A Thesis Submitted for the Degree of Master of Philosophy at

Harper Adams University

HARPER ADAMS UNIVERSITY

THE EFFECT OF AGRICULTURAL MANAGEMENT ON COLLEMBOLA COMMUNITIES IN AGROECOSYSTEMS

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A thesis submitted in partial fulfilment of the requirements for the degree of Master of Philosophy

29th September 2017

PUBLICATIONS & PRESENTATIONS

Sconce, FB; Ashton,T; Jeffery, S; Leather, SR, (2017) The impact of Cultivation on Soil Arthropods and Associated Functions. Talk, Ento'17, Newcastle University

Sconce, FB; Leather, SR, Grove IG (2014) Collembola and agriculture: untangling the web. Poster, British Ecological Society Annual Meeting, Lille

Sconce, FB; Leather, SR, Grove IG (2014) Springing away? Collembola responses to different traffic and tillage farming systems. Poster 1st Global Soil Biodiversity Conference, Dijon

Sconce, FB; Leather, SR, Grove IG (2014) Diversity in a detritivore community: an agroecosystem context. European Congress of Entomology, York

Sconce, FB; Leather, SR, Grove IG (2014) Collembola at Harper Adams. Talk, Royal Entomological Society Postgraduate Forum, York

Sconce, FB; Leather, SR, Grove IG (2013) Collembola community assemblages in agroecosystems: what's the story? Poster, Royal Entomological Society Annual Meeting, St Andrews

Sconce, FB; Leather, SR, Grove IG (2013) Response of Collembola communities to different agricultural management practices. Poster, INTECOL London, British Ecological Society

Sconce, FB; Leather, SR, Grove IG (2013) Springing into action? Collembola in agroecosystems. Aspects of Applied Biology 118:307

Sconce, FB; Leather, SR, Grove IG (2013) Springing into action? Collembola in agroecosystems. Poster, 'Environmental Management on Farmland', Association of Applied Biologists

ABSTRACT

Collembola are soil dwelling arthropods that are beneficial for soil health, contributing to rates of decomposition and nutrient cycling. They exhibit different life forms living within different soil niches, and make up an important component of soil mesofauna and can indicate overall soil biodiversity community.

Agroecosystems are environments managed for production of resources for human benefit, with interventions such as agrochemical application and ploughing (tillage) of soil, using specialised agricultural vehicles. Management intensity can vary with the frequency of interventions and effects of each intervention on soil.

The effect of agricultural management on Collembola and the wider mesofauna community was investigated in three ways. Firstly with surveys of Collembola and mesofauna in fields of different management intensity, secondly by sampling Collembola and mesofauna in an experiment on the effects different tillage and traffic regimes and thirdly by sampling Collembola in an experiment on the effects of tillage and no till systems.

Management intensity did not affect Collembola abundance and species richness or mesofauna abundance and taxonomic order richness overall. Sampling date and soil moisture had a significant effect the abundance and species richness of the soil mesofauna. Collembola of different life forms showed different responses related to their life history traits.

Different traffic and tillage regime combinations did not affect Collembola abundance and species richness or mesofauna abundance and taxonomic order richness overall. Sampling date did significantly affect Collembola abundance and diversity and Collembola of different life forms showed different responses.

Tillage system had a significant effect on Collembola abundance and species richness and mesofauna abundance and taxonomic order richness one month after tillage treatment, but numbers recovered to pre-treatment levels after six months. Collembola of different life forms showed different responses to tillage system and sampling date.

Results are discussed in relation to wider research and future focus within soil biodiversity.

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ACKNOWLEDGEMENTS

I would very much like to thank my Director of Studies Prof. Simon Leather who has been a mentor to me for many years and has provided many opportunities for me to develop as an entomologist and a researcher. I would also like to thank my second supervisor Dr. Ivan Grove who welcomed me to Harper Adams and introduced me to the world of agriculture.

I am grateful to Harper Adams University for funding my studentship and to all the departments who have provided equipment, materials and assistance. I would also like to thank Emily Smith, Paula Misiewcz, Tim Ashton and Simon Jeffery for allowing me to collaborate with their research.

I am indebted to friends amongst past and current students and staff at Harper Adams, to my family and to my partner Jasper. Your encouragement, support and patience have helped me through challenging times.

1. LITERATURE REVIEW

Collembola characteristics, taxonomy & diversity

Collembola (springtails) are six-legged arthropods that live predominantly in soil and are grouped within soil mesofauna, with the Acari and Nematoda. Defining characteristics (Figure 1) of the group are body size generally of around a few mm, mouthparts retracted into the head (entognathous), simple eyes (ocelli), 6 or fewer abdominal segments, a ventral tube (collophore) and a springing or jumping organ (furcula) (Hopkin, 1997).

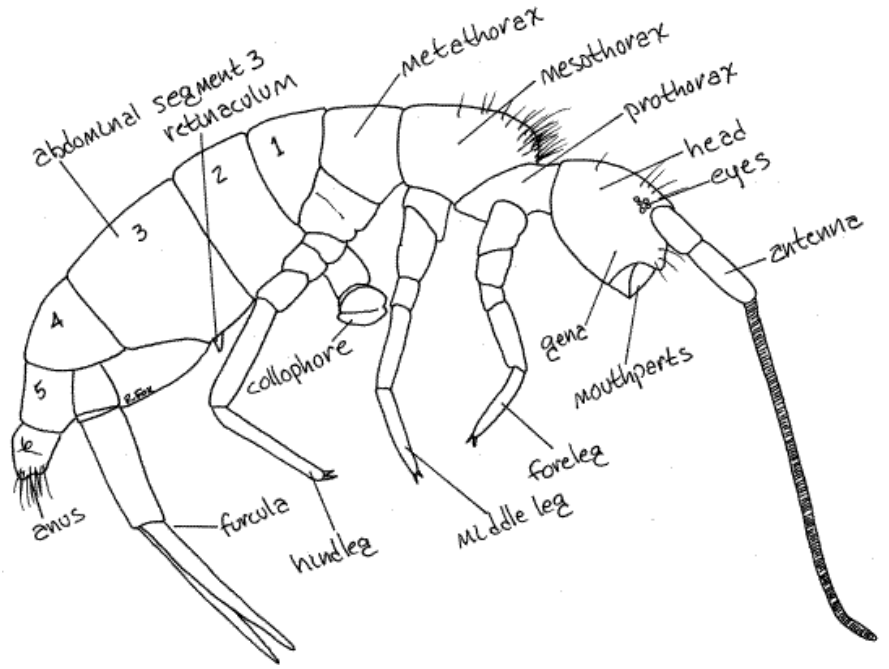

Figure 1 Collembola anatomy (Fox, 2001)

There is evidence that Collembola are the oldest evolved hexapods with fossils dating at 400 million years old, but it is disputed whether the group are a taxonomic class (Deharveng, 2004) or an order next to the Protura and Diplura within Class Entognatha (Trautwein *et al.*, 2012). Collembola are subgrouped (Figure 2) by to their morphology into: Poduromorpha (flat body), Entomobryomorpha (long and thin body), Symphypleona (globular body) and Neelipleona (hunched body), which is supported by molecular phylogeny (Xiong *et al.*, 2008).

Figure 2 Collembola subgroups, clockwise from top left: Poduromorpha, Symphypleona, Entomobryomorpha and Neelipleona (Wikimedia, 2017)

Globally there are over 8000 described Collembola species (Janssens, 2017) though actual diversity could be over 50,000 (Cicconardi, Fanciulli & Emerson, 2013), in the UK over 250 species have been recorded (Hopkin, 2007).

Collembola life cycle and ecology

The life cycles of Collembola do not involve metamorphosis; juveniles resemble adults except that they lack genitalia, they undergo up to eight growth phases and moults to reach maturity, after which they will continue to moult through their lifetime, which can be a few days in tropical ecosystems up to a few years at the poles (Hopkin, 1997). Some Collembola species reproduce parthenogenetically and others sexually. Spermatophores are laid in soil and females release hormones to activate them and take them into their bodies to fertilise eggs, these are laid in patches or separately in the soil habitat.

Collembola exhibit life forms related to vertical niches within soil. Epedaphic Collembola live on the soil surface and in leaf litter, they have large body sizes and reproduce sexually in certain seasons laying many small eggs. Euedaphic Collembola live within soil pores, they have small body sizes and reproduce parthenogenetically throughout the year laying a few large eggs. Hemedaphic Collembola are intermediary lifeforms living in leaf litter or the very top layers of soil, they exhibit both epedaphic and euedaphic characteristics (Petersen, 2002). Collembola can occur in densities of up 100,000 individuals per square metre (Petersen & Luxton, 1982b).

Abiotic influences on Collembola

Temperature affects Collembola physiological and reproductive processes. Higher temperatures, as with other hexapoda, increase the rate of these processes, until a maximum or thermal death point is reached when the organism dies. Lower temperatures decrease the rate of these processes until a minimum or supercooling point when the organism dies (Hopkin, 1997). Different Collembola lifeforms respond in different ways to temperature change: epedaphic species are more sensitive and have larger temperature ranges (thermobiological spans) than euedaphic species, this reflects adaptation to the stability of environments on the soil surface or within soil (Van Straalen, 1994).

Soil moisture levels are important for Collembola and generally they are more abundant in damp soils. They can also use the collophore to regulate water uptake and loss. Euedaphic Collembola are more sensitive to water than epedaphic, they can drown in floods as soil pore space becomes filled with water and the proportion of those with air decreases, they can also die in droughts if there is no water film on the surface of soil pores. Some Collembola have specific adaptations to control water loss such as long hairs on the body surface in Neanuridae which increase water adhesion and desiccation resistant eggs (Hopkin, 1997).

Soil structure, the arrangement of soil particles and aggregates to form soil pores, affects the ease of movement of euedaphic Collembola through soil (Heisler & Kaiser, 1995). Dense, highly compacted soils with small pores are likely to hamper the movement and distribution of Collembola.

Collembola species show preference for particular soil pHs and soil types. Different species assemblages are recorded in habitats with extremes of pH (Loranger *et al.*, 2001; Cassagne *et al.*, 2006) and Collembola will react to experimental pH treatment solutions by retracting the ventral tube to control concentrations of water in their bodies (Van Straalen & Verhoef, 1997).

Organic matter levels strongly influence Collembola. Collembola densities positively correlate with organic matter levels (Vreeken-Buijs, Hassink & Brussaard, 1998; Eaton *et*

al., 2004) and organic matter is an important influence in the organisation of Collembola communities (Hasegawa, 2001).

Biotic influences on Collembola

Collembola are predominantly generalist detritivores, they feed on dead and decaying organic matter such as fungal hyphae and dead plants (Petersen, 2002). As Collembola feed they fragment organic matter and ingest it, digest it with gut microbial flora and then excrete it out into soil as small particles, with some of the microbial flora (Rusek, 1998). This process both increases the overall surface area of the organic matter and distributes decomposer microbes around soil (Seastedt, 1984), this can increase the rate of decomposition and nutrient cycling (Filser, 2002) and influence Nitrous oxide emissions (Kuiper *et al.*, 2013).

A few Collembola species feed on live plant matter and in high enough numbers can be damaging to commercial crops. *Onychiurus* species feed on sugar beet roots and are controlled with pesticide seed dressings (Baker & Dunning, 1975). *Sminthurus viridis* feeds on alfalfa and clover and in the Southern Hemisphere, where it has been introduced, it regularly reaches damaging levels and more recently outbreaks have been recorded in the UK (Crotty *et al.*, 2016a).

Predators of Collembola on the soil surface range from small vertebrates such as juvenile grey partridge (Southwood & Cross, 2002), to generalist predatory arthropods such as carabid and staphylinid beetles, lycosid spiders and harvestmen (Bilde, Axelsen & Toft, 2000), for which they can be important alternative prey and help contribute to maintenance of conservation biocontrol (Agusti *et al.*, 2003). Below the soil, euedaphic Collembola are predated on by predatory mites such as the *Neomolgus capillatus,* which has been used as a biocontrol agent against Sminthurus viridis (Ireson *et al.*, 2002).

As well as responding to predator pressure Collembola populations can show density dependent effects, with matrix population modelling showing oscillations in relation to previous densities (Longstaff, 1976).

Collembola and the wider mesofauna community can indicate overall ecosystem health (Parisi *et al.*, 2005; Greenslade, 2007; Wu *et al.*, 2011).

Agroecosystems

Agroecosystems are environments managed to grow resources such as edible crops, livestock or biofuels (Warren, Lawson & Belcher, 2008). Land area under agricultural management has decreased over the last 70 years, but advances in agricultural equipment and agrochemicals have meant that production yields have increased fourfold (Robinson & Sutherland, 2002).

Practitioners make trade off decisions when using different agricultural techniques to manage agroecosystems, choosing between provisioning services such as the yield of crops or growth of livestock, ecosystem services such as soil fertility or levels of natural enemies for biological control, and ecosystem 'disservices' such as loss of wildlife habitat and biodiversity (Power, 2010).

Agrochemicals include herbicides to reduce unwanted plant species, pesticides to reduce levels of animals feeding on crops at damaging levels, fungicides to reduce levels of pathogenic fungi and fertilisers to increase soil nutrient levels. These are usually applied over a field in liquid solutions with a sprayer on a vehicle, some are applied in solid form with pellets spread over the field.

Tillage is the ploughing of soil in preparation for crop seed sowing. This can vary in mode of action with different tillage equipment attached to an agricultural vehicle to form furrows in the soil, lift and drop soil, or turn soil. Each technique results in varying levels of soil mixing and percentage of previous crop residue remaining on the soil surface (Titi, 2003). Tillage aims to alleviate soil compaction, mix organic matter vertically through soil and increase water infiltration rates. Soil functioning however can be negatively affected by tillage, with decreases in soil stability, resilience, the production of new soil (pedogenesis) and overall organic matter levels due to increases in soil erosion (Lal, 1993).

'No-till' systems do not involve ploughing of the soil and instead use specialised crop seed sowing equipment to insert seeds below the soil surface, 'direct drills' drive a narrow furrow into soil, drop seeds at a regular interval and then roll the soil. No till systems often require extra herbicide applications as weeds are not broken down by plough action and populations may increase (Titi, 2003).

Traffic is the frequency of movement of agricultural vehicles over soil. The development of the internal combustion engine in the 20th century led to the use of mechanised vehicles in agriculture, replacing horse drawn equipment. Vehicles have increased in weight with advancements in technology, the traffic of which can lead to compaction of soil (Soane & van Ouwekerk, 1994).

Controlled traffic farming (CTF) involves the use of global positioning systems to guide vehicle routes over agricultural fields, reducing the trafficked area in a field. CTF also involves investment to use vehicles, such as tractors and combine harvesters, with wheels the same distances apart, so as to establish permanent wheel way areas and intact untrafficked areas in the field (Kingwell & Fuschbichler, 2011).

Vehicle tyre inflation pressure can also be varied to reduce soil compaction effects of vehicles. Higher tyre pressure results in narrower wheel ways under higher forces of compaction. If tyre pressure is decreased then the force per unit area exerted by tyres on

soil will decrease even though the wheelway will be wider, and this decreases the effects of soil compaction (Hamza & Anderson, 2005).

Management systems of agroecosystems can be positioned along a continuum of management intensity, according to the disturbance effect on the habitat of management interventions (Ponge *et al.*, 2013). High intensity systems have frequent agrochemical applications, limited variation in crop rotation and deep soil tillage. Low intensity systems have fewer agrochemical applications, more variation in crop rotation and minimum or no tillage.

Agricultural management and Collembola

Soils in agroecosystems are altered by the management interventions used by practitioners, and this effect increases in higher intensity systems. Soil physics, chemistry and biology change and the beneficial ecosystem services can decrease, leading to a need for further interventions such as artificial inputs to alleviate nutrient declines (Giller *et al.*, 1997). Pesticide use decreases soil mesofauna abundance and diversity in the short term (Fountain *et al.*, 2007) and long term (Ewald *et al.*, 2015). Collembola abundances decrease with the use of fungicides (Filser, 1995) and insecticides (Alvarez, Frampton & Goulson, 1997).

Conventional tillage decreases Collembola abundance and diversity (House, 1985; Kladivko, 2001; Miyazawa *et al.*, 2002; Chang *et al.*, 2013) and this is thought to be due to changes in soil texture (van Capelle, Schrader & Brunotte, 2012). Some Collembola groups however respond positively or negatively to tillage (Sabatini *et al.*, 1997). Under a reduced tillage system 'ECOtillage' Collembola abundance increased but diversity did not change (Brennan, Fortune & Bolger, 2006). Collembola have been recorded to initially decrease after tillage treatment and then later increase, with those under no till treatments having stable populations (Loring, Snider & Robertson, 1981).

Agricultural traffic can lead to soil compaction, that is a decrease in soil pore size, the interconnectedness of pores and the overall proportion of air filled pores (Didden, 1987), Compaction can therefore decrease the 'habitable space' for Collembola (Larsen, Schjønning & Axelsen, 2004). Mesofauna densities decrease with increased agricultural traffic (Heisler & Kaiser, 1995; Larsen, Schjønning & Axelsen, 2004) and with measured soil compaction of agricultural machinery (Heisler & Kaiser, 1995; Schrader & Lingnau, 1997).

Management intensity and Collembola

Management intensity strongly influences soil biodiversity (Gardi, Jeffery & Saltelli, 2013), with assessments showing high threats to soil biodiversity in areas of intense agricultural activity (Jeffery *et al.*, 2010) affecting the resilience of soil food webs (de Vries *et al.*, 2012).

Soil organisms decrease in abundance and diversity with increasing management intensity (Tsiafouli *et al.*, 2014). Multiple studies have found lower Collembola abundances and species diversity under more intensive management techniques (Frampton, 2000; Petersen, 2002; Bedano, Cantu & Doucet, 2006). Ponge *et al.*, (2013)found that Collembola numbers decrease along an increasing gradient of agricultural intensity, although epedaphic species increased.

Collembola species diversity can decrease but abundance has been shown to increase with increasing management (Schrader *et al.*, 2006; Alvarez, Frampton & Goulson, 2001). This is because different Collembola subgroups respond to different extents, for example euedaphic Onychiuridae decrease in abundance more than epedaphic Isotomidae (Larsen, Schjønning & Axelsen, 2004; Niwranski, Kevan & Fjellberg, 2002).

Whether management is conventional or organic does influence Collembola but there is no clear pattern. Steiner *et al*. (1986) found higher Collembola abundances in integrated-farm managed than in conventionally managed fields of cereals and sugar beet, but Brussaard *et al.* (1990) found integrated and conventionally managed plots favouring different species of edaphic Collembola. Paoletti *et al.* (1992) and Moreby *et al.* (1994) found higher Collembola abundances in organic than conventionally cereal fields, but in the latter case only in one of 2 sampling years. Large-scale regional studies in cereals (Reddersen, 1997) and other arable crops (Dekkers *et al.*, 1994; Czarnecki and Paprocki, 1997) found no differences in Collembola abundance between organic and conventional fields.

Sustainable agricultural management

Ecosystem functioning is strongly linked to biodiversity levels (Hooper *et al.*, 2005). Agroecosystems are needed to be productive with functioning ecosystem services in a world with a growing population undergoing global climate change (Lal, 2009), as soils underpin many ecosystem services (Bardgett, 2005) strategies that conserve soil biodiversity should be prioritised (Garnett & Godfray 2012; Nielsen, Wall & Six, 2015).

OBJECTIVES OF RESEARCH

This thesis looks at the effect of agricultural management on Collembola communities, firstly by sampling Collembola in fields along a continuum of conventional management intensity, then by investigating the interaction of agricultural traffic and tillage on Collembola and lastly by comparing Collembola in tilled and no till systems. It is hypothesised that Collembola abundance and density will decrease with: increasing management intensity, higher amounts of agricultural traffic and deeper tillage regimes.

2. SOIL MESOFAUNA IN DIFFERENT AGRICULTURAL MANAGEMENT SYSTEMS

2.1 INTRODUCTION

Soil underpins ecosystem functions including nutrient cycling and decomposition and the organisms living within it make up a high proportion of total biodiversity (Brussaard, de Ruiter & Brown, 2007; Kibblewhite, Ritz & Swift, 2008; de Vries *et al.*, 2012). Up to 20% of soil biodiversity is comprised of arthropods (Culliney, 2013), the most abundant of which are mesofauna such as Collembola (springtails) which can occur in densities of over 100,000 per m^2 (Petersen & Luxton, 1982a) and range from 0.1 to 3mm in body length (Hopkin, 1997).

Collembola can increase rates of decomposition in soil; as detritivores, they feed on dead and decaying organic matter particles, increasing the surface area of matter for processing by microbes (Rusek, 1998; Petersen, 2002). They also harbour microbial colonies in the gut, which are excreted and spread around the habitat as they feed, further adding the recycling process (House, 1985; Thimm *et al.*, 1998). Soil arthropods such as carabid beetles and spiders predate Collembola as well as small vertebrates including birds (Bilde, Axelsen & Toft, 2000). Collembola are therefore a crucial link between the food webs above and below the soil surface and can indicate ecosystem health of the these systems (Parisi *et al.*, 2005; Greenslade, 2007; Wu *et al.*, 2011;).

Agricultural management intensity has increased over the last fifty years whilst land area under agricultural management has decreased: technological developments in soil ploughing, crop seed sowing and harvesting change the soil physical structure to a greater extent; increase in agrochemical frequency of applications and strength of mode of action can greater influence soil chemical makeup; and advances in farm livestock breeding, nutrition and health mean animals grow to higher masses and at a faster rate (Robinson & Sutherland, 2002). Farmers and practitioners choose crop and animal varieties based on the soil types of the land available, economic viability, equipment available and historic site management; this involves deciding trade-offs on the 'services' of the agricultural ecosystem for production such as nutrient recycling and the 'disservices' to it such as loss of habitat and therefore biodiversity (Power, 2010).

Ecosystem services are replaced with artificial inputs as agricultural management intensity increases (Giller *et al.*, 1997), this is a major factor influencing soil biodiversity (Gardi, Jeffery & Saltelli, 2013), in particular affecting the resilience of soil food webs (de Vries *et al.*, 2012).

Soil organisms generally respond negatively with increasing management intensity (Tsiafouli *et al.*, 2015). Pesticide use decreases the abundance and diversity of fauna in the short term (Fountain *et al.*, 2007) and long term (Ewald *et al.*, 2015). The soil fauna is also affected by the physical aspects of cultivation; the action of agricultural traffic reduces faunal densities (Heisler & Kaiser, 1995; Larsen, Schjønning & Axelsen, 2004), and tillage lowers fauna abundance and diversity (House, 1985; Kladivko, 2001; Miyazawa *et al.*, 2002; Chang *et al.*, 2013).

This study aims to look at seasonal changes in soil mesofauna, with a particular focus on Collembola, across fields in conventional agriculture with three different management types along an intensity continuum. It is hypothesised that higher abundance and diversity of mesofauna will be recorded in fields under lower intensity management.

2.2 METHODS

Study site and history

The experiment was carried out at Harper Adams University, Shropshire, UK (SJ711206, Figure 3).

Figure 3 location of study site in the UK

Survey design

Three management types were surveyed: permanent pasture with grass for more than five year (low intensity), short-term ley with grass for under five years (mid intensity), and long-term arable (high intensity). Three fields of each management type were selected based on similarity of management history (Table 1) and field area, a total of nine fields were surveyed (Figure 4).

Table 1 management details of field surveyed at Harper Adams University in 2014 (University, 2014; Cranfield, 1995)

FIELD	system	area /ha	Crop	Tillage	Soil type	Agrochemical inputs
Upper Wood Leasow	Arable	6.07	Wheat (Diego Anchor)	Flatlift subsoiler	Very slightly stony sandy loam	Herbicide, insecticide, fertiliser, fungicide
Black Britch	Arable	6.65	Winter barley (Cassia Anchor)	Flatlift subsoiler	Very slightly stony sandy loam	Herbicide, insecticide, fertiliser, fungicide
Garden	Arable	2.92	Wheat (Diego Anchor)	Flatlift subsoiler	Very slightly stony clay loam	Herbicide, insecticide, fertiliser, fungicide
Cottage	Pasture	2.96	Grass	-	Very slightly stony clay loam	Fertiliser
The Lawn	Pasture	0.85	Grass	-	Very slightly stony clay loam	Fertiliser
Pit Ancellor	Pasture	1.5	Grass	-	Very slightly stony clay loam	Fertiliser
Far Broad	Grass Ley	5.84	Grass	-	Stoneless clay	Fertiliser
Near Broad	Grass Ley	5.1	Grass Westerwold Lifloria	-	Very slightly stony clay loam	Fertiliser, Herbicide
Cote Ussock	Grass Ley	4.68	Grass	-	Very slightly stony clay loam	Fertiliser

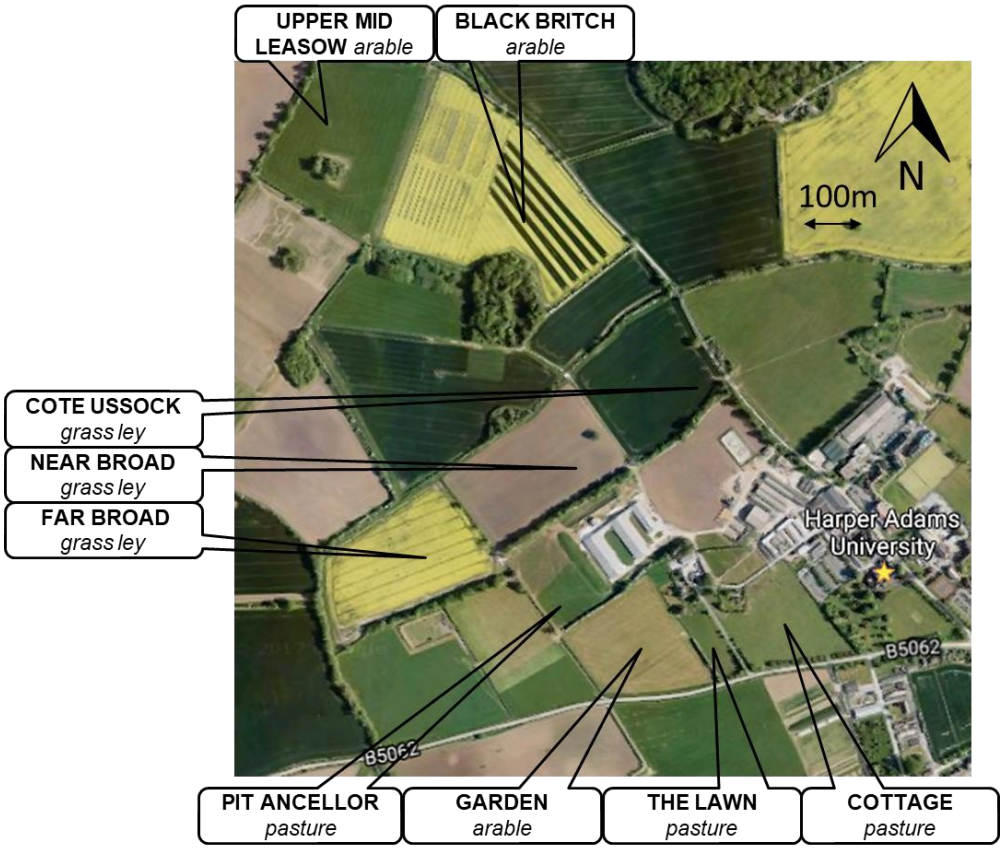

Figure 4 Fields and agricultural management types surveyed at Harper Adams University in 2014 (Google, 2017)

Soil mesofauna sampling

Four soil cores of 100mm high x 65 mm width were sampled from each of the nine fields on 28 April 2014, 28 May 2014, 8 July 2014 (before harvest in arable fields) and 13 August 2014 (after harvest in arable fields.) Cores were taken from the corners of a $1m^2$ square at least 30m from the field edges and at least 3m from wheel ways and headlands. In each successive month the core square was moved 2m along the length of the field.

Soil mesofauna were extracted into 50ml sample tubes holding 20ml of 70% Industrial Methylated Spirits (IMS) solution, by placing soil cores in Berlese-Tullgren funnels BS00290 (Burkard, 2013) on $2mm^2$ square holed gauze under 40W power lightbulbs for 7 days.

Samples were examined in 100mm diameter Petri dishes under a Microtec HM-2 dissection microscope at X20 magnification. All arthropod specimens were identified to taxonomic order with Tilling (1987), Collembola specimens were further examined with a drop of 70% IMS in 40mm wide square watch glasses under a Microtec HM-2 dissection microscope at X40 magnification or (for specimens with body length smaller than 1mm) in glass slides with single concave depressions of 16mm diameter and 0.5mm depth with a drop of 70% IMS under a Olympus CX31 compound microscope at x100 magnification, and identified to species using Hopkin (2007). The specimens for each sample were retained as a voucher records in a 10ml sample tube with 5ml 70% IMS.

Mesofauna abundance and taxonomic order richness, Collembola abundance and species richness were recorded for each sample.

Soil moisture

One extra soil core 100mm high x 65 mm width was taken from the centre of each soil mesofauna core square and used to measure gravimetric soil moisture content (Brady & Weil, 2008). Core mass was weighed with a Precisa XT1220M balance on day of sampling, cores were placed in an 105 °C oven for seven days and then reweighed. The ratio of the mass of water lost against mass of dry soil was then calculated in $g\ g^{-1}$.

Statistical analysis

Datasheets with mean abundance and taxonomic order richness of soil mesofauna and species richness of Collembola were constructed in Microsoft Excel (Microsoft, 2013). Statistical analysis and graphics drawing was done with R statistics package (Core Team, 2014).

General linear models with mesofauna abundance, Collembola abundance, mesofauna order richness, Collembola species richness as response variables were fitted, with field management type, date and field as categorical explanatory variables and soil moisture as continuous explanatory variable. Quasipoisson family error structure was used to account for overdispersion in the count data. Interactions were removed and models simplified to

find the minimal adequate model. The effect of field management type and date on soil moisture content was tested with ANCOVA.

2.3 RESULTS

Soil moisture

Arable fields had the lowest mean soil moisture contents at 0.06 g g^{-1}, 0.22 g g^{-1}, 0.18 g g^{-1}, 0.19 g g^{-1} on all dates (Figure 5), in April and May soil moisture contents in grass ley and pasture were not significantly different, in July and August pasture fields had the highest soil moisture contents at 0.44 g g^{-1} and 0.37 g g^{-1}. Management and date significantly affected soil moisture content (F= 39.48 (17,126), Adjusted R-squared = 0.820, p-value < 2.2e-16).

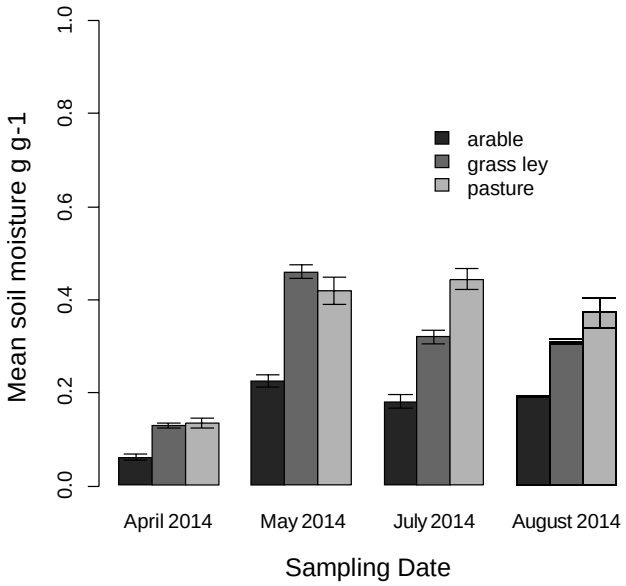

Figure 5 Mean gravimetric soil moisture content in three field management types across 4 sampling dates in 2014

Soil mesofauna

7993 soil mesofauna individuals from 17 taxonomic orders were recorded, Acari were the most abundant order making up 47% of all individuals, Collembola were the second most abundant making up 38% of all individuals.

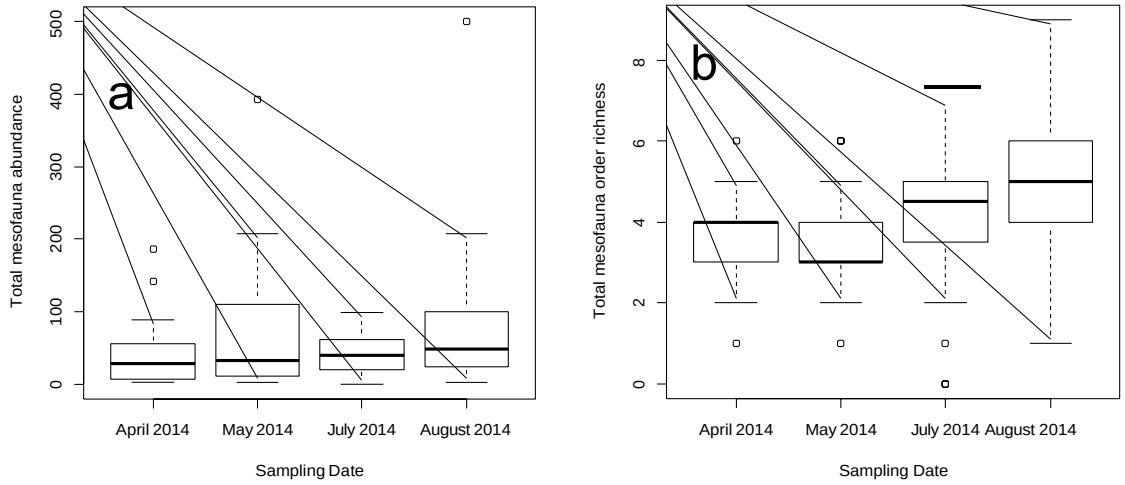

Figure 6 Total mesofauna abundance (a) and taxonomic order richness (b) across all fields at Harper Adams University

Total mesofauna median abundance (Figure 6a) in April was 39.0 individuals, which increased in May to 32.0, and further in July to 39.0 and in August to 48.0. Total mesofauna median taxonomic order richness (Figure 6b) in April was 4 orders, which decreased in May to 3, increased in July to 4.5 and further increased in August to 5.0.

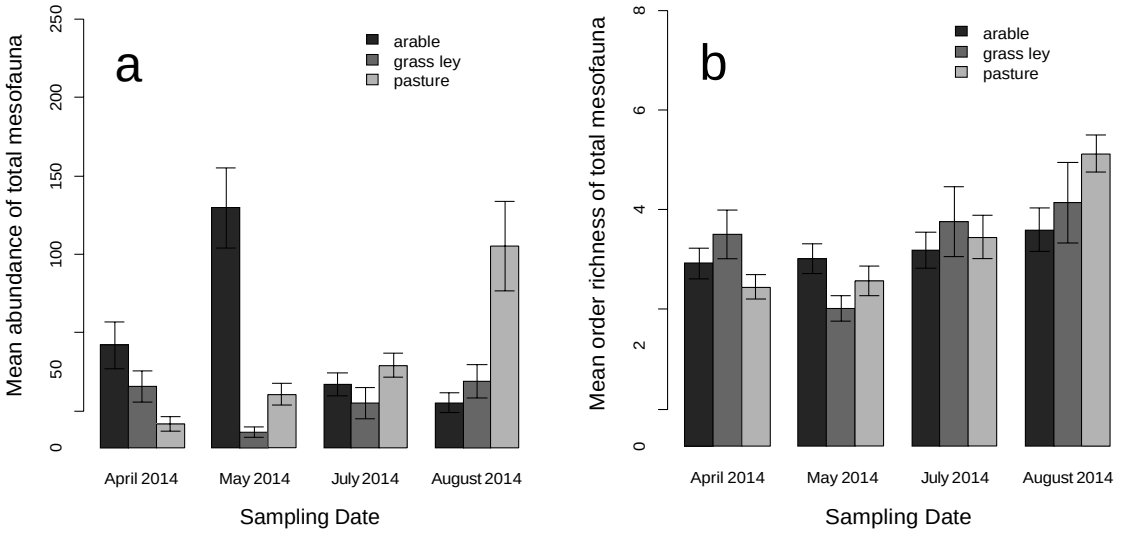

Figure 7 Mean abundance (a) and order richness (b) of all recorded soil mesofauna groups from 3 field management types on 4 sampling dates in 2014, bars represent ± one standard error.

Mean total mesofauna abundance (Figure 7a) in April was highest in arable fields at 65.3 individuals and lowest in pasture at 15.0; in May mean total mesofauna abundance was highest in arable fields at 153.0 individuals and lowest in grass ley at 33.8, in July mean

total mesofauna abundance was highest in pasture at 52.5 individuals and lowest in grass

ley at 28.0 and in August mean total mesofauna abundance was highest in pasture at 128.6 individuals and lowest in arable at 28.6. There was a significant effect of date in May (T = 3.64, p-value = 0.000397), and of water (T = -2.72, p-value = 0.00752) on total mesofauna abundance.

Mean total mesofauna order richness (Figure 7b) in April was highest in grass ley at 4.3 orders and lowest in pasture at 3.7 orders; in May mean total mesofauna order richness was highest in arable fields at 4.4 orders and lowest in grass ley at 3.4 orders; in July mean total mesofauna order richness was highest in grass ley at 4.8 and lowest in pasture at 4.2 orders and in August mean total mesofauna order richness was highest in pasture at 5.8 orders and lowest in grass ley at 4.9 orders. There was no interaction between or effect of field management on mesofauna abundance.

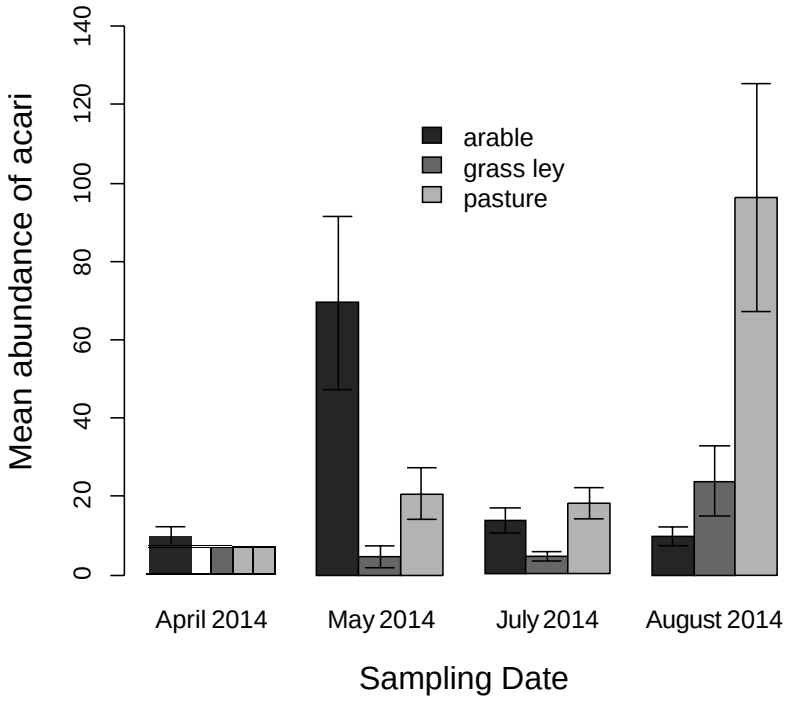

Figure 8 Mean acari abundance from 3 field management types on 4 sampling dates in 2014, bars represent ± one standard error

Acari abundances (Figure 8) were not significantly different across field management types in April; in May highest abundance were in arable fields at 69.4 and lowest in grass ley at 4.5; acari abundance in arable and pasture was not significantly different in July but lowest in grass ley at 4.1 and in August pasture had the highest acari abundance at 96.4 and arable lowest at 9.9. There was no overall effect of management on acari abundance, but date in May significantly affected acari abundance (T = 3.03, p-value = 0.00298) and there was a significant interaction of date and management in August (T = 2.74, p-value = 0.00708).

Collembola

3070 Collembola individuals were recorded from 8 taxonomic families and 23 species. The Isotomidae were the most abundant family making up 69% of all individuals. The Hypogasturidae were the second most abundant family making up 13% of all individuals and the Bourletiellidae were the third most abundant family making up 11%.

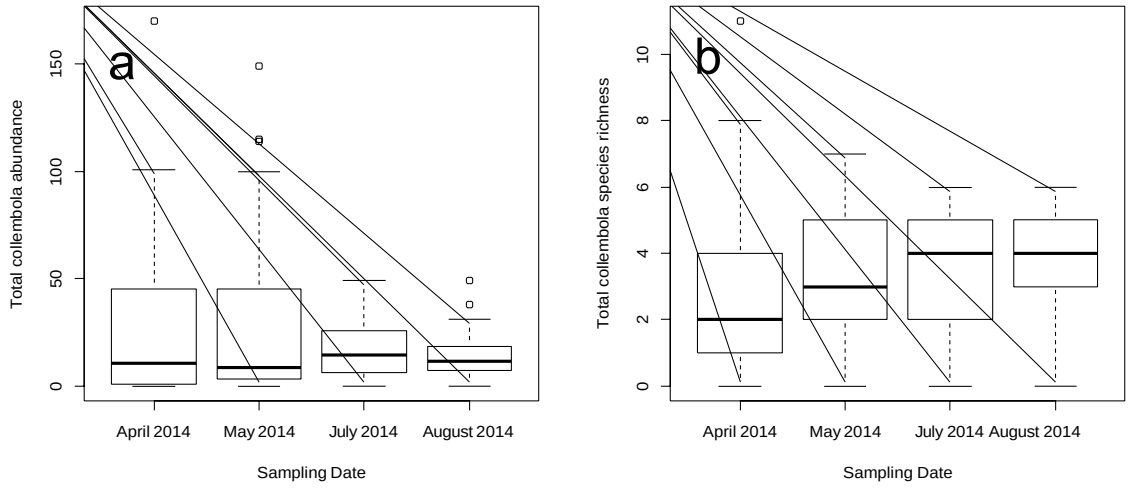

Figure 9 Total Collembola abundance (a) and species richness (b) across all plots in Large Marsh field

Total Collembola median abundance in April was 10.5 individuals which decreased to 8.5 in May, increased to 14.5 July and decreased to 11.5 November (Figure 9a). Total Collembola median species richness in April was 2 species, which increased in May to 3 and further increased in July to 4 and remained constant in August at 4 (Figure 9b).

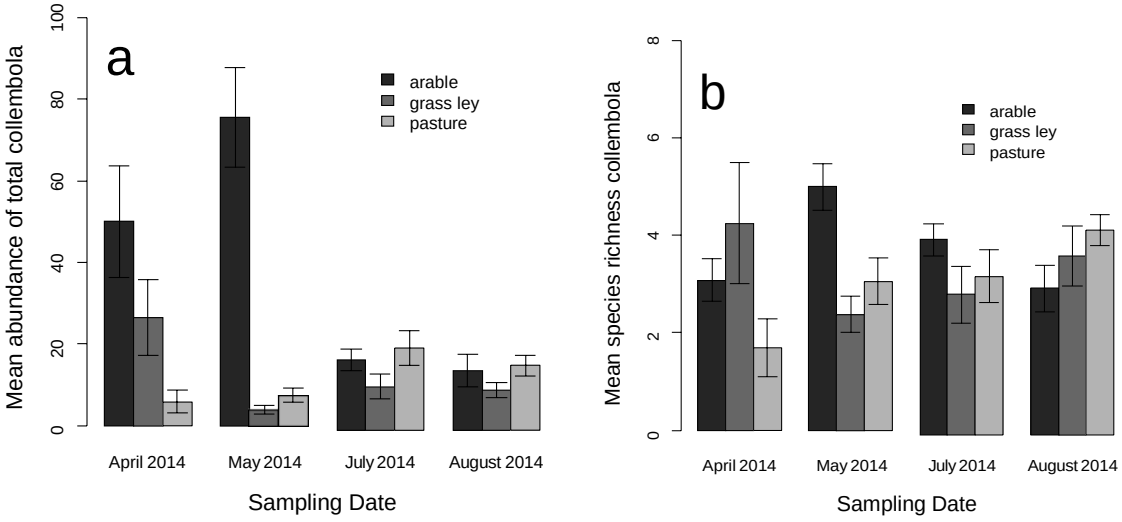

Figure 10 Mean abundance (a) and species richness (b) of all recorded Collembola across 3 field types on 4 sampling dates at Harper Adams University in 2014; bars represent ± one standard error.

Mean Collembola abundance (Figure 10a) in April was highest in arable at 50 individuals and lowest in pasture at 5.8; in May abundance was again highest in pasture at 75.7 individuals at lowest in grass ley with 3.9; Collembola abundance were not significantly different across field management types in July and August. There was a significant effect of Date in May on Collembola abundance (T = 4.24, p-value = 4.4e-05), and a significant effect of pasture (T= -3.75, p-value = 0.000268) and water (T = -3.81, p-value = 0.000220) and an interactive effect of these (T = 3.03, p-value = 0.002989).

Mean Collembola species richness (Figure 10b) in April was highest in grass ley at 4.3 species and lowest in pasture at 1.7; in May species richness was highest in arable at 5.0 and grass ley and pasture were not significantly different; species richness were not significantly different in July and August. Soil moisture significantly affected Collembola species diversity (T = -2.21, p-value = 0.026887).

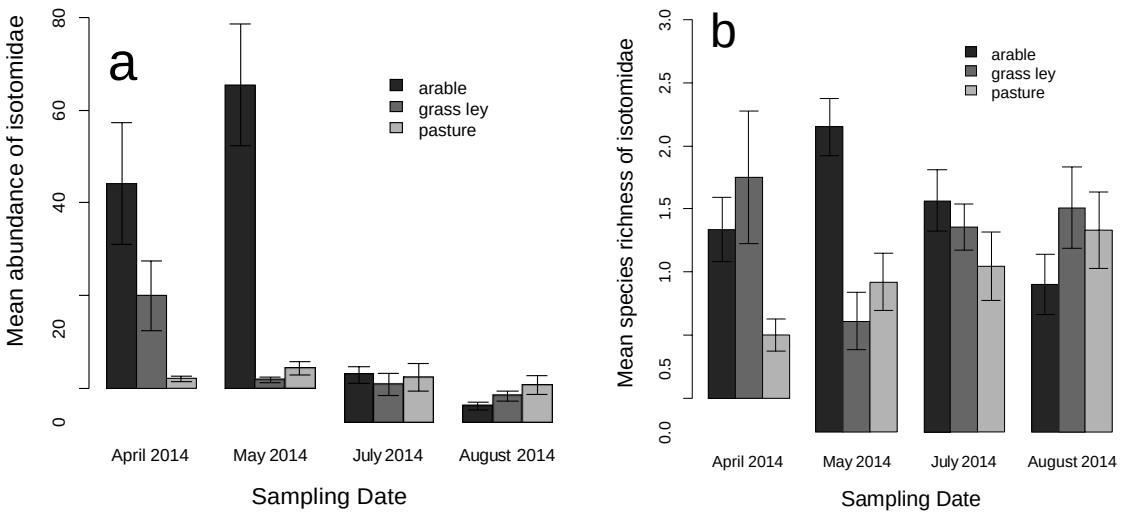

Figure 11 Mean abundance (a) and species richness (b) of Isotomidae in 3 field management types across 4 sampling dates at Harper Adams University in 2014 bars represent ± one standard error.

Mean Isotomidae abundance (Figure 11a) was highest in April in arable fields at 44.1 individuals and lowest in pasture fields at 1.9; in May abundance was highest in arable fields at 65.4 individuals and lowest in grass ley at 1.2; mean Isotomidae abundances were not significantly different across field management types in July and August. There was a significant effect of Date in May (T = 4.401, p-value = 2.23e-05) and of soil moisture (T = -4.01, p-value = 0.000104) on Isotomidae abundance.

Mean Isotomidae species richness (Figure 11b) was lowest in April in pasture at 1.8 species; highest in May in arable at 2.4 species, in July and August species richness were

not significantly different across field management type. Soil moisture significantly affected Isotomidae species richness (T = -2.50, p-value = 0.01241).

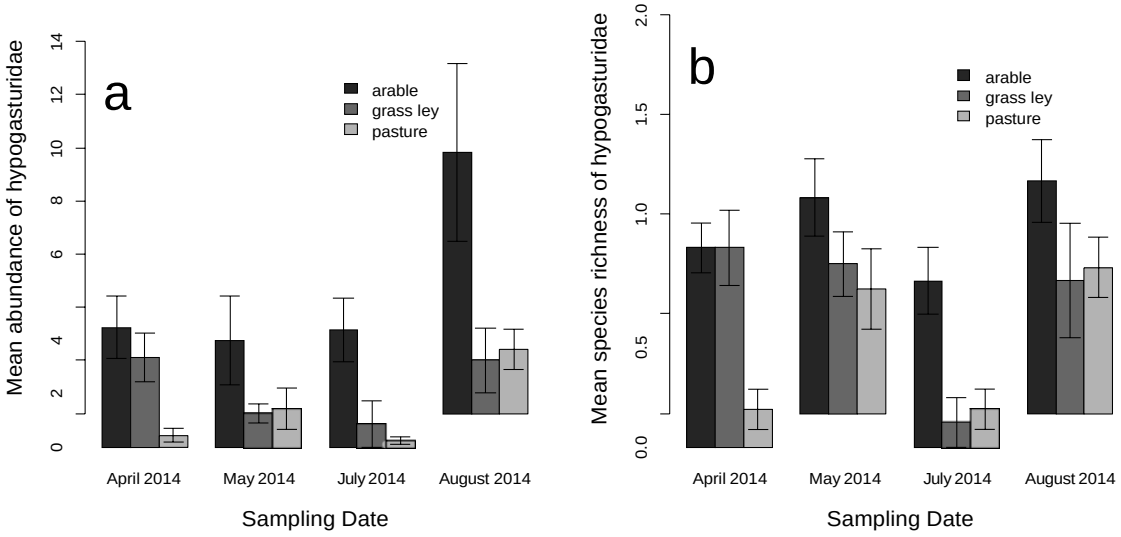

Figure 12 Mean abundance (a) and species richness (b) of Hypogasturidae in 3 field management types across 4 sampling dates at Harper Adams University in 2014 bars represent ± one standard error.

Mean Hypogasturidae abundance (Figure 12a) was highest in at all dates in arable fields at 4.5, 4.0. 4.4, and 9.8 individuals. Pasture management type had a significant effect on abundance (T = -2.30, p-value = 0.02310).

Mean Hypogasturidae species richness (Figure 12b) was highest at all dates in arable fields at arable 0.1, 0.2, 0.2 and 0.2 species. There was a significant effect of Date in July (T = -2.25, p-value = 0.024210), pasture management type (T = -3.61, p-value = 0.000303) and grass ley (T = -2.55, p-value = 0.010663) on species richness.

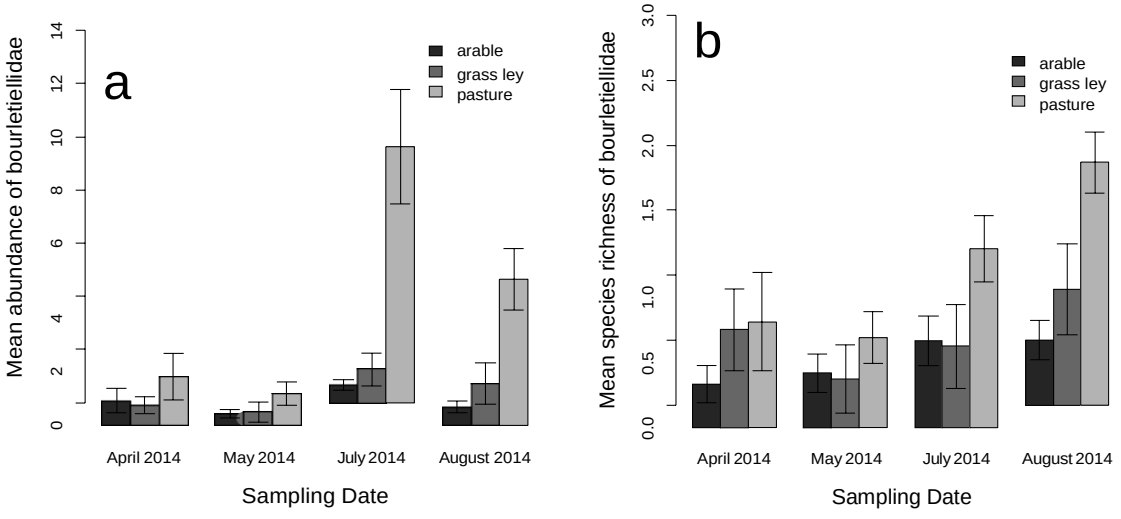

Figure 13 Mean abundance (a) and species richness (b) of Bourletiellidae in 3 field management types across 4 sampling dates at Harper Adams University in 2014 bars represent ± one standard error.

Mean abundance of Bourletiellidae (Figure 13a) was highest in pasture field management type across all sampling dates at 1.8, 1.2, 9.6 and 5.5 individuals. Date in August significantly affected abundance (T = 2.00, p-value = 0.04746) and pasture management type significantly affected abundance (T = -2.88, p-value = 0.00465).

Mean species richness of Bourletiellidae (Figure 13b) was highest in pasture field management type across all sampling dates at 0.8, 0.4, 0.6 and 0.9 species. Pasture field management type significantly affected species richness (T = -2.05, p-value = 0.0405).

2.4 DISCUSSION

Acari and collembola were the most abundant soil mesofauna groups recorded in the soil cores, this was expected as these are the most common mesofauna groups in soil and extracted from samples in Berlese-Tullgren funnels (Schinner & Margesin, 1996). The Isotomidae, Hypogasturidae and Bourletiellidae were the most common taxonomic families of Collembola recorded, the Isotomidae were dominated by the closely related *Isotoma viridis* and *Isotoma anglicana* and by *Isotomiella minor* which are common species in the UK (Hopkin, 2007).

Field management type significantly affected soil moisture. This could be an effect caused by soil type as all the pasture fields surveyed had clay soil which holds more water, but as one of the arable and two of the grass ley fields also had clay soil, this is unlikely. Mesofauna abundance, Collembola abundance and diversity were significantly affected by soil moisture, which agrees with some previous studies (Verhoef & van Selm 1983; van Capelle, Schrader & Brunotte, 2012).

Mesofauna taxonomic order richness, Collembola species richness and Mesofauna, Acari and Collembola abundance were not significantly affected by field management type overall, in May Acari and Collembola and (as these were the most dominant groups) total mesofauna abundance had significantly higher abundances in arable fields, this was also unexpected and was in contrast to the hypothesis and the intensity effect found by Tsiafouli (2015). Density dependence has been recorded as important for Collembola populations fluctuations (Vegter, Joosse & Ernsting, 2012), and perhaps this is what drives the increase to and higher numbers in May.

The three most abundant families of Collembola inhabit different soil niches and were affected in different ways by management type. The Isotomidae are epedaphic, living on the soil surface and leaf litter with brightly coloured bodies (Hopkin, 2007), abundance and species richness of Isotomidae were highest in May in arable fields and in other months were not significantly different across fields. The Hypogasturidae are hemiedaphic, living in the top layers of the soil with shorter body lengths and smaller jumping organs (furcula) than

Isotomidae (Hopkin, 2007); abundance and species richness of

Hypogasturidae were highest in arable fields than other field types across sampling dates, but the highest numbers were in August rather than May, and pasture and grass ley management types significantly affected species richness. Bourletiellidae are epedaphic like Hypogasturidae but are globular springtails, with round-shaped bodies and short jumping organs (Hopkin, 2007); Bourletiellidae abundance and species diversity were highest in pasture fields and there was a significant effect of pasture field management type, in contrast to the Isotomidae and Hypogasturidae.

It would be interesting to assess the results in a landscape context, Tscharntke *et al* (2005) suggested that increased landscape complexity can compensate for negative effects of high intensity agricultural management on biodiversity. Collembola lifeforms respond differently to landscape diversity, Querner (2013) for example, found that epedaphic species were more influenced by landscape diversity than euedaphic.

Future work that addresses the importance of the different groups of Collembola in determining soil health, perhaps based on trait analysis, could inform future initiatives that seek to enhance the biodiversity of agroecosystems.

3. TRAFFIC AND TILLAGE EFFECTS ON SOIL MESOFAUNA

3.1 INTRODUCTION

Organisms living in soil are vital for nutrient cycling and overall ecosystem functioning (Brussaard, de Ruiter & Brown, 2007; de Vries & Shade, 2013;). Arthropods make up 20% of soil fauna and the mesofauna groups Collembola (springtails) and Acari (mites) are some of the most abundant of these groups (Culliney, 2013). Mesofauna perform several functions such as transforming litter, fragmenting particles of dead and decaying organic matter, increasing surface areas for action of microbes and enabling increased rates of decomposition (Culliney, 2013).

Collembola are one of the most abundant groups of soil mesofauna with densities recorded of over 100,000 per m^2 (Petersen & Luxton, 1982a). Inhabiting the soil litter surface and top soil layers they act as intermediaries of the above and below ground food webs (Hopkin, 1997), feeding on dead and decaying organic matter and themselves predated on by other soil mesofauna, multiple studies have shown that they can indicate wider soil biodiversity and ecosystem health (Parisi *et al.*, 2005; Greenslade, 2007; Wu *et al.*, 2011;).

Agricultural traffic is the movement of machinery over soil, since the advent of internal combustion engines in the early C20th mechanised vehicles pulling ploughs have been widely used globally and have increased in weight with advancements in technology (Soane & van Ouwekerk, 1994).

The weight of vehicle wheels running over a field can compact soil, decreasing porosity and permeability (Soane & van Ouwekerk, 1994). With each vehicle pass over a field for different agricultural interventions soil will be affected, and if vehicles are of different widths then a greater area of soil will be influenced and multiple wheel ways established.

Decrease in pore sizes reduces the overall habitable space for organisms to live and function in soil (Elliott *et al.*, 1980; Young & Ritz, 2000), can reduce connectivity between pores (Larsen, Schjønning & Axelsen, 2004) and availability for gas exchange of soil organisms and for soil organisms to live.

Controlled traffic farming systems aim to reduce the effects of soil compaction by vehicle wheels by constraining all vehicles to the same wheel ways in a field. This requires initial investment in vehicles with wheels the same distances apart but studies have shown crop yield and quality increases (Kingwell & Fuschbichler, 2011).

Lowering wheel inflation pressure is another strategy to reduce soil compaction effects from agricultural machinery. Wheel area in contact with soil will increase with decreasing inflation pressure, but the force applied per unit area will decrease, reducing the effects of soil compaction (Hamza & Anderson, 2005).

Only a few studies look at the effects agricultural traffic on soil fauna, Heisler and Kaiser (1995) found that increasing traffic reduced Collembola densities, which was linked to a decrease in soil porosity. Experiments by Larsen, Schjønning & Axelsen (2004)investigating the interactions between varying bulk densities and several Collembola species found that soil compaction and habitable soil space directly influence Collembola densities.

Ploughing (tillage) can involve parting, lifting or turning of soil and different tillage techniques vary in the mode of action on the soil and the percentage on the soil surface of previous crop residues (Titi, 2003). Tillage aims to alleviate soil compaction, to mix soil organic matter through the soil layers and to increase water infiltration rates (Lal, 1993). Soil functioning can however be detrimentally affected by tillage, with decreases in stability, resilience, the production of new soil (pedogenesis) and levels of organic matter, due to increases in soil erosion (Lal, 1993).

Many more studies have looked at tillage than agricultural traffic effects on soil biodiversity. Soil organisms generally occur in lower abundance and diversity in conventional than no tillage (House, 1985; Kladivko, 2001; Chang *et al.*, 2013) or reduced tillage systems (Miyazawa *et al.*, 2002). Manetti (2010) however found abundance and diversity unaffected by tillage and Sabatini *et al.* (1997) and Brennan *et al.* (2006) found decreased abundance but no changes in diversity. Loring, Snider & Robertson (1981)recorded Collembola initially decreasing after tillage treatments and then recovering, and Ponge *et al.* (2013) found different groups of Collembola responding positively or negatively to tillage.

There is an increasing need for sustainable agricultural practices that will feed a growing global population whilst maintaining soil health (Powlson *et al.*, 2011). These practices should take into account soil biodiversity (Lal, 2009; Nielsen, Wall & Six, 2015).

No previous studies have been found that look at the interaction of agricultural traffic and tillage on soil biodiversity. Mele (2013) proposed that fields with conventional tillage and uncontrolled traffic will have the lowest levels of soil diversity, fields with no tillage and uncontrolled traffic will have higher levels and that systems with both no till and controlled traffic with have the highest levels of soil biodiversity.

This study investigated the response of soil mesofauna, with a particular focus on Collembola, to combinations of different agricultural traffic and tillage intensities. It is hypothesised that in the lowest intensity treatment combinations there will be the highest abundance and diversity of soil mesofauna and Collembola.

3.2 METHODS

Study site and history

The experiment was carried out on ‘Large Marsh’, an 8.5ha field at Harper Adams University, Shropshire, UK (SJ711206) (Figure 14). The soil type is Claverley very slightly stony sandy loam (Cranfield, 1995).

Figure 14 location of study site in the UK

Experimental design

Three types of farming traffic system: random traffic farming (RTF), controlled traffic farming (CTF) and low ground pressure (LGP), were compared with three types of tillage: conventional (deep 250mm), minimum (shallow 100mm) and zero or no tillage, resulting in nine treatment combinations (Figure 15).

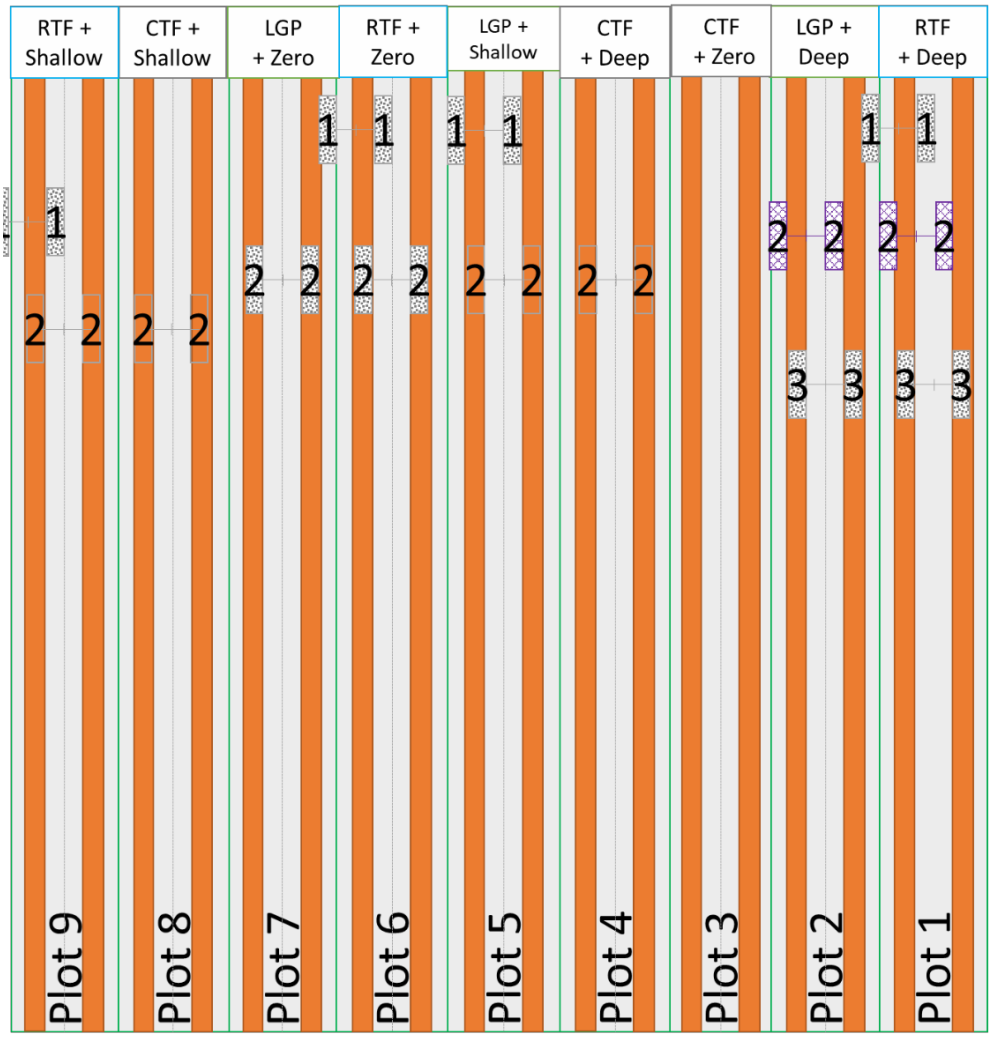

Figure 15 traffic and tillage treatment combinations within one experimental block, red strips are primary wheel ways, numbers 1, 2 and 3 show machinery passes for traffic treatments

Four blocks of nine plots of 4m wide and 84m length were established in 2012, each plot with one treatment combination, treatments were randomly allocated to plots within blocks, making a total of 36 plots (Figure 16). Different numbers of machinery passes were used to apply traffic treatments (Figure 15), random traffic farming treatment was carried out with conventional Michelin MachXbib tyres inflated to 1.2b (front) and 1.5b (rear) and low ground pressure at 0.7b (front and rear). Deep and shallow tillage was carried out with a Vaderstad Top Down cultivator and in the zero tillage treatment no tillage was carried out. In 2012 a Vaderstad Rapid direct seed drill was used to sow winter wheat (*Triticum aestivum* var.Duxford) in all plots. The crop was harvested in 2013 and then winter barley (*Hordeum vulgare* var. Cassia) was sown in 2013 and 2014. Full plot establishment details are described in Smith, Misiewicz, Chaney & White *et al.* (2013) .

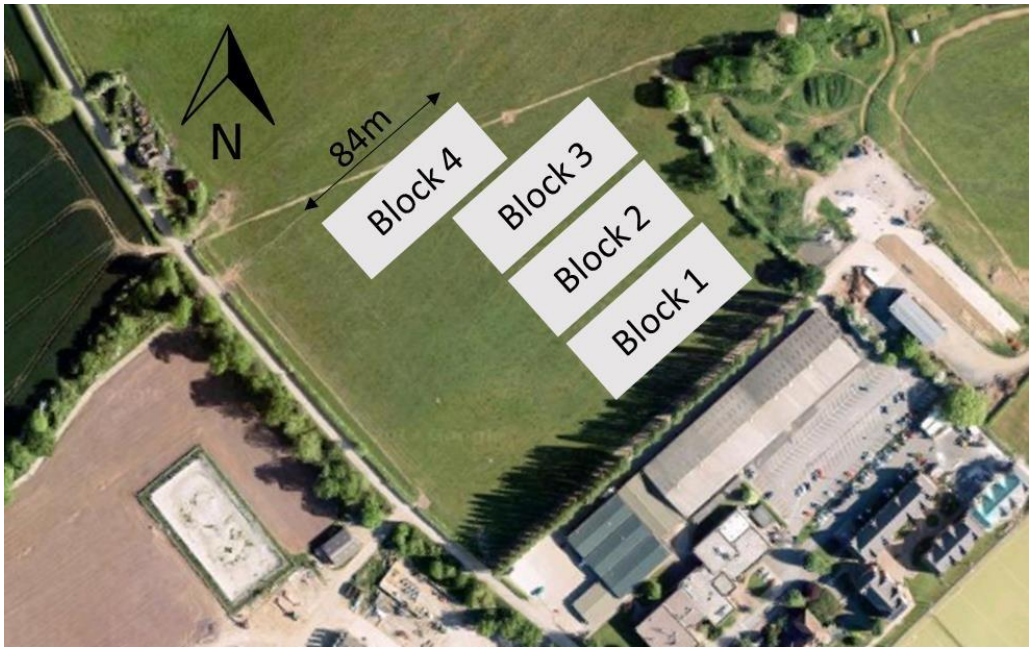

Figure 16 Location of experimental blocks on Large Marsh Field

Soil mesofauna sampling

Thirty-six soil cores of 100mm high x 65 mm width were sampled on 5 June 2014 (before harvest), 25 July 2014 (after harvest) and 13 November 2014. One core was taken from each plot, atleast 10m from the end and from the centre strip to account for differing numbers of machinery passes across treatment combinations.

Soil mesofauna were extracted into 50ml sample tubes holding 20ml of 70% Industrial Methylated Spirits (IMS) solution, by placing soil cores in Berlese-Tullgren funnels BS00290 (Burkard, 2013) on 2mm^2 square holed gauze under 40W power lightbulbs for 7 days.

Samples were examined in 100mm diameter Petri dishes under a Microtec HM-2 dissection microscope at X20 magnification. All arthropod specimens were identified to taxonomic order with Tilling (1987), Collembola specimens were further examined with a drop of 70% IMS in 40mm wide square watch glasses under a Microtec HM-2 dissection microscope at X40 magnification or (for specimens with body length smaller than 1mm) in glass slides with single concave depressions of 16mm diameter and 0.5mm depth with a drop of 70% IMS under a Olympus CX31 compound microscope at x100 magnification, and identified to species using Hopkin (2007). The specimens for each sample were retained as a voucher records in a 10ml sample tube with 5ml 70% IMS.

Mesofauna abundance and taxonomic order richness, Collembola abundance and species richness were recorded for each sample.

Statistical analysis

Datasheets with mean abundance and taxonomic order richness of soil mesofauna and species richness of Collembola were constructed in Microsoft Excel (Microsoft, 2013). Statistical analysis and graphics drawing was done with R statistics package (Core Team, 2014).

General linear modelling with mesofauna or Collembola abundance or diversity as the response variable and traffic treatment, tillage treatment as categorical explanatory variables, with date and block as covariates. Quasiposson family error structure was used where residual deviance was greater than degrees of freedom.

3.3 RESULTS

Soil mesofauna

8700 soil mesofauna individuals from 16 taxonomic orders were recorded, Collembola were the most abundant making up 55% of all individuals, Acari were the second most abundant order making up 39% of all individuals.

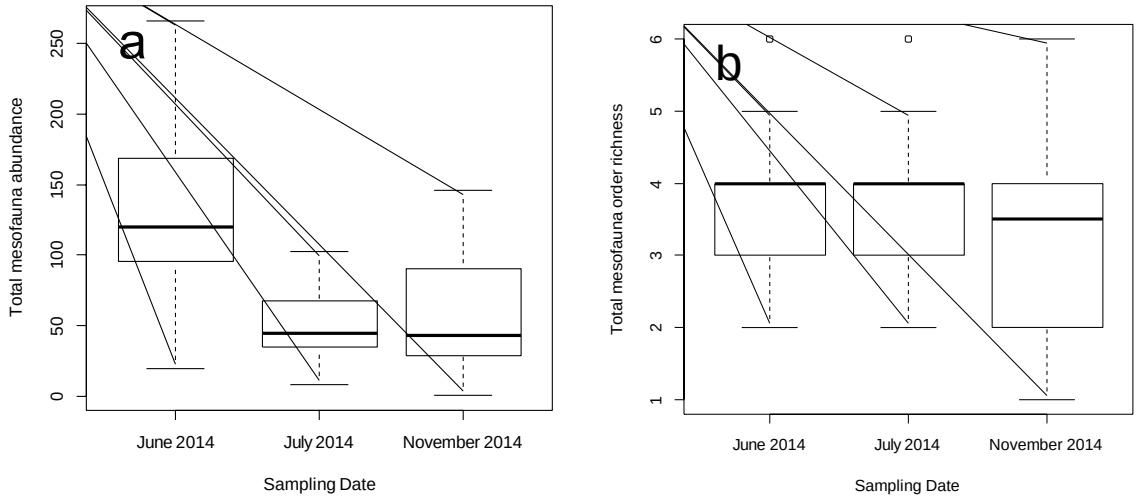

Figure 17 Total mesofauna abundance (a) and taxonomic order richness (b) across all plots in Large Marsh field

Total mesofauna median abundance in June was 120 individuals which decreased to 45 in July and to 43 in November (Figure 17a). Total mesofauna median taxonomic order richness in June was 4.0 orders, which stayed constant in at July 4.0 and decreased in November to 3.5 (Figure 17b).

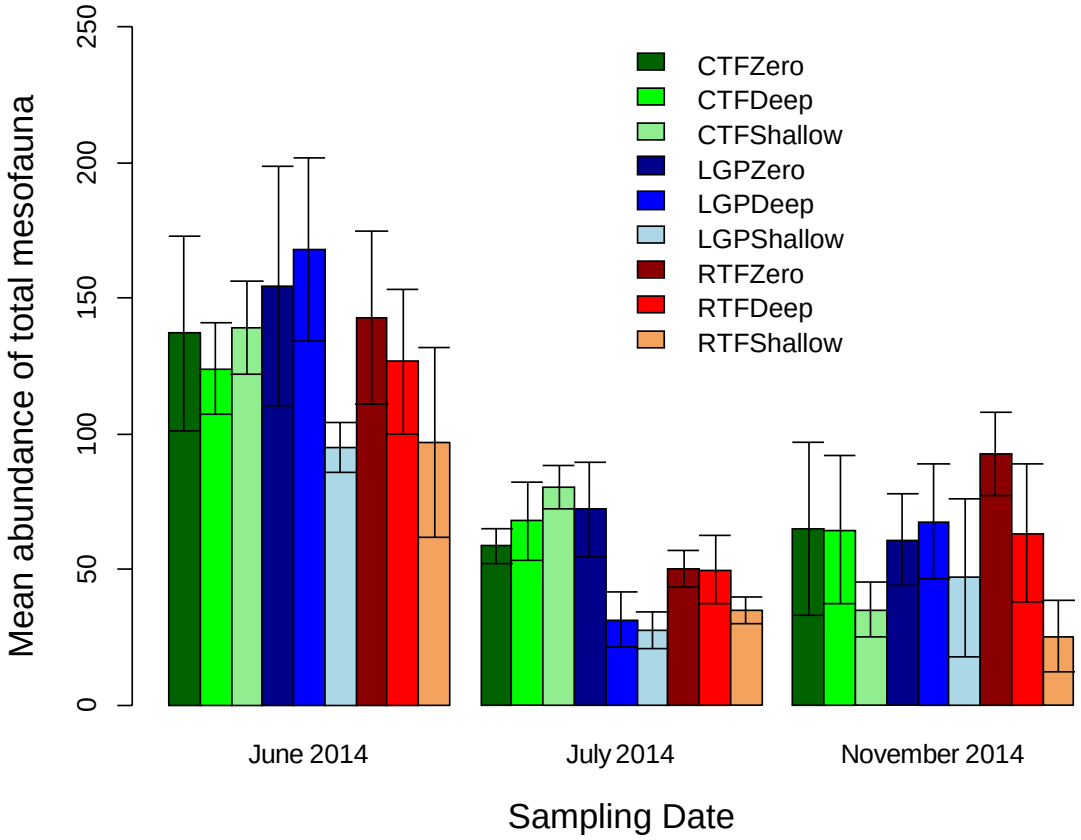

Figure 18 Mean abundance of all recorded soil mesofauna groups across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean total mesofauna abundance (Figure 18) in all June samples was highest in low ground pressure plots with zero tillage at 95.0 individuals and lowest in low ground pressure plots with shallow tillage in at 168.0 individuals; mean total mesofauna abundance in all July samples was highest in controlled traffic farming plots with zero tillage at 80.3 individuals and lowest in low ground pressure plots with zero tillage in at 27.5 individuals; mean total mesofauna abundance in all November samples was highest in random traffic farming plots with deep tillage at 92.5 individuals and lowest in random traffic farming plots with zero tillage in at 25.0 individuals. There was no interaction between or effect of traffic and tillage treatments on mesofauna abundance, but sampling date did significantly affect mesofauna abundance in July (T = -4.13, p-value = 7.65e-05) and November (T = -3.46, p-value = 0.000804).

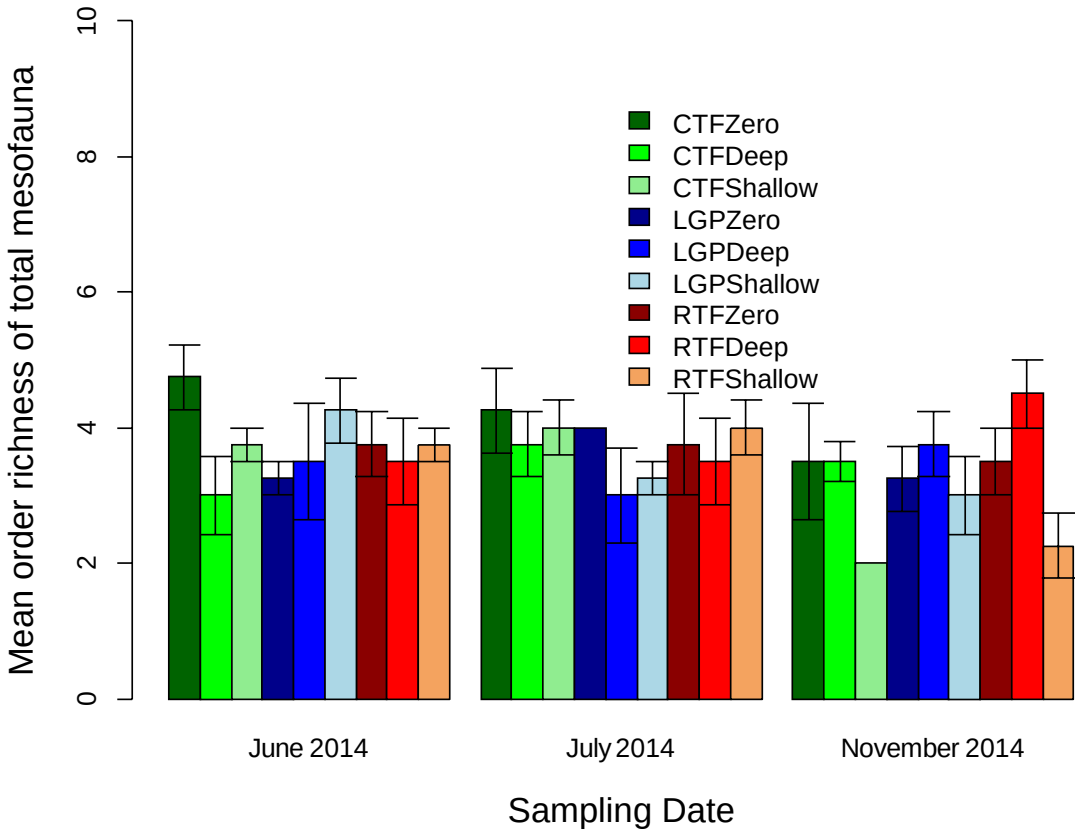

Figure 19 Mean taxonomic order richness of all recorded soil mesofauna groups across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean mesofauna taxonomic order richness (Figure 19) in all June samples was highest in controlled traffic farming plots with deep tillage at 4.8 orders and lowest in controlled traffic farming pots with shallow tillage at 3.0 orders; mean mesofauna taxonomic order richness in all July samples was highest in controlled traffic farming plots with deep tillage at 4.3 orders and lowest in low ground pressure plots with shallow tillage in at 3.0 orders; mean mesofauna taxonomic order richness in all November samples was highest in random traffic farming plots with shallow tillage at 4.5 orders and lowest in random traffic farming plots with zero tillage in at 2.25 orders. There was no interaction between or effect of traffic and tillage treatments or date on mesofauna order richness.

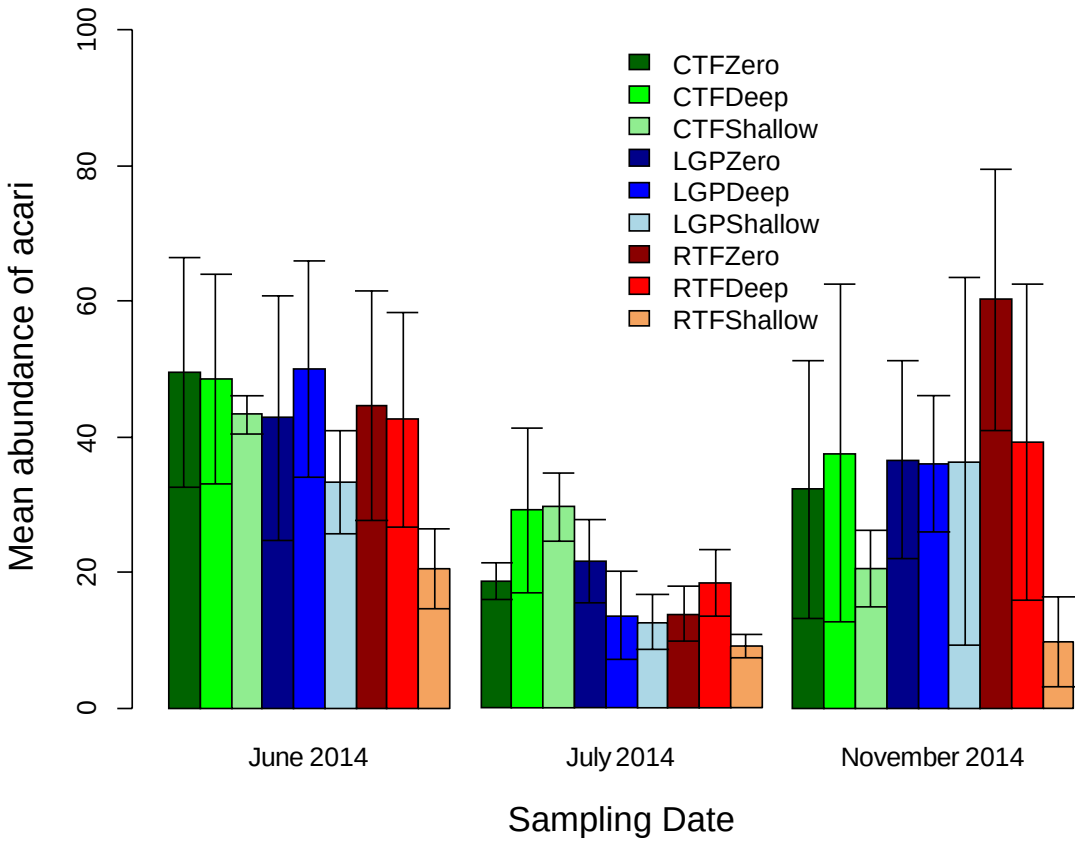

Figure 20 Mean abundance of Acari across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Acari abundance (Figure 20) in all June samples was highest in low ground pressure plots with deep tillage at 18.1 individuals and lowest in controlled traffic farming plots with zero tillage at 2.7 individuals; mean Acari abundance in all July samples was highest controlled traffic farming plots with shallow plots 15.6 and lowest in random traffic farming plots with zero tillage at 1.8 individuals; mean Acari abundance in all November samples was highest in low ground pressure farming plots with zero tillage at 27.1 individuals and lowest in controlled traffic farming plots with zero tillage at 5.6 individuals . There was no interaction between or effect of traffic and tillage treatments on Acari abundance, but sampling date did significantly affect Acari abundance in July (T = -3.98, p-value = 0.000129).

Collembola

4810 Collembola individuals were recorded from 8 taxonomic families and 16 species. The Isotomidae were the most abundant family making up 72% of all individuals. The Entomobryidae were the second most abundant family making up 10% of all individuals.

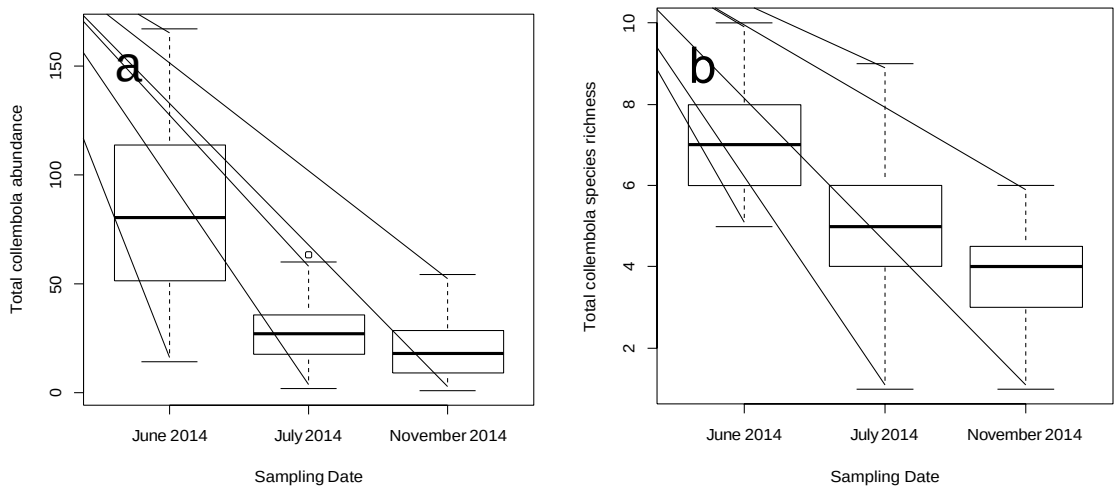

Figure 21 Total Collembola abundance (a) and species richness (b) across all plots in Large Marsh field

Total Collembola median abundance in June was 80.5 individuals which decreased to 27.0 in July and to 18.0 in November (Figure 21a). Total Collembola median species richness in June was 7 species, which decreased in July to 5 and further decreased in November to 4 (Figure 21b).

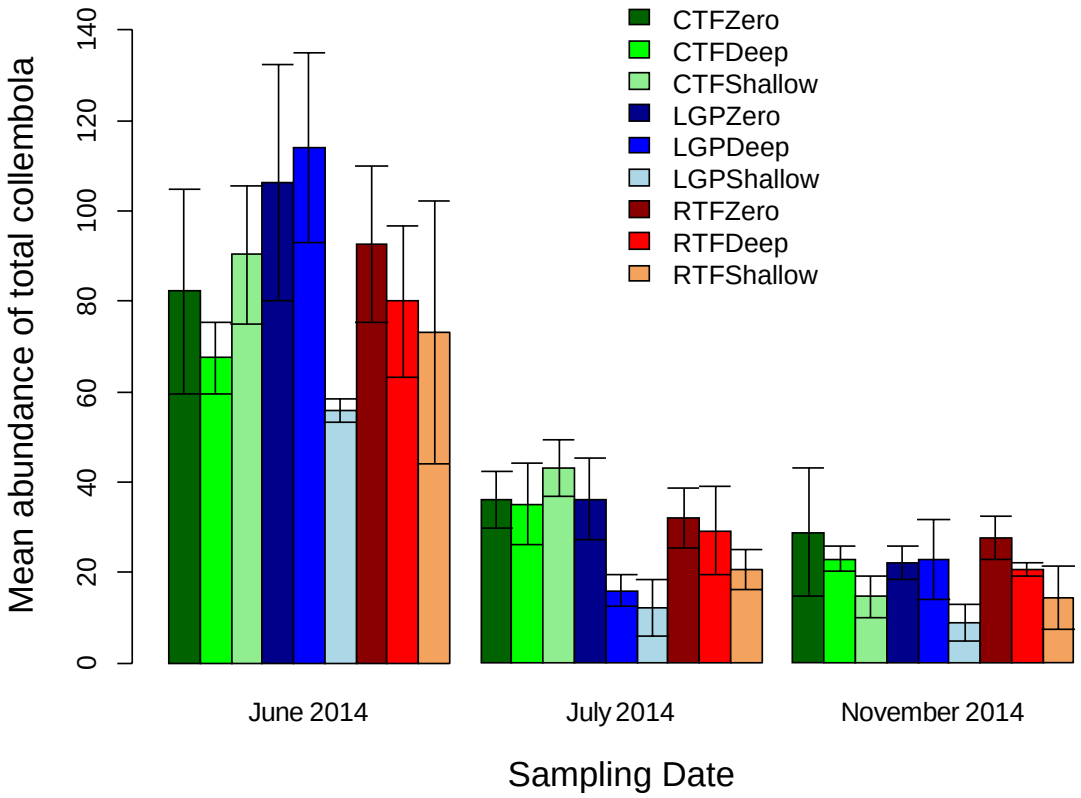

Figure 22 Mean abundance of all recorded Collembola across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Collembola abundance (Figure 22) in all June samples was highest in random traffic farming plots with zero tillage at 29.1 individuals and lowest in low ground pressure plots with zero tillage at 2.59 individuals; mean Collembola abundance in all July samples was highest in random traffic farming plots with shallow tillage at 9.76 individuals and lowest in random traffic farming plots with zero tillage at 4.3 individuals; mean Collembola abundance in all November samples was highest in controlled traffic farming with deep tillage at 14.1 individuals and lowest in random traffic farming plots with shallow tillage at 1.5 individuals. There was no interaction between or effect of traffic and tillage treatments on Collembola abundance , but sampling date did significantly effect Collembola abundance in July ($T = -2.49$, p-value = 0.01506) and November ($T = -2.92$, p-value = 0.00461).

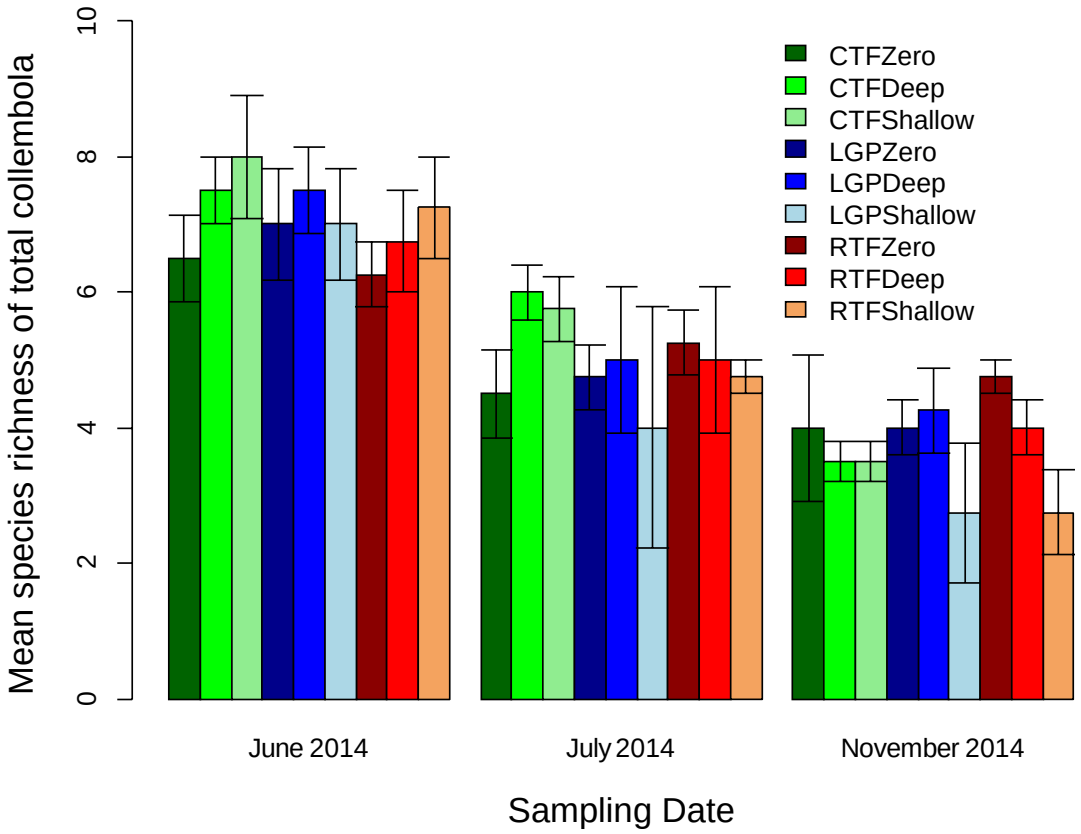

Figure 23 Mean species richness of all recorded Collembola across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Collembola species richness (Figure 23) in all June samples was highest in controlled traffic farming plots with zero tillage at 0.9 species and lowest in random traffic farming plots with deep tillage at 0.47 species; mean Collembola species richness in all July samples was highest in low ground pressure farming plots with zero tillage at 1.8 species and lowest in random traffic farming plots with zero tillage at 0.3 species; mean species richness abundance in all November samples was highest in controlled traffic farming with deep tillage at 1.1 species and lowest in controlled traffic farming plots with zero and shallow tillage at 0.3 species . There was no interaction between or effect of traffic and tillage treatments on Collembola species richness, but sampling date did significantly effect Collembola species richness in July (T = -3.58, p-value = 0.000346) and November (T = -6.03, p-value = 1.64e-09).

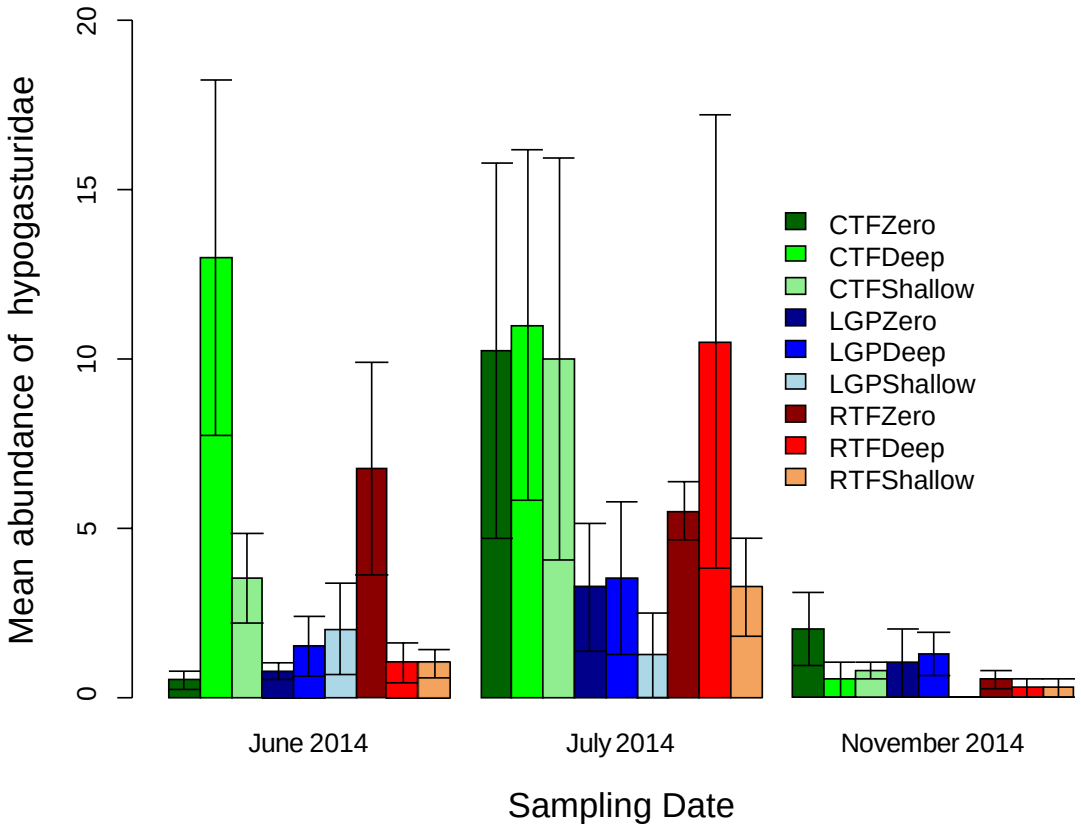

Figure 24 Mean abundance of Hypogasturidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Hypogasturidae abundance (Figure 24) in all June samples was highest in controlled traffic farming plots with shallow tillage at 13.0 individuals and lowest in controlled traffic farming plots with deep tillage at 0.5 individuals; mean Hypogasturidae abundance in all July samples was highest in the controlled traffic farming plots with shallow tillage at 13 individuals and lowest in the low ground pressure plots with zero tillage at 1.3 individuals; mean Hypogasturidae abundance in all November samples was highest in controlled traffic farming with deep tillage at 2.0 individuals and lowest in low ground pressure plots with zero tillage at 0.0 individuals. There was no interaction between or effect of traffic and tillage treatments on Hypogasturidae abundance but sampling date did significantly effect Hypogasturidae abundance in July (T = -2.49, p-value = 0.01506) and November (T = -2.92, p-value = 0.00461).

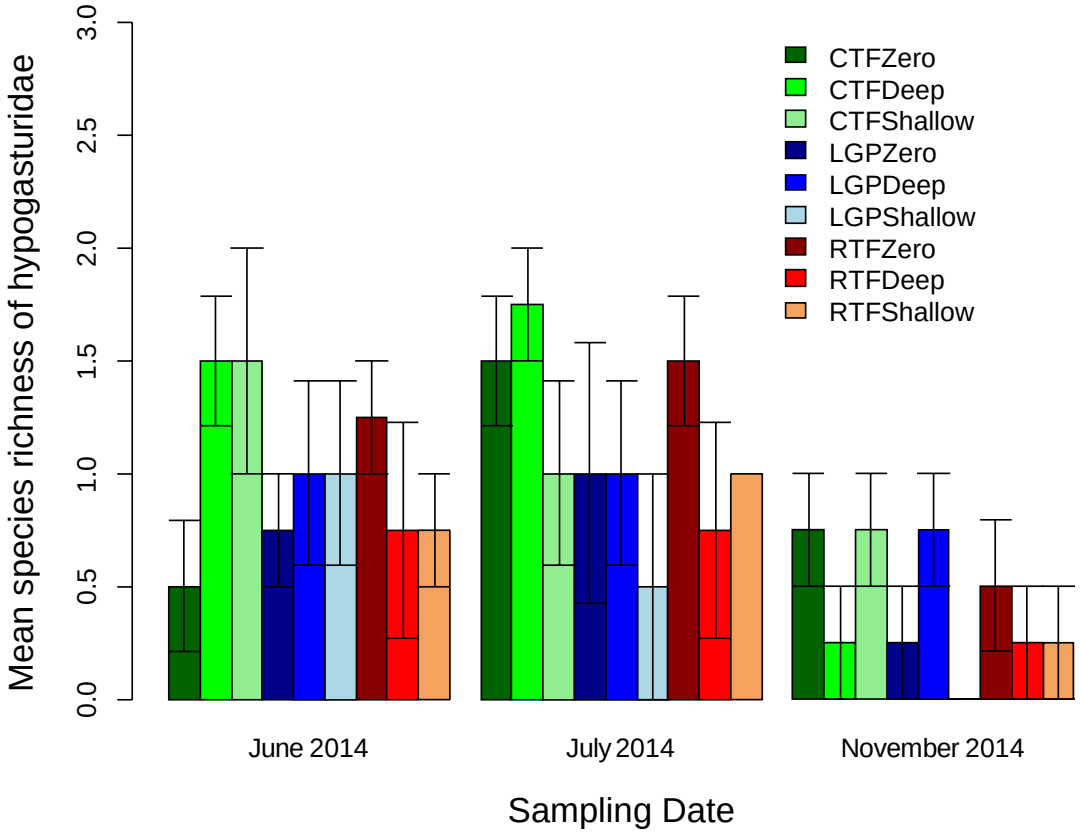

Figure 25 Mean species richness of Hypogasturidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Hypogasturidae species richness (Figure 25) in all June samples was highest in controlled traffic farming plots with zero and shallow tillage at 1.5 species and lowest in controlled traffic deep plots at 0.5 species; mean Hypogasturidae species richness in all July samples was highest in controlled traffic farming plots with shallow tillage at 1.8 species and lowest in low ground pressure farming plots with zero tillage at 0.5 species; mean Hypogasturidae species richness in all November samples was highest in controlled traffic farming with deep and shallow tillage and in low ground pressure farming plots with shallow tillage at 0.75 species and lowest in low ground pressure farming plots with zero tillage at 0.0 species. There was no interaction between or effect of traffic and tillage treatments on Hypogasturidae species richness , but sampling date did significantly effect Hypogasturidae species richness in November (T = -2.85, p-value = 0.00439).

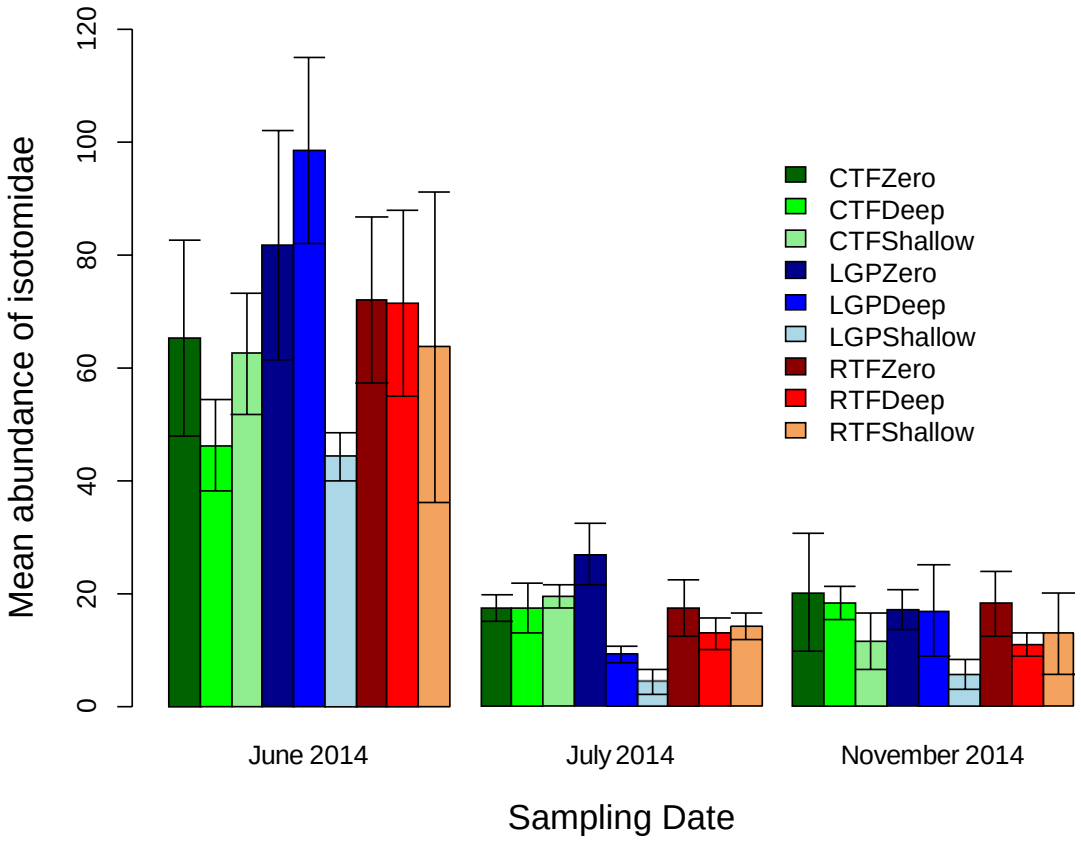

Figure 26 Mean abundance of Isotomidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Isotomidae abundance (Figure 26) in all June samples was highest in low ground pressure plots with shallow tillage at 98.5 individuals and lowest in low ground pressure farming plots with zero tillage at 44.2 individuals; mean Isotomidae abundance in all July samples was highest in low ground pressure farming plots with deep tillage at 26.7 individuals and lowest in low ground pressure farming plots with zero tillage at 4.3 individuals; mean Isotomidae abundance in all November samples was highest in controlled traffic farming deep tillage at 20.0 individuals and lowest in low ground pressure plots with zero tillage at 5.5 individuals . There was no interaction between or effect of traffic and tillage treatments on Isotomidae abundance (Figure 7), but sampling date did significantly effect Isotomidae abundance in July (T = -10.43, p-value = <2e-16) and November (T = -10.58, p-value = <2e-16).

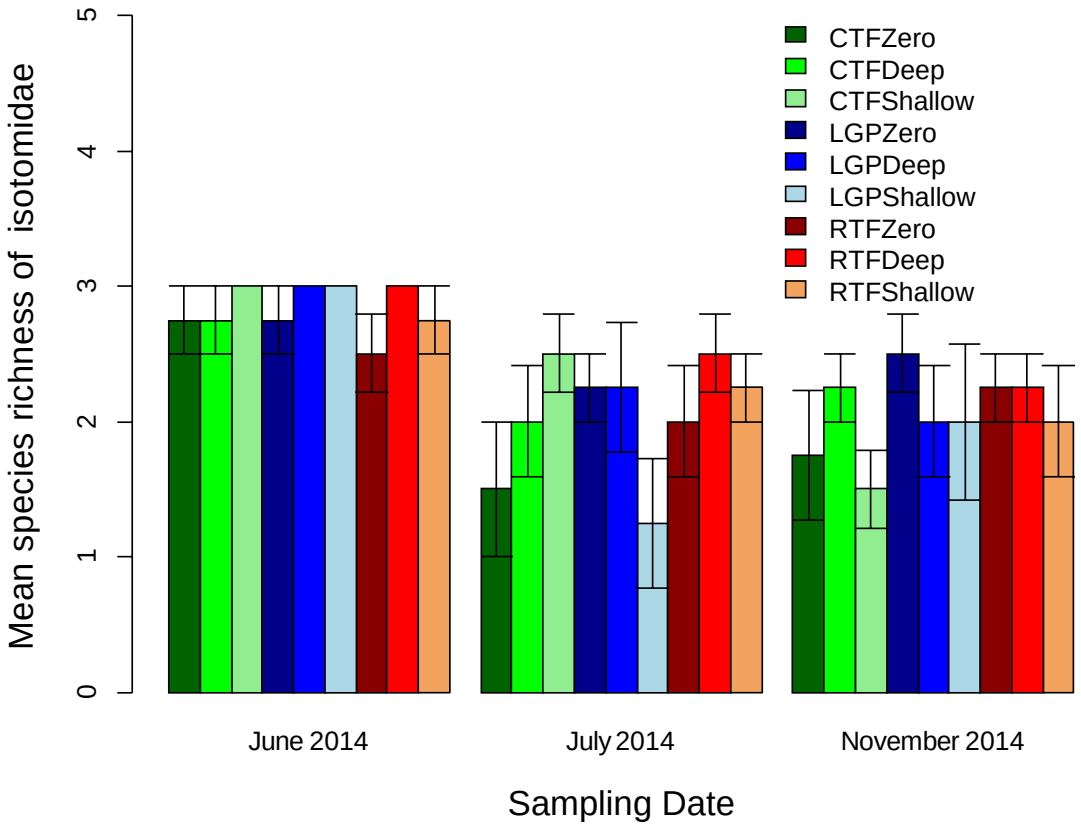

Figure 27 Mean species richness of Isotomidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Isotomidae species richness (Figure 27) in all June samples was highest in random traffic farming plots with deep tillage at 0.3 species and lowest in controlled traffic farming plots with zero tillage, low ground pressure plots with shallow and zero tillage, and random traffic controlled farming with shallow tillage all at 0.0 species; mean Isotomidae species richness in July samples was highest in controlled traffic farming plots with deep tillage at 0.5 species and lowest in random traffic farming plots with zero tillage and low ground pressure farming plots with deep tillage at 0.3 species; mean Isotomidae species richness in all November samples was highest in low ground pressure farming plots with zero tillage at 0.6 species and lowest in low ground pressure farming plots with deep tillage and random traffic farming plots with deep and shallow tillage 0.3 species. There was no interaction between or effect of traffic and tillage treatments on Isotomidae species richness, but sampling date did significantly effect Isotomidae species richness in July (T=-2.10, p-value = 0.0356) and in November (T = -2.10, p-value = 0.0356).

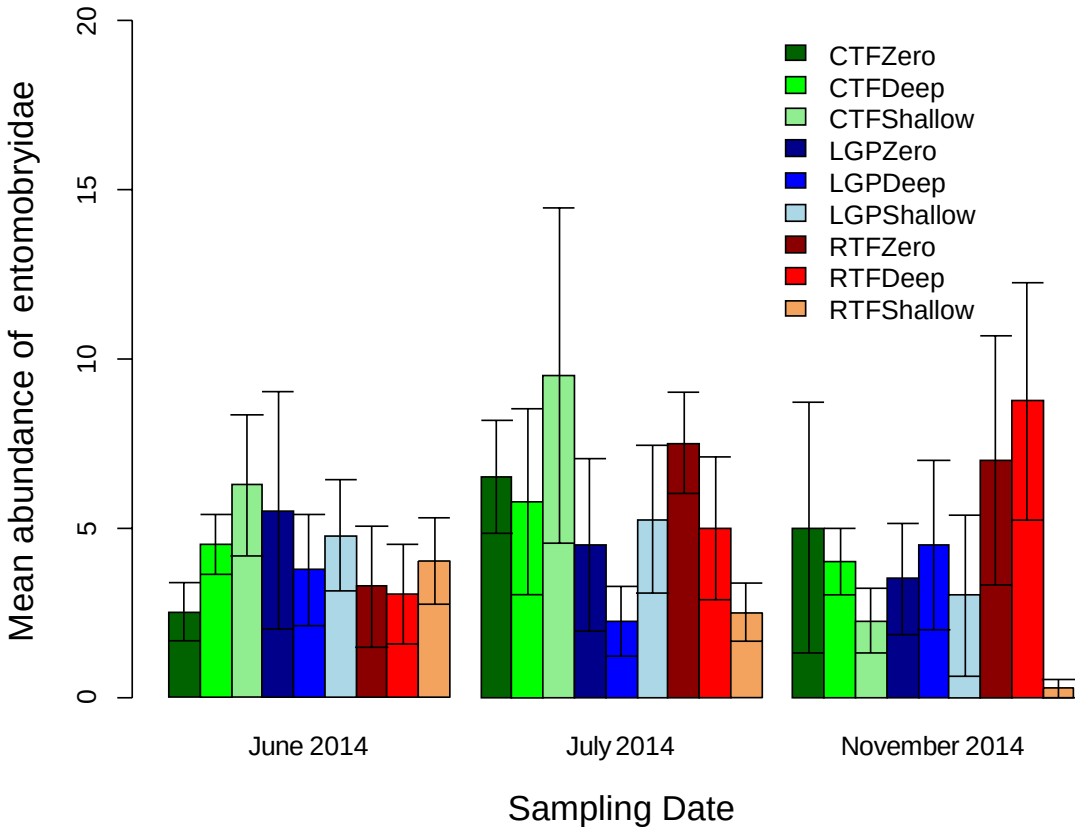

Figure 28 Mean abundance of Entomobryidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Entomobryidae abundance (Figure 28) in all June samples was highest in controlled traffic farming plots with zero tillage at 6.2 individuals and lowest in controlled traffic farming plots with deep tillage at 2.5 individuals; mean Entomobryidae abundance in all July samples was highest in controlled traffic farming plots with zero tillage at 9.5 individuals and lowest in low ground pressure farming plots with shallow tillage at 2.2 individuals; mean Entomobryidae abundance in all November samples was highest in random traffic farming plots with shallow tillage at 8.75 individuals and lowest in random traffic farming plots with zero tillage at 0.25 individuals. There was no interaction between or effect of traffic and tillage treatments on Entomobryidae abundance , but sampling date did significantly effect Entomobryidae abundance in June ($T = 2.63$, p-value = 0.0101).

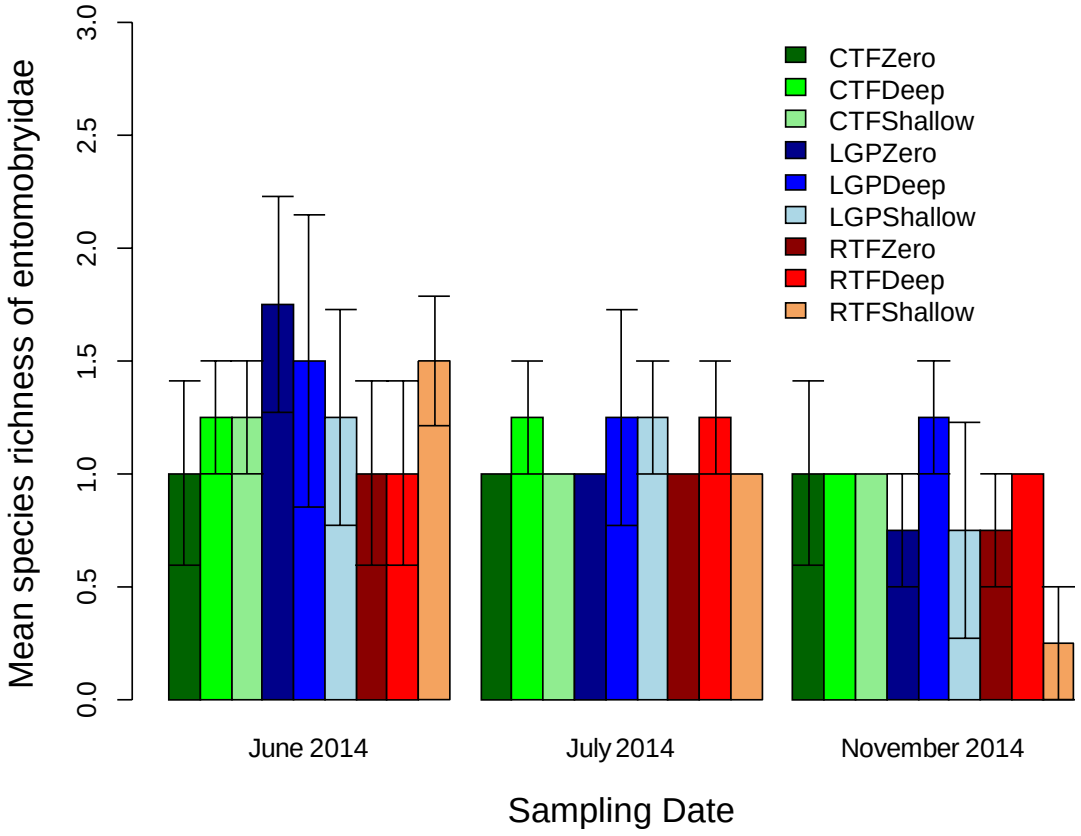

Figure 29 Mean species richness of Entomobryidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Entomobryidae species richness (Figure 29) in all June samples was highest in low ground pressure farming with deep tillage at 1.8 species and lowest in random traffic farming plots with shallow and deep tillage and controlled traffic farming plots with deep tillage at 1.0 species; mean Entomobryidae species richness in July samples was highest in controlled traffic farming plots with shallow tillage and low ground pressure lots with shallow and zero tillage and random traffic farming plots with shallow tillage all at 1.25 species and lowest in all other plots at 1 species; mean Entomobryidae species richness in all November samples was highest in low ground pressure plots with shallow tillage at 1.25 species and lowest in random traffic farming plots with zero tillage at 0.25 species. There was no interaction between or effect of traffic and tillage treatments or date on Entomobryidae species richness.

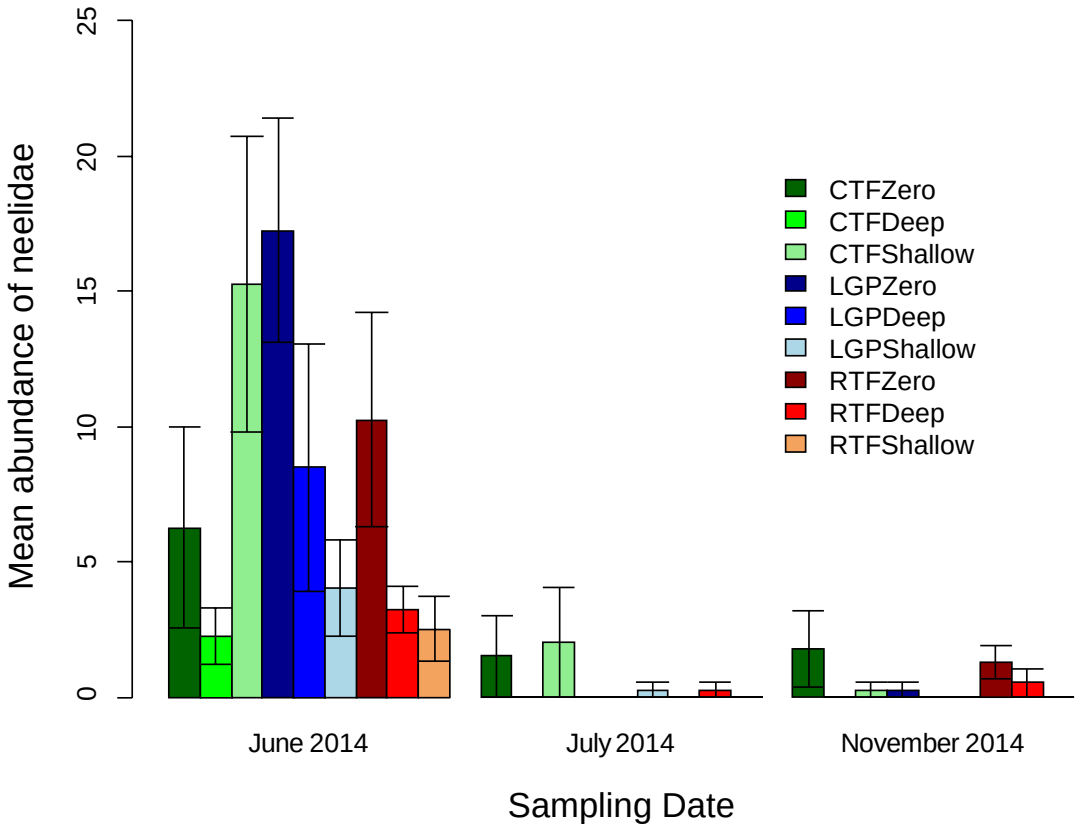

Figure 30 Mean abundance of Neelidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Neelidae abundance in all June samples was highest in low ground pressure plots with deep tillage at 17.25 individuals and lowest in controlled traffic farming plots with shallow tillage at 2.25 individuals; mean Neelidae abundance in all July samples was highest in controlled traffic farming plots with zero tillage at 2.0 individuals and lowest in controlled traffic farming plots with shallow tillage and low ground pressure plots with deep and shallow tillage and random traffic farming plots with deep and zero tillage at 0 individuals; mean Neelidae abundance in all November samples was highest in controlled traffic farming plots with deep tillage at 1.75 individuals and lowest in controlled traffic farming plots with shallow tillage and in low ground pressure plots with shallow and zero tillage and in random traffic farming plots with zero tillage at 0 individuals. There was no interaction between or effect of traffic and tillage treatments or date on Neelidae abundance.

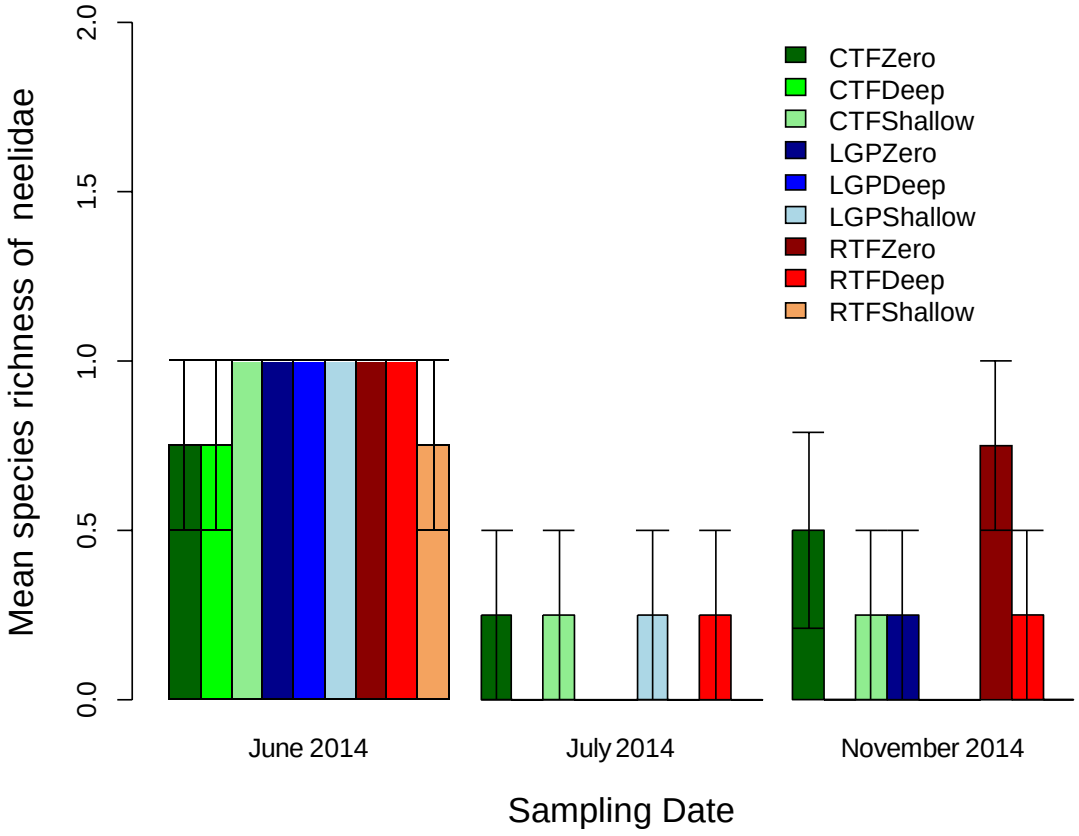

Figure 31 Mean species richness of Neelidae across 9 plot treatment combinations in June, July and November 2014; CTF=Controlled Traffic Farming, LGP = Low Ground Pressure and RTF = Random Traffic Farming; bars represent ± one standard error.

Mean Neelidae species richness (Figure 31) in all June samples was one species in all plots except for controlled traffic farming plots with deep and shallow tillage and random traffic farming plots with zero tillage where the mean was 0.8 species; mean Neelidae species richness in July samples was 0.25 species in controlled traffic farming with deep and zero tillage and in low ground pressure farming plots with zero tillage and in random traffic farming plots with shallow tillage, mean species were 0 in remaining plots; mean Neelidae species richness in all November samples was highest in random traffic farming plots with deep tillage at 0.75 species and lowest at 0 species in controlled traffic farming lots with shallow tillage, low ground pressure farming plots with shallow and zero tillage and in random traffic farming plots with zero tillage. There was no interaction between or effect of traffic and tillage treatments on Neelidae species richness but sampling date significantly affected species richness in June (T= -3.99, p-value = 6.72e-05) and July (T=-3.59, p-value = 0.000323.

3.4 DISCUSSION

Collembola and Acari were the most abundant groups recorded. This was expected as these are the most common mesofauna groups in soil and extracted from samples in Berlese-Tullgren funnels (Schinner & Margesin, 1996). The Isotomidae were the most abundant Collembola family and these were dominated by the closely related *Isotoma viridis* and *Isotoma anglicana* and by *Isotomiella minor* which are common species in the UK (Hopkin, 2007).

Sampling date significantly affected: overall mesofauna abundance in July and November, Acari abundance in July, and overall Collembola abundance and species richness in July and November. Collembola families representing all life forms (Hopkin, 1997) in soil were significantly affected by season. The abundance of surface dwelling (epedaphic) Hypogasturidae were affected in July and November and their species richness in November. The top soil dwelling (hemiedaphic) Isotomidae abundance and species richness were affected in July and November and Entomobryidae abundance in June. Collembola dwelling deeper in the soil (euedaphic) were affected in July and November. Previous studies have also recorded seasonal differences in soil biodiversity with peaks in fauna at different times of the season (Kanal, 2004; Gudleifsson & Jarnadottir, 2008; Anu, Sabu & Vineesh, 2009).

Mesofauna abundance and taxonomic order richness, Collembola abundance and species richness, and abundance and species richness of the most abundant Collembola families did not respond to traffic or tillage treatments. This was unexpected and in marked contrast to multiple studies on the detrimental effects of traffic (Heisler & Kaiser, 1995; Larsen, Schjønning & Axelsen, 2004) and of tillage (House, 1985; Kladivko, 2001; Chang *et al.*, 2013) or reduced tillage (Miyazawa *et al.*, 2002). The results do however, agree with Manetti (2010) who also found no effects of tillage on soil biodiversity.

On each date, sampling was limited to one soil core per plot due to constraints in available numbers of Tullgren Funnels. Block did not significantly affect abundance or diversity or mesofauna or Collembola, therefore future sampling could focus on fewer blocks in Large Marsh to allow for soil core replication within each plot. This would hopefully reduce the standard error around mean of abundance and diversity and provide a clearer picture of the effects of traffic and tillage.

The effects of farm traffic and tillage on Collembola and other soil groups remain equivocal. More work on this topic in different geographical regions and different soil types may provide a clearer picture of the potential impacts of intensive agriculture on soil biodiversity.

4. TILLAGE EFFECTS ON SOIL MESOFAUNA

4.1 INTRODUCTION

Agriculture has intensified since the 1940s, agricultural land area has decreased but the yield of this land has increased fourfold with use of modern agrochemicals and equipment (Robinson & Sutherland, 2002).

The agricultural process involves farmers making agroecosystem trade-off decisions on provisioning services such as food, ecosystem services such as nutrient recycling, decomposition and soil fertility and ecosystem 'disservices' such as loss of biodiversity and wildlife habitat (Power, 2010). Soil organisms interact to maintain functions of healthy soils: carbon transformation, nutrient cycling, soil structure maintenance and disease regulation; farmers must conserve these functions whilst producing economically viable crop yields (Kibblewhite, Ritz & Swift, 2008). As agricultural management increases natural processes break down and must be replaced by artificial inputs (Giller *et al.*, 1997).

Soil tillage has been used for thousands of years to modify soil conditions to provide a suitable environment to grow crops; different types of tillage vary in the action exerted on the soil and the percentage of crop residue remaining on the soil surface (Titi, 2003). Tillage can benefit soil by increasing water infiltration rates, alleviating soil compaction and by mixing soil organic matter within the sub soil (Lal, 1993).

Tillage can however negatively affect soil structure, stability and resilience: increasing soil erosion, reducing the production of new soil (pedogenesis), levels of organic matter and biodiversity present (Lal, 1993). Land use for agriculture and the intensity of it are the main pressures on soil biodiversity (Gardi, Jeffery & Saltelli, 2013). Nielsen et al (2010) concluded that actions such as tillage that homogenise soil and decrease species richness of mesofauna such as Collembola, do not however, decrease evenness of microfauna such as bacteria and fungi. Tillage affects vertical distribution of organisms within soil; with conventional tillage fauna were equally distributed throughout top soil, without tillage fauna were in the top 3cm (van de Bund, 1970). A review by Decaens (2010) concluded that soil heterogeneity directly influenced the number of niches available for fauna and therefore levels of biodiversity.

Soil biota contribute to Carbon and Nitrogen cycling (de Vries *et al.*, 2013) and are important for ecosystem functioning (Brussaard, de Ruiter & Brown, 2007). Arthropods make up 20% of soil fauna and the mesofauna groups Collembola and Acari are one the most abundant groups of these (Culliney, 2013). Arthropods can perform litter transformation, fragmenting dead and decaying organic matter, thus increasing the surface area for decomposition and mineralisation by microfauna (Culliney, 2013).

Increasing land use intensity reduced soil diversity and reduced the complexity of soil food webs (fewer taxonomic groups) and species richness of Collembola (Tsiafouli *et al.*, 2015).

Collembola are a soil arthropod group with over 8000 species worldwide (Janssens, 2017) and over 250 species in the UK (Hopkin, 2007). Classed as mesofauna due to their body size of between 0.25 and 17mm, they are recognised as beneficial organisms within the soil food web. Collembola can increase the area of soil organic matter (Seastedt, 1984; Rusek, 1998) and inoculate it with microbial cultures from their guts as they ingest and excrete matter (Rusek, 1998). Collembola increase rates of decomposition (Hendrix *et al.*, 1986) and increase nutrient cycling rates (Filser, 2002; Zhang *et al.*, 2007). Along with other soil fauna groups Collembola can influence Nitrous oxide emissions (Kuiper *et al.*, 2013)

Soil mesofauna and Collembola specifically, can act as indicators of above and below ground biodiversity and thus as indicators or overall ecosystem health (Wu *et al.*, 2011). Soil microarthropods have been used in indicator indices of soil health (Parisi *et al.*, 2005). Collembola have been used as indicators of ecosystem health (Greenslade, 2007).

A summary by Kladivko (2001) showed that soil organisms have higher abundance in no till and that larger sized organisms are more sensitive than smaller. Multiple studies show that Collembola increase in abundance with decreasing farming intensity (Stinner & House, 1990), reducing pesticide use increased numbers of *Isotoma viridis* (Frampton, 2000) and Collembola numbers increased in lower input systems (Bedano, Cantú & Doucet, 2006). Collembola contribute to soil microsculpturing and this action is decreased in soil compacted by tillage (Schrader, Langmaack & Helming, 1997). Higher densities of Collembola were recorded in no till than conventional tillage systems (House, 1985). In rice plantation tillage experiments Collembola abundance and diversity decreased as tillage intensity increased (Chang *et al.*, 2013).

There is evidence for both top-down and bottom-up effects of tillage on soil fauna (Wardle, 1995). Manetti *et al* (2010) found that soil fauna density and composition was not affected by tillage treatments. Some Collembola groups respond positively or negatively to tillage and fertilisation treatments (Sabatini *et al.*, 1997). Stockdale and Watson (2012) and Key (2013) summarise defects of different interventions of soil management on soil biodiversity.

Overall Collembola numbers are found in lower numbers when sampling along an increasing gradient of agricultural intensity, except for epigeic groups which increase (Ponge *et al.*, 2013). With reduced tillage, under an 'ECOtillage' system Collembola abundance increased but diversity did not change (Brennan, Fortune & Bolger, 2006). Higher Collembola abundances were found under reduced tillage regimes by Miyazawa (2002). Reviewing data from multiple studies van Capelle *et al* (2012) found that Collembola

abundance and species diversity decreased with increasing tillage intensity, via a mechanism of soil texture.

Collembola have been recorded to initially decrease after tillage and then increase, with those under no till having stable populations (Loring, Snider & Robertson, 1981).

Methods to increase soil biodiversity are needed in a world with a growing population and the threat of global change (Lal, 2009). Future management practices should focus on conserving beneficial soil biodiversity (Nielsen, Wall & Six, 2015).

'No-till' systems involve no tillage or ploughing of the soil and then crop seed planting with specialist 'direct drill' equipment, which drives a narrow slot into the soil, drops in seeds at regular intervals and afterwards roles the soil (Titi, 2003). Developed in the 1960s and 1970s uptake of the system was slow until efficient herbicides and direct drills had been developed (Derpsch, 2001).

The following studies reports on an experiment comparing soil mesofauna responses to conventional and no till. It is hypothesised that under no till there will be a decrease in mesofauna abundance and taxonomic diversity.

4.2 METHODS

Study site and history

The experiment was located at Soulton Hall, North Shropshire, UK, (SJ541303, Figure 32). 'Nursery Field' has a sandy loam soil type and an area of 1.645 ha and a history of minimum tillage for 10 years until 2013, then under no till with a spring wheat rotation, awinter oil seed rape from 2013 to 2014, winter wheat from 2014 to 2015 and then an oat cover crop in 2015, which was desiccated with glyphosphate in January 2016, spring beans were planted in early 2016 and harvested in Summer 2016.

Figure 32 location of study site in the UK

Experimental design

Remaining crop residues and weeds in the field were desiccated with glyphosphate and the whole field was rolled. Experimental plots were established on 24 Sept 2016. The corners of six rectangular plots of 130m long and 3m width were marked along the field, three plots were randomly allocated the tilled treatment and the three remaining receiving no till

treatment (Figure 33). Tilled plots were ploughed to a depth of 150mm with a stubble cultivator and then rolled, no till plots were not ploughed.

Figure 33 Experimental treatment plots on Nursery field at Soulton Hall, satellite image from Google Maps (2009)

Winter wheat 'Crusoe' seed with Redigo Deter insecticide and fungicide dressing was sown on 6 Oct 2016 with Weaving GD 3m direct drill across the whole field over all plots and the whole field was then rolled. During sowing tilled plots had less resistance to the direct drill vehicle wheel pressure, seeds in these plots were found to have been sown at a depth of 75mm, lower than the no till plot seed depth of 40mm. Ferric phosphate slug pellets were applied at half rate in late Oct 2016. See Appendix A for images of crop growth.

Soil mesofauna sampling

30 soil cores of 100mm high x 65 mm width were sampled along a w-shaped transect, to cover heterogeneity in the field (Wheater, Bell & Cooke, 2011), on 21 Sept 2016 (prior to plot establishment), avoiding previous crop tramlines and headlands.

Further sampling was carried out on 22 Nov 2016 and 23 May 2017 with 5 soil cores of 100mm high x 65 mm width taken from random locations within the centre 1m strip of each of the 6 plots, making a total of 30 cores from each sampling date.

Soil mesofauna were extracted into 50ml sample tubes holding 20ml of 70% Industrial Methylated Spirits (IMS) solution, by placing soil cores in Berlese-Tullgren funnels BS00290 (Burkard, 2013) on 2mm^2 square holed gauze under 40W power lightbulbs for 7 days.

Samples were examined in 100mm diameter Petri dishes under a Microtec HM-2 dissection microscope at X20 magnification. All arthropod specimens were identified to taxonomic order with Tilling (1987), Collembola specimens were further examined with a drop of 70% IMS in 40mm wide square watch glasses under a Microtec HM-2 dissection microscope at X40 magnification or (for specimens with body length smaller than 1mm) in glass slides with

single concave depressions of 16mm diameter and 0.5mm depth with a drop of 70% IMS under a Olympus CX31 compound microscope at x100 magnification, and identified to species using Hopkin (2007). The specimens for each sample were retained as a voucher records in a 10ml sample tube with 5ml 70% IMS.

Mesofauna abundance and taxonomic order richness, Collembola abundance and species richness were recorded for each sample.

Statistical analysis

Datasheets with mean abundance and taxonomic order richness of soil mesofauna and species richness of Collembola were constructed in Microsoft Excel (Microsoft, 2013). Statistical analysis and graphics drawing was done with R statistics package (Core Team, 2014).

One-way Analysis of Variance was used to test for differences in mean abundance and taxonomic order richness of soil mesofauna and species richness of Collembola between till and no till treatments. T-tests were used to test for differences in mean abundance and taxonomic order richness of soil mesofauna and species richness of Collembola between the same treatments on different dates. An random subset of 15 data points from the September pre tillage treatment sampling was selected using the r function sample() for equal comparison with 15 tilled or no tilled data points from other dates.

4.3 RESULTS

Soil mesofauna

8240 mesofauna individuals from twelve taxonomic orders were recorded across the three sampling dates in the soil cores.

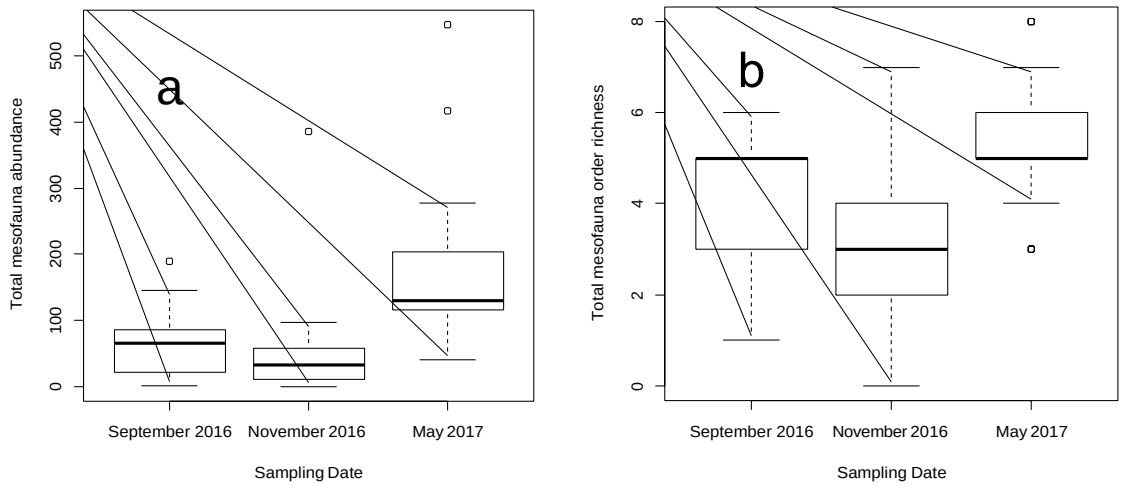

Figure 34 Total mesofauna abundance (a) and taxonomic order richness (b) in the w-shaped walk before tillage (September 2016) and after in both tilled and no till plots (November 2016 and May 2017) at Soulton Hall.

Total mesofauna median abundance was 65 individuals per soil core in September 2016, decreasing to 32 in November 2016 and then increasing to 130.5 in May 2017 (Figure 34a). A similar pattern was seen in total mesofauna order richness with a median of five orders in September 2016, decreasing to three in November 2016 and increasing, but with a lesser extent than of abundance, to five in May 2017 (Figure 34b).

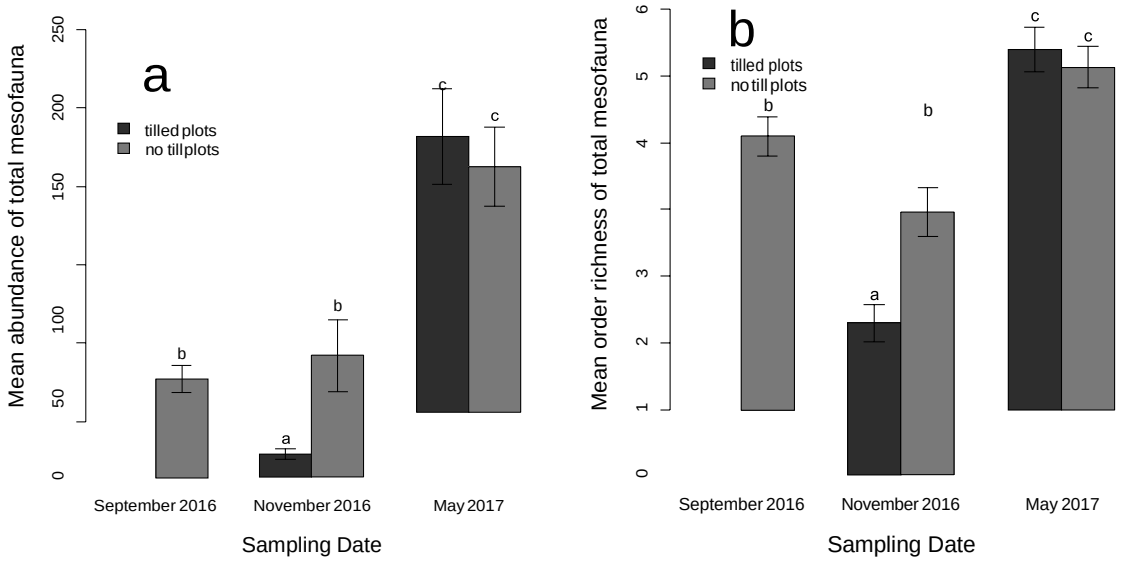

Figure 35 Mean abundance (a) and taxonomic order richness (b) of all recorded soil mesofauna groups before tillage (September 2016) and after in tilled and no till plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total soil mesofauna individuals (Figure 35a) in the w-shaped walk sample in September was 63.0; this significantly decreased in November (t = 4.48, df = 15.81, p-value = 0.00039) in tilled plots soil core samples to 14.3 individuals, but showed a non-significant (t = -0.79, df = 19.813, p-value = 0.44) increase in no till plots to 77.2 individuals. In May mean abundance of total mesofauna individuals significantly increased in tilled plots (t = -5.25, df = 14.318, p-value = 0.0001153) to 175.5 individuals and in no till plots (t = -2.33, df = 27.718, p-value = 0.02737) to 156.5 individuals; these levels were not significantly different from each other (F (1,28) = 0.23 p-value = 0.635).

Mean taxonomic order richness of total soil mesofauna individuals (Figure 35b) in the w-shaped walk sample in September was 4.1; this significantly decreased in November (t = 3.37, df = 22.823, p-value = 0.002704) in tilled plots soil core samples to 2.3 orders, but showed a non-significant (t = -0.358, df = 27.405, p-value = 0.7277) decrease in no till plots to 3.9 orders. In May mean abundance of total mesofauna individuals significantly increased in tilled plots (t = -7.1, df = 27.263, p-value = 1.079e-07) to 5.4 orders and in no till plots (t = -2.49, df = 27.034, p-value = 0.0191) to 5.1 orders; these levels were not significantly different from each other (F (1,28) = 0.345 p-value = 0.562).

Collembola

4565 Collembola individuals from 7 taxonomic families and 14 species were recorded from the Berlese-Tullgren funnel soil core extracts.

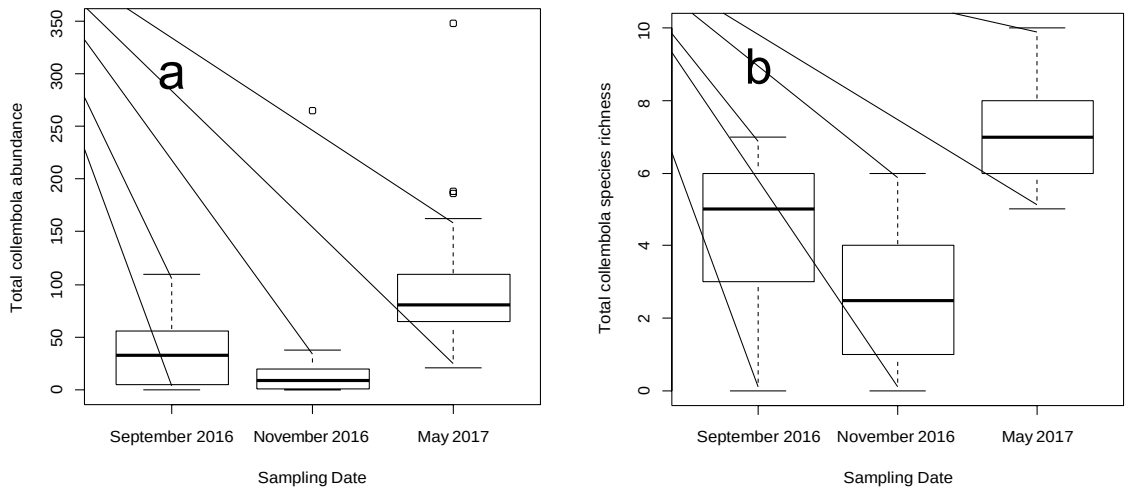

Figure 36 Total collembola abundance (a) and collembola species richness (b) in the w-shaped walk before tillage (September 2016) and after in both tilled and no till plots (November 2016 and May 2017) at Soulton Hall

Total Collembola median abundance (Figure 36a) was 32.5 individuals per soil core in September 2016, decreasing to 8.6 in November 2016 and then increasing to 81 individuals in May 2017. A similar pattern was seen in total Collembola order richness (Figure 36b) with a median of 5 species in September 2016, decreasing to 2.5 in November 2016 increasing to 7 orders in May 2017.

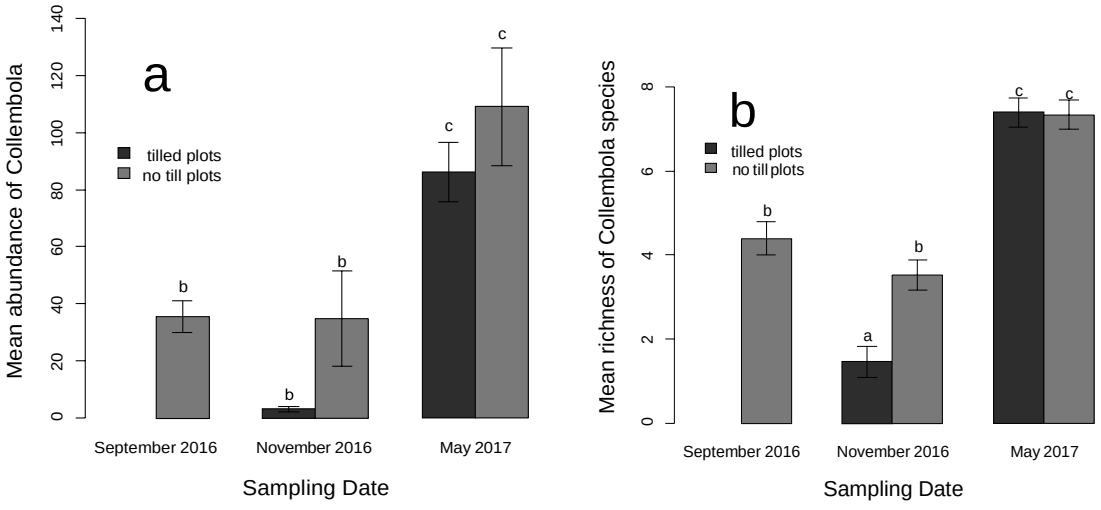

Figure 37 Mean abundance (a) and species richness (b) of Collembola before tillage (September 2016) and after in tilled and no till plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Collembola individuals (Figure 37a) in the w-shaped walk sample in September was 35.6; this significantly decreased in November (t = 3.51, df = 14.723, p-

value = 0.003209) in tilled plots soil core samples to 3.1 individuals, but showed a non-

significant (t = -0.15, df = 19.29, p-value = 0.8822) decrease in no till plots to 34.8 individuals. In May mean abundance of total Collembola individuals significantly increased in tilled plots (t = -7.94, df = 14.231, p-value = 1.345e-06) to 86.1 individuals and in no till plots (t = -2.79, df = 26.75, p-value = 0.009528) to 109.1 individuals; these levels were not significantly different from each other (F (1,28) = 0.345 p-value = 0.562).

Mean species richness of total Collembola individuals (Figure 37b) in the w-shaped walk sample in September was 4.4 species; this significantly decreased in November (t = 5.85, df = 27.554, p-value = 2.896e-06) in tilled plots soil core samples to 1.5 species, but showed a non-significant (t = 1.20, df = 24.071, p-value = 0.2412) decrease in no till plots to 3.5 species. In May mean abundance of total mesofauna individuals significantly increased in tilled plots (t = -11.56, df = 27.845, p-value = 3.862e-12) to 7.4 species and in no till plots (t = -7.56, df = 27.943, p-value = 3.149e-08) to 7.3 species; these levels were not significantly different from each other (F (1,28) = 0.018 p-value = 0.893).

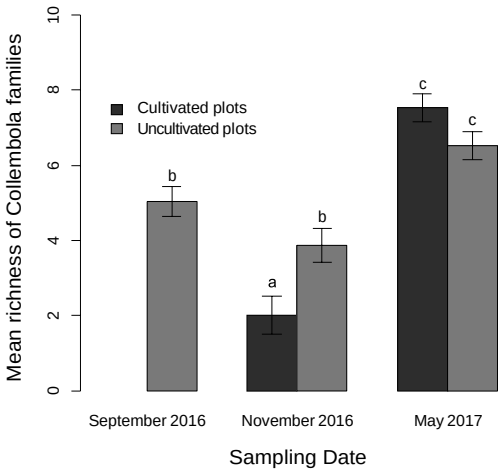

Figure 38 Mean richness of Collembola families before tillage (September 2016) and after in tilled and no till plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean taxonomic family richness of total Collembola individuals (Figure 38) in the w-shaped walk sample in September was 5.0 families; this significantly decreased in November (t = 4.89, df = 27.987, p-value = 3.796e-05) in tilled plots soil core samples to 2.0 families, but showed a non-significant (t = 2.05, df = 25.49, p-value = 0.0504) decrease in no till plots to 3.9 families. In May taxonomic family richness of total Collembola individuals significantly increased in tilled plots (t = -8.87, df = 25.379, p-value = 2.99e-09) to 7.5 families and in no till plots (t = -4.51, df = 27.019, p-value = 0.0001139) to 6.5 families and these levels were not significantly different from each other (F (1,28) = 3.654 p-value = 0.0662).

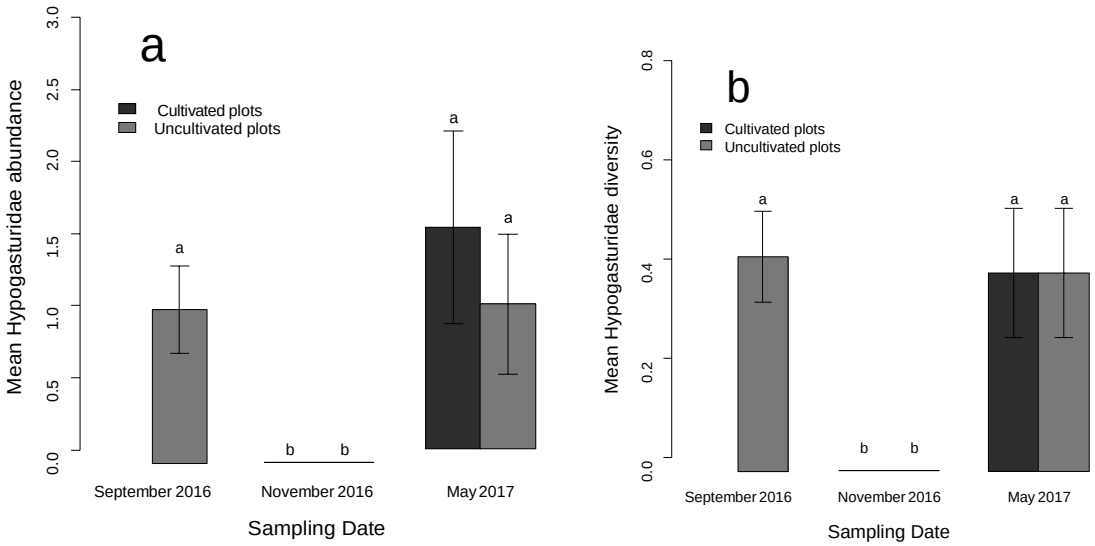

Figure 39 Mean abundance (a) and species diversity (b) of Hypogasturidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Hypogasturidae individuals (Figure 39a) in the w-shaped walk sample in September was 1.1; this significantly decreased in November in tilled plots (t = 2.35, df = 14, p-value = 0.03391) soil core samples to 0 and in no till plots (t = 2.61, df = 14, p-value = 0.02073) to 0. In May mean abundance of total Hypogasturidae individuals increased in tilled plots (t = -2.29, df = 14, p-value = 0.0377) to 1.5 but notno till plots (t = -2.05, df = 14, p-value = 0.05965) to 1; these levels were not significantly different from each other (F (1,28) = 0.416 p-value = 0.524) or from those in September in the tilled (t = -0.42 df = 23.449, p-value = 0.6758) or no till (t = 0.57, df = 27.993, p-value = 0.5698) plots.

Mean species richness of total Hypogasturidae individuals (Figure 39b) in the w-shaped walk sample in September was 0.4 species; this significantly decreased in November in tilled plots (t = 3.5, df = 14, p-value = 0.003535) to 0, and in no till plots (t = 3.06, df = 14, p-value = 0.008564) to 0. In May species richness of total Hypogasturidae individuals significantly increased in tilled plots (t = -3.06, df = 14, p-value = 0.008564) to 0.4 species and in no till plots (t = -3.06, df = 14, p-value = 0.008564) to 0.4 species; these levels were not significantly different from each other (F (1,28) = 0 p-value = 1) or from those in September in the tilled (t = 0.36, df = 27.991, p-value = 0.724) or no till (t = -0.37, df = 27.959, p-value = 0.7165) plots.

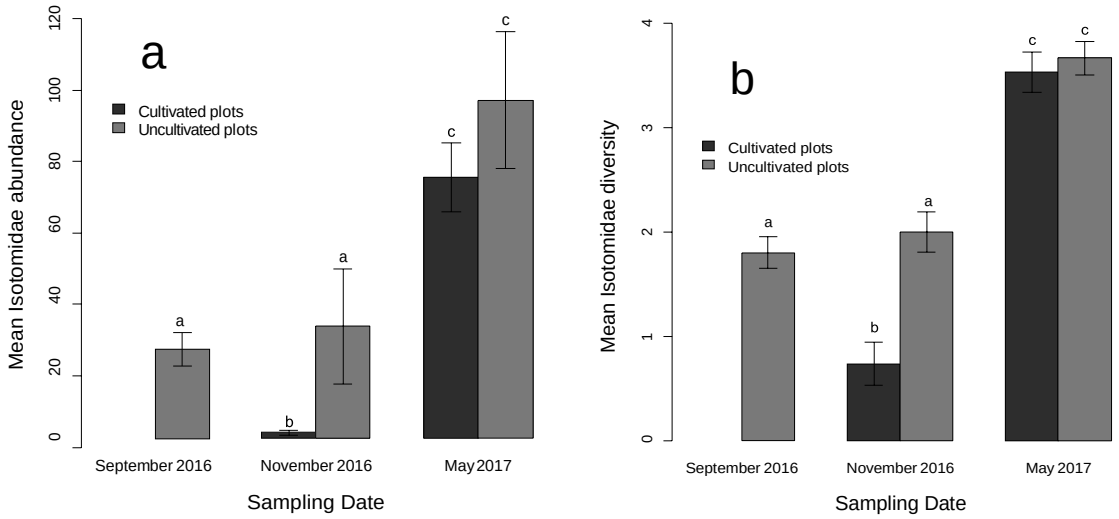

Figure 40 Mean abundance (a) and species diversity (b) of Isotomidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Isotomidae individuals (Figure 40a) in the w-shaped walk sample in September was 25.0; this significantly decreased in November in tilled plots (t = 3.28, df = 14.222, p-value = 0.005381) soil core samples to 1.5 and increased but not significantly in no till plots (t = -0.59, df = 16.746, p-value = 0.5614) to 31.2. In May mean abundance of total Isotomidae individuals significantly increased in tilled plots (t = -7.38, df = 14.145, p-value = 3.273e-06) to 72.9 and in no till plots (t = -2.54, df = 27.236, p-value = 0.01716) to 94.5; these levels were not significantly different from each other (F (1,28) = 0.416 p-value = 0.524). Isotomidae were the most abundant Collembola family recorded in the study.

Mean species richness of total Isotomidae individuals (Figure 40b) in the w-shaped walk sample in September was 1.8 species; this significantly decreased in November in tilled plots (t = 4.75, df = 26.96, p-value = 5.984e-05) to 0.7, and increased but not significantly in no till plots (t = -1.25, df = 26.237, p-value = 0.2233) to 2. In May species richness of total Isotomidae individuals significantly increased in tilled plots (t = -6.61, df = 26.923, p- value = 4.325e-07) to 3.5 species and in no till plots (t = -6.61, df = 26.923, p-value = 4.325e-07) to 3.7 species; these levels were not significantly different from each other (F (1,28) = 0.416 p-value = 0.524).

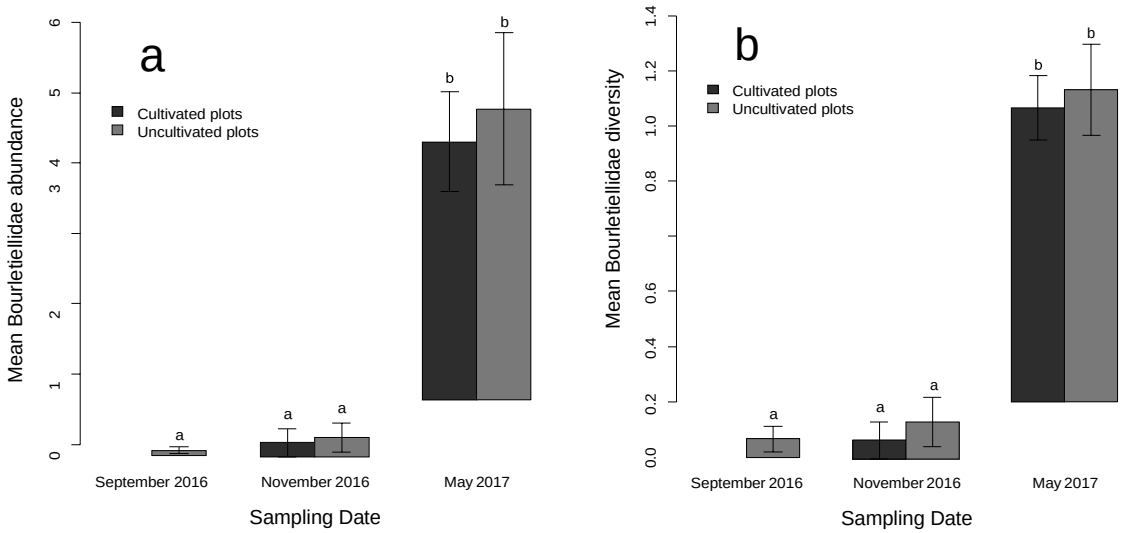

Figure 41 Mean abundance (a) and species diversity (b) of Bourletiellidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Bourletiellidae individuals (Figure 41a) in the w-shaped walk sample in September was 0.1; this increased but not significantly in November in tilled plots (t = -0.63, df = 17.073, p-value = 0.5355) soil core samples to 0.2 and in no till plots (t = -0.92, df = 16.894, p-value = 0.3692) to 0.3. In May mean abundance of total Bourletiellidae individuals significantly increased in tilled plots (t = -4.67, df = 16.178, p-value = 0.0002492) to 3.7 and in no till plots (t = -3.52, df = 15.025, p-value = 0.003055) to 4.1; these levels were not significantly different from each other (F (1,28) = 0.13 p-value = 0.721).

Mean species richness of total Bourletiellidae individuals (Figure 41b) in the w-shaped walk sample in September was 0.1 species; this remained constant in November in tilled plots (t = 0, df = 28, p-value = 1) at 0.1, and in no till plots (t = -0.5916, df = 25.688, p-value = 0.5593) at 0.1. In May species richness of total Bourletiellidae individuals significantly increased in tilled plots (t = -7.34, df = 22.09, p-value = 2.187e-07) to 1.1 species and in no till plots (t = -5.30, df = 21.756, p-value = 2.627e-05) to 1.1 species; these levels were not significantly different from each other (F (1,28) = 0.108 p-value = 0.745).

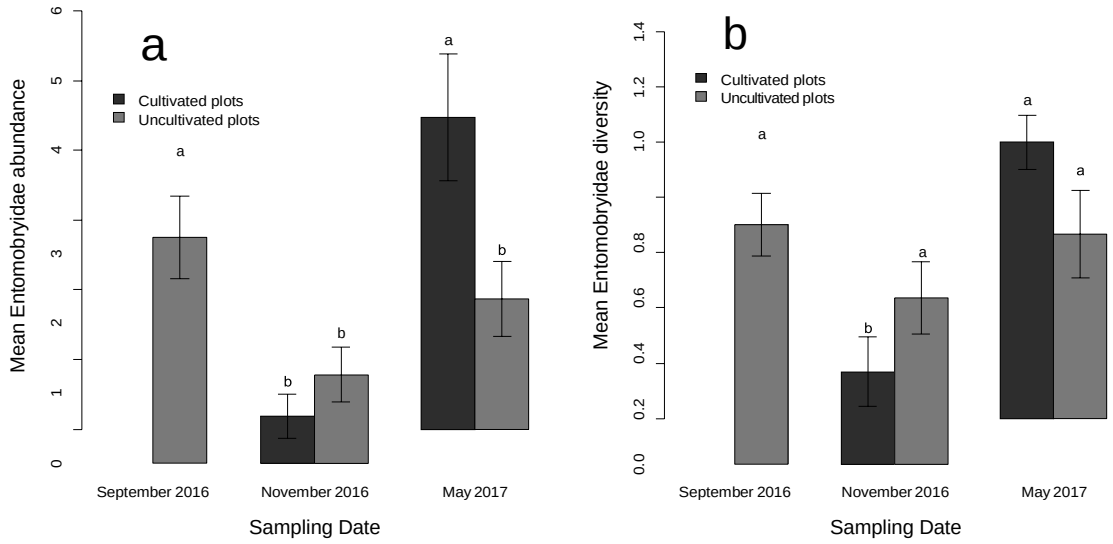

Figure 42 Mean abundance (a) and species diversity (b) of Entomobryidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Entomobryidae individuals (Figure 42a) in the w-shaped walk sample in September was 3.2; this significantly decreased in November in tilled plots (t = 3.14, df = 17.633, p-value = 0.005734) soil core samples to 0.6 and in no till plots (t = 2.84, df = 21.285, p-value = 0.009786) to 1.2 and these levels were not significantly different from each other (F (1,28) = 1.393, p-value = 0.248) In May mean abundance of total Entomobryidae individuals significantly increased in tilled plots (t = -3.94, df = 17.387, p-value = 0.001011) to 4.5 and in increased but not significantly in no till plots (t = -0.90, df = 25.839, p-value = 0.3747) to 1.9; these levels were not significantly different from each other (F (1,28) = 1.393 p-value 0.248) or from levels in September in tilled plots (t = -1.05, df = 27.975, p-value = 0.3019) but were significantly different to those in September no till plots (t = -1.05, df = 27.975, p-value = 0.3019).

Mean species richness of total Entomobryidae individuals (Figure 42b) in the w-shaped walk sample in September was 0.9 species; this significantly decreased in November in tilled plots (t = 2.17, df = 25.471, p-value = 0.03973) to 0.3, and decreased but not significantly in no till plots (t = 1.43, df = 27.991, p-value = 0.1646) to 0.6 and these levels were not significantly different from each other (F (1,28) = 2.154, p = 0.153). In May species richness of total Entomobryidae individuals significantly increased in tilled plots (t = -4.18, df = 26.353, p-value = 0.0002831) to 1.0 species and increased but not significantly in no till plots (t = -0.32, df = 26.984, p-value = 0.749) to 0.7 species; these levels were not significantly different from each other (F (1,28) = 3.182 p-value = 0.0853).

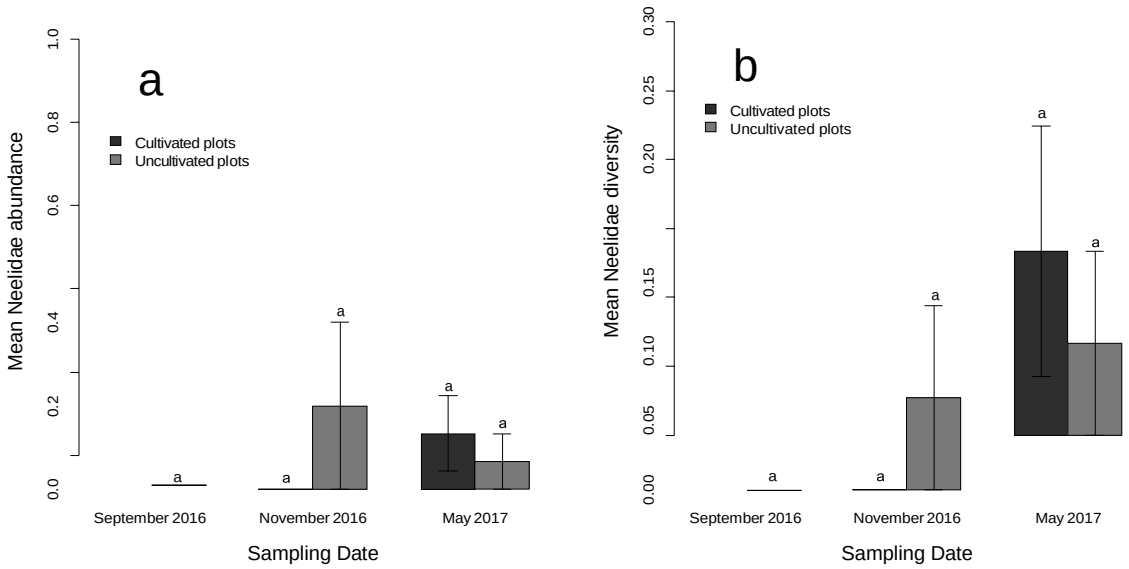

Figure 43 Mean abundance (a) and species diversity (b) of Neelidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Neelidae individuals (Figure 43a) in the w-shaped walk sample in September was 0; this did not change in November in tilled plots (t = NaN, df = NaN, p-value = NA) soil core samples and increased but not significantly in no till plots (t = -1, df = 14, p-value = 0.3343) to 0.2 and these levels were not significantly different from each other (F (1,28) = 1 p-value = 0.326). In May mean abundance of total Neelidae individuals increased but not significantly in tilled (t = -1.47, df = 14, p-value = 0.1643) to 0.1 and in no till plots (t = 0.63, df = 17.073, p-value = 0.5355) to 0.1; these levels were not significantly different from each other (F (1,28) = 0.35 p-value = 0.559).

Mean species richness of total Neelidae individuals (Figure 43b) in the w-shaped walk sample in September was 0 species; this stayed constant in November in tilled plots at 0, and increased but not significantly in no till plots (t = -1, df = 14, p-value = 0.3343) to 0 and these levels were not significantly different from each other (F (1,28) = 1, p-value = 0.326). In May species richness of total Neelidae individuals increased but not significantly in tilled plots (t = -1.47, df = 14, p-value = 0.1643) to 0.1 species and in no till plots (t = 0, df = 28, p-value = 1) to 0.1 species; these levels were not significantly different from each other (F (1,28) = 0.35, p-value = 0.559).

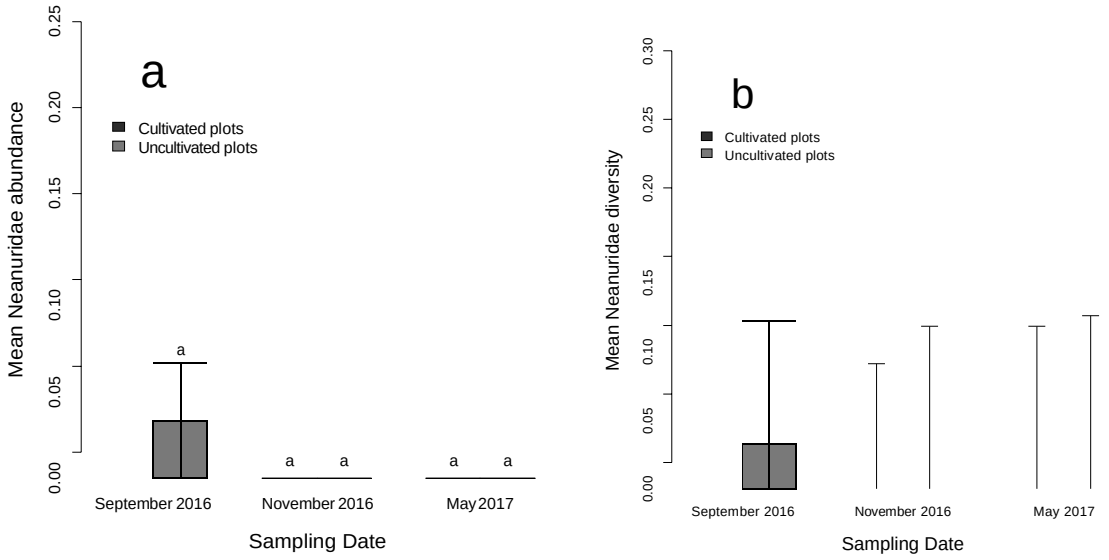

Figure 44 Mean abundance (a) and species diversity (b) of Neanuridae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Neanuridae individuals (Figure 44a) in the w-shaped walk sample in September was 0.03; this decreased to 0 but not significantly in November in both tilled) and no till plots (t = 1, df = 14, p-value = 0.3343). In May mean abundance of total Neanuridae individuals did not change in both in tilled

Mean species richness of total Neanuridae individuals (Figure 44b) in the w-shaped walk sample in September was 0.03 species; this decreased to 0 in November in tilled plots and no till plots (t = -1, df = 14, p-value = 0.3343) to 0. In May species richness of total Neanuridae individuals did not change in both tilled and no till plots (t = -1.47, df = 14, p-value = 0.1643) to 0.1 species and in no till plots (t = 0, df = 28, p-value = 1).

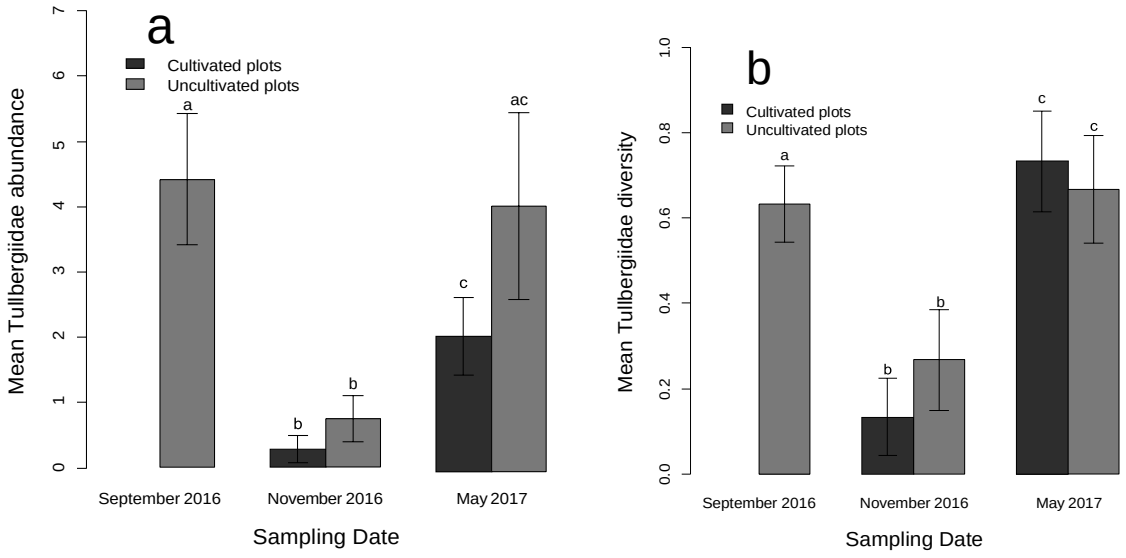

Figure 45 Mean abundance (a) and species diversity (b) of Tullbergiidae before cultivation (September 2016) and after in cultivated and uncultivated plots (November 2016 and May 2017) at Soulton Hall, bars represent ± one standard error.

Mean abundance of total Tullbergiidae individuals (Figure 45a) in the w-shaped walk sample in September was 4.4; this significantly decreased in November in tilled plots (t = 2.99, df = 14.379, p-value = 0.009526) to 0.3 soil core samples and in no till plots (t = 2.40, df = 15.22, p-value = 0.0297) to 0.7 and these levels were not significantly different from each other (F (1,28) = 1.275, p-value 0.268). In May mean abundance of total Tullbergiidae individuals significantly increased in tilled plots (t = -2.84, df = 17.291, p-value = 0.01098) to 2.1 and in no till plots (t = -2.26, df = 15.743, p-value = 0.03856) to 4.1; these levels were not significantly different from each other (F (1,28) = 1.661, p-value = 0.208) but were significantly different to September in tilled plots (t = 2.33, df = 18.252, p-value = 0.03122 and but not in tilled (t = -0.1315, df = 28, p-value = 0.8963).

Mean species richness of total Tullbergiidae individuals (Figure 45b) in the w-shaped walk sample in September was 0.6 species; this significantly decreased in November in tilled plots (t = 2.93, df = 24.944, p-value = 0.007178) to 0.1, and decreased in no till plots (t = 2.79, df = 28, p-value = 0.009332) to 0.3 and these levels were not significantly different from each other (F (1,28) = 0.8, p-value = 0.379). In May species richness of total Tullbergiidae individuals significantly increased in tilled (t = -4.02, df = 26.263, p-value = 0.0004316) to 0.73 species and in no till plots (t = -2.32, df = 27.886, p-value = 0.02816) to 0.1 species; these levels were not significantly different from each other (F (1,28) = 0.149, p-value = 0.702).

4.4 DISCUSSION

Overall mesofauna and Collembola abundance and diversity median numbers showed seasonal changes. Numbers declined between September and November and then increased in May to higher numbers than in September, this follows early summer Collembola peaks recorded in other environments by (Anu, Sabu & Vineesh, 2009), but is in contrast to Kanal (2004) and Gudleifsson & Jarnadottir (2008) who found peaks in late summer.

Tillage significantly reduced mean abundance and order richness of soil mesofauna and Collembola in the first month after treatment. This agrees with studies by (House, 1985; Chang *et al.*, 2013; Miyazawa *et al.*, 2002; van Capelle, Schrader & Brunotte, 2012; Kladivko, 2001) but is in contrast with (van Capelle, Schrader & Brunotte, 2012) who found increases in Collembola with tillage, (Manetti *et al.*, 2010) who found no changes, and with (Brennan, Fortune & Bolger, 2006) who found decreases in Collembola abundance but not species richness.

Mean abundance and order richness of Mesofauna and mean abundance, family and species richness of Collembola recovered in tillage treated plots 6 months after treatments, as found by (Loring, Snider & Robertson, 1981) who recorded stable populations in no till treated areas compared with tilled. Other studies however have shown that effects of tillage can remain for several years (Crotty *et al.*, 2016b; Hirsch *et al.*, 2016).

Collembola families living on the soil surface (epedaphic) were unaffected by tillage treatments. These organisms are more mobile than those deeper in soil, with larger jumping organs (furcula), they are often brightly coloured and have many eyes (Hopkin, 1997). Hypogasturidae decreased in both till and no till in November and recovered in May. Bourletiellidae were unchanged by tillage in November and then increased in May in both plot types.

Collembola families living in the top layer of the soil and the soil surface (hemiedaphic) are intermediate between epedaphic and euedaphic lifeforms (Hopkin, 1997). They respond to tillage in different ways: the Isotomidae decreased in tilled plots in November and recovered in May to the same level as in no till plots, the Entomobryidae decreased both in till and no till plots in November following the overall seasonal trend and then increased by May to higher numbers in tilled plots than no till plots, the Neanuridae decreased in November and then did not recover in May in both till and no till plots.

Collembola families living deeper in the soil (euedaphic) are adapted to this niche with small body sizes and small or no furcula so as to manoeuvre through limited soil space, few or no eyes and pale colourless body colour as there are lower light levels (Hopkin, 2007). We would expect these groups to be most affected by tillage as they have limited dispersal

ability and their habitat is disturbed the most. The Neelidae however did not significantly change over the study period, though it maybe the low numbers recorded meant that tillage effect comparisons were not possible. The Tullbergiidae decreased in November in both tilled and no till plots and then recovered in May to September levels.

Soil physical and chemical properties, as well as soil organisms (Kibblewhite, Ritz & Swift, 2008), would have informed us of the mechanisms of the tillage effects seen in this study. Soil bulk density is directly related to tillage with past studies recording higher bulk densities in no till systems than conventional (Osunbitan, Oyedele & Adekalu, 2005). We would expect soil mesofauna abundance and order diversity to be positively related to bulk density as there is more soil pore space and diversity of pore sizes for fauna to inhabit (Larsen, Schjønning & Axelsen, 2004). No till systems are also recorded to have higher soil organic matter levels and soil stratification than conventional systems (House, 1985; Stinner & House, 1990), and this information would show forage available for detritivorous soil mesofauna such as Collembola (Beare *et al.*, 1992). Soil moisture and temperature levels affect soil mesofauna, particularly Collembola which are prone to desiccation (Petersen & Luxton, 1982a), this data might help us see potential interactions of tillage and climate.

Plots were arranged along the length of Nursery field at Soulton Hall for ease of establishment and 'real world' effect. A grid of plots, with treatments carried out at random would have reduced potential bias in the soil changes across the field, from the edge of the road to neighbouring fields.

Epedaphic Collembola respond to habitat architecture and heterogeneity (Alvarez, Frampton & Goulson, 1997). This study sampled in the centre metre of 3m wide plots but sampling and analysis that takes into account plot edge effects might show how no till systems interact with field margins compared with conventional.

GENERAL DISCUSSION

Soils have more biodiversity per unit than in any aboveground ecosystem (Brussaard, 1997) and provide vital ecosystem services such as decomposition and nutrient cycling (de Vries *et al.*, 2013; Wagg *et al.*, 2014). Whilst there is however, extensive historic literature on soil chemistry and physics, soil biology has been understudied and many faunal groups remain elusive to science, in part because of their small size but also because of few economic valuations of soil biodiversity, which might drive energies towards studies. Recently Pascual *et al* (2015) summarised the links between soil biodiversity value and ecosystem services, they highlighted that may of the services are involved in regulating and supporting processes, and that there may be shared benefit from a service even if generated locally.

Community building organisations such as the Global Soil Biodiversity Initiative in 2011 and UK efforts such as the Soil Biology Group of the Association of Applied Biologists in 2016, aim to connect researchers, practitioners and policy makers working with soil biodiversity. This is important as multidisciplinary studies are needed to tackle a question from many angles and to also encompass different motives of researchers and practitioners. Ecologists might focus on biodiversity measures, ecosystem functioning and landscape connectivity; farmers however, would consider the cost benefits of agricultural interventions and inputs in relation to crop quality and yield. In the Soulton Hall tillage study the landowner's focus was not the soil fauna recorded, but on the cost of carrying out tillage in relation to crop yield (e.g. kilo weight) and grain quality (e.g. Hagberg falling number) from different plot treatments, which did not in fact significantly differ between tilled and no-till plots.

The studies presented in this thesis contribute to knowledge on Collembola and the wider mesofauna biology in agroecosystems. Abundance and diversity of mesofauna and specific groups of Collembola responded in different ways to a range of different management systems and experimental traffic and tillage treatments at Harper Adams University and tillage treatments at Soulton Hall. Further mesofauna sampling and more environmental data could improve these studies to clarify the mechanisms of agricultural management and intervention effects.

Agricultural traffic and tillage experiments need to be replicated across different soil types and climates, to fully understand the positives and negatives of these strategies for sustainable soil management. In areas where there are soil fungal pathogens, no till systems can cause these to increase (Sharma-Poudyal *et al.*, 2017), as fungal hyphae are not broken up by the action of a plough. The traffic and tillage experiment at Harper Adams University, is currently being partially replicated at a site in Zambia, with the same random

and controlled traffic and low ground pressure treatments, but instead with three tillage techniques commonly used in Zambia.

Specimen identification using (Hopkin, 2007) produced new biological records of Collembola species on the sites studied in this thesis, and species were newly recorded in the region of the UK surveyed. The high abundances of Acari recorded across the studies, highlight this mesofauna group as another avenue for mesofauna research. The unresolved Acari taxonomy and lack of reliable comprehensive identification resources is however a challenge, although dichotomous keys are currently being developed (Shepherd & Crotty, 2015). Surveys of organisms such as predatory Carabid and Staphylinid beetles, spiders, and different fungal groups, which sit at the trophic levels above and below mesofauna and to which mesofauna provide a crucial link in the soil food web, would provide further information on both bottom up or top down pressures on soil biodiversity in agroecosystems (Buchkowski, 2016).

An investigation into variation of species traits along a management intensity gradient, such as change in Collembola body length, furcula length, number of eyes and number of fused body segments, in individuals from fields under different management regimes, had been an aim of this thesis, using specimens drawn from the three other studies and specimens from elsewhere from the UK. Farska *et al.* (2013) found increasing numbers of Collembola with increasing management intensity in a forest ecosystem and Hedde *et al.* (2012) found that soil invertebrate traits described a soil disturbance of pollution better than density or diversity of the community. Salmon *et al.* (2014) looked at Collembola species traits in sites across Europe and found species with epedaphic traits in more open habitats and those with euedaphic in woodland and forest habitats.

Several of the studies presented here found seasonal effects on mesofauna. With global change altered phenology of seasons and extreme weather events areexpected; this presents another avenue for future research of soil biodiversity, particularly on interactions with human land use and manipulation (Smith *et al.*, 2015). A number of studies have found range shifts of organisms in response to changing climatic envelopes (Hickling *et al.*, 2006). These were however, on highly dispersive mobile species with an extensive biological record history gathered from professional and amateur natural historians. Accurate distribution maps for soil invertebrates are largely unavailable, even for many of the well-known groups such as earthworms. Manipulative controlled environment experiments and/or replicated experiments in different global climates can provide data for use in modelling the responses of soil fauna to different climate scenarios (Wall *et al.*, 2008).

Standardisation of soil biology sampling is crucial for providing comparable data. The EcoFINDERS project established techniques for monitoring soil biodiversity and ecosystem functioning using indicator species and groups across Europe (Stone *et al.*, 2016), this can

provide data on baseline ecosystem health for use in future soil policy frameworks (Römbke *et al.*, 2016). Molecular biology techniques are decreasing in cost and some methods can provide information on species presence and abundance (Orgiazzi *et al.*, 2015), as well as actual trophic links between species via gut content analysis (Morriën, 2016) and soil functioning via active enzymes (Caldwell, 2005). In relation to the studies in this thesis, a UK database of Collembola COI barcodes is in development and specimens from these studies have been contributed to this (Shaw & Benefer, 2015). Researchers in Japan are also developing similar methods (Saitoh, Fujii & Takeda, 2013).

Precision farming technologies will revolutionise soil biodiversity and environmental sampling and monitoring. Automated environmental data measuring is now possible with remote temperature and soil moisture sensors embedded in a habitat whilst communicating with data servers. Kits to sequence in DNA in the field are already on the market and robotic tillage, seed sowing and crop harvesting technologies are in development. Perhaps the farm of the future will have autonomous vehicles regularly sampling soil, identifying the life within it and monitoring agroecosystem management effects.

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APPENDIX A

Tillage plot progress at Soulton Hall.

Figure 46 Nursery Field on 21 September 2016 before tillage treatments

Figure 47 Plot tillage treatments visible on September 24 2016, looking across the field plot 1 is on the far right.

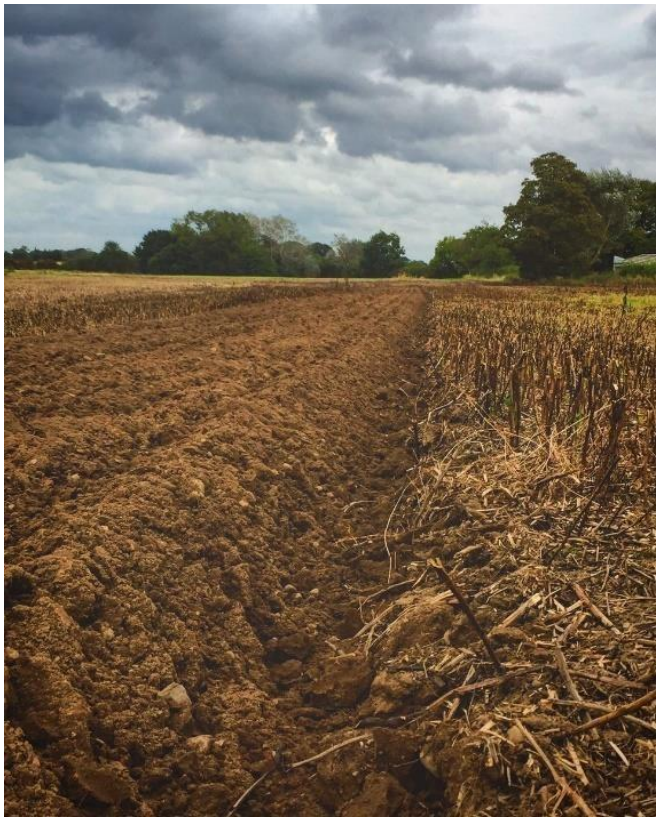

Figure 48 Edge of Plot 1 with tilled treatment after plot establishment on 24 September 2016

Figure 49 Crop plant growth on 21 October 2016, looking along length of the field with plot 1 on the far left.

Figure 50 No till plot on 23 March 2017

Figure 51 Till plot on 23 March 2017


Figure 52 Till plots on 16 May 2017


Figure 53 No till plots on 16 May 2017

Figure 54 Nursery field on 7 September 2017, with volunteer plants after harvest on 24 August 2017

APPENDIX B

Raw data chapter2

Raw data chapter3

SAMPLE	DATE	BLOCK	TRAFFIC T	TILLAGE T	COMBINE	TOTAL AB	ORDER DI	ACARI	ANNELID	APHID	ARANEAE	COLEOPTE	CARABID	COLEOPTE	OTHER CO	STAPHYLI	NEMATOD	DIPTERA L	DIPLOPOD	DIPLOPOD	DIPLOPOD	SYMPHYLA
Block1CTF	01-Jun-17	Block1	CTF	Zero	CTFZero	131	4	36	0	0	0	2	0	0	0	2	0	0	0	0	0	0
Block1CTF	01-Jun-17	Block1	CTF	Shallow	CTFShallo	127	2	47	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1CTF	01-Jun-17	Block1	CTF	Deep	CTFDeep	93	4	37	0	0	0	2	1	1	0	0	0	0	0	0	0	0
Block1LGP	01-Jun-17	Block1	LGP	Zero	LGPZero	108	5	45	0	0	0	1	0	1	0	0	1	0	1	1	0	0
Block1LGP	01-Jun-17	Block1	LGP	Shallow	LGPShallo	266	6	92	0	0	2	1	0	1	0	0	0	1	0	0	0	0
Block1LGP	01-Jun-17	Block1	LGP	Deep	LGPDeep	113	3	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1RTF	01-Jun-17	Block1	RTF	Zero	RTFZero	20	3	5	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Block1RTF	01-Jun-17	Block1	RTF	Shallow	RTFShallo	188	2	85	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1RTF	01-Jun-17	Block1	RTF	Deep	RTFDeep	98	3	29	0	0	0	3	0	2	0	1	0	0	0	0	0	0
Block2CTF	01-Jun-17	Block2	CTF	Zero	CTFZero	171	4	47	0	0	0	3	0	3	0	0	1	0	0	0	0	0
Block2CTF	01-Jun-17	Block2	CTF	Shallow	CTFShallo	92	4	27	0	0	0	1	0	0	0	1	0	0	0	0	0	0
Block2CTF	01-Jun-17	Block2	CTF	Deep	CTFDeep	61	4	19	0	0	0	0	0	0	0	0	0	0	2	1	1	0
Block2LGP	01-Jun-17	Block2	LGP	Zero	LGPZero	99	3	28	0	0	0	3	0	3	0	0	0	0	0	0	0	0
Block2LGP	01-Jun-17	Block2	LGP	Shallow	LGPShallo	139	3	16	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block2LGP	01-Jun-17	Block2	LGP	Deep	LGPDeep	262	4	90	0	0	1	4	0	3	0	1	0	0	0	0	0	0
Block2RTF	01-Jun-17	Block2	RTF	Zero	RTFZero	168	4	34	0	0	1	1	0	1	0	0	0	0	0	0	0	0
Block2RTF	01-Jun-17	Block2	RTF	Shallow	RTFShallo	61	3	17	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2RTF	01-Jun-17	Block2	RTF	Deep	RTFDeep	131	4	18	0	0	0	0	0	0	0	0	0	0	2	2	0	0
Block3CTF	01-Jun-17	Block3	CTF	Zero	CTFZero	160	3	48	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block3CTF	01-Jun-17	Block3	CTF	Shallow	CTFShallo	108	2	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block3CTF	01-Jun-17	Block3	CTF	Deep	CTFDeep	213	6	98	1	0	0	0	0	0	0	0	0	3	1	0	1	0
Block3LGP	01-Jun-17	Block3	LGP	Zero	LGPZero	105	5	46	0	0	0	2	0	2	0	0	0	1	1	1	0	0
Block3LGP	01-Jun-17	Block3	LGP	Shallow	LGPShallo	112	3	39	0	0	0	2	0	1	0	1	0	0	0	0	0	0
Block3LGP	01-Jun-17	Block3	LGP	Deep	LGPDeep	184	3	51	0	0	0	2	1	1	0	0	0	0	0	0	0	0
Block3RFT	01-Jun-17	Block3	RTF	Zero	RTFZero	143	4	23	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block3RTF	01-Jun-17	Block3	RTF	Shallow	RTFShallo	111	4	48	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Block3RTF	01-Jun-17	Block3	RTF	Deep	RTFDeep	106	3	37	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Block4CTF	01-Jun-17	Block4	CTF	Zero	CTFZero	94	4	42	0	0	0	1	0	1	0	0	1	0	0	0	0	0
Block4CTF	01-Jun-17	Block4	CTF	Shallow	CTFShallo	169	4	93	0	0	0	0	0	0	0	0	0	1	27	26	1	0
Block4CTF	01-Jun-17	Block4	CTF	Deep	CTFDeep	181	5	44	0	0	0	1	0	1	0	0	1	1	0	0	0	0
Block4LGP	01-Jun-17	Block4	LGP	Zero	LGPZero	68	4	14	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Block4LGP	01-Jun-17	Block4	LGP	Shallow	LGPShallo	155	2	53	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block4LGP	01-Jun-17	Block4	LGP	Deep	LGPDeep	59	3	22	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Block4RTF	01-Jun-17	Block4	RTF	Zero	RTFZero	57	4	20	1	0	0	1	0	1	0	0	0	0	0	0	0	0
Block4RTF	01-Jun-17	Block4	RTF	Shallow	RTFShallo	146	5	20	1	0	0	2	0	2	0	0	0	0	0	0	0	0
Block4RTF	01-Jun-17	Block4	RTF	Deep	RTFDeep	236	5	94	0	0	0	1	0	1	0	0	1	0	0	0	0	0
Block1CTF	02-Jul-17	Block1	CTF	Zero	CTFZero	74	4	29	0	0	0	5	1	3	0	1	0	5	0	0	0	0
Block1CTF	02-Jul-17	Block1	CTF	Shallow	CTFShallo	63	4	29	1	0	0	1	0	1	0	0	0	0	0	0	0	0
Block1CTF	02-Jul-17	Block1	CTF	Deep	CTFDeep	60	6	23	1	0	1	1	1	0	0	0	0	0	1	1	0	0
Block1LGP	02-Jul-17	Block1	LGP	Zero	LGPZero	38	4	14	0	0	0	2	2	0	0	0	0	1	0	0	0	0
Block1LGP	02-Jul-17	Block1	LGP	Shallow	LGPShallo	16	2	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1LGP	02-Jul-17	Block1	LGP	Deep	LGPDeep	44	4	10	0	0	0	1	1	0	0	0	0	0	1	0	1	0
Block1RTF	02-Jul-17	Block1	RTF	Zero	RTFZero	24	4	4	0	0	0	2	2	0	0	0	1	0	0	0	0	0
Block1RTF	02-Jul-17	Block1	RTF	Shallow	RTFShallo	81	2	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1RTF	02-Jul-17	Block1	RTF	Deep	RTFDeep	59	3	10	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Block2CTF	02-Jul-17	Block2	CTF	Zero	CTFZero	65	4	17	1	0	0	1	0	0	0	1	0	0	0	0	0	0
Block2CTF	02-Jul-17	Block2	CTF	Shallow	CTFShallo	31	3	10	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block2CTF	02-Jul-17	Block2	CTF	Deep	CTFDeep	71	3	16	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Block2LGP	02-Jul-17	Block2	LGP	Zero	LGPZero	36	3	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2LGP	02-Jul-17	Block2	LGP	Shallow	LGPShallo	16	2	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2LGP	02-Jul-17	Block2	LGP	Deep	LGPDeep	40	4	13	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Block2RTF	02-Jul-17	Block2	RTF	Zero	RTFZero	29	4	12	0	0	1	1	0	1	0	0	0	0	0	0	0	0
Block2RTF	02-Jul-17	Block2	RTF	Shallow	RTFShallo	58	4	29	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block2RTF	02-Jul-17	Block2	RTF	Deep	RTFDeep	63	6	19	1	0	1	1	0	1	0	0	0	1	0	0	0	0
Block3CTF	02-Jul-17	Block3	CTF	Zero	CTFZero	102	5	42	1	2	0	1	0	0	0	1	0	0	0	0	0	0
Block3CTF	02-Jul-17	Block3	CTF	Shallow	CTFShallo	77	3	14	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block3CTF	02-Jul-17	Block3	CTF	Deep	CTFDeep	62	4	23	0	0	0	1	0	0	0	1	0	0	3	0	3	0
Block3LGP	02-Jul-17	Block3	LGP	Zero	LGPZero	28	3	23	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block3LGP	02-Jul-17	Block3	LGP	Shallow	LGPShallo	35	3	9	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Block3LGP	02-Jul-17	Block3	LGP	Deep	LGPDeep	103	4	27	0	0	0	16	0	16	0	0	0	0	2	0	2	0
Block3RTF	02-Jul-17	Block3	RTF	Zero	RTFZero	46	5	9	1	0	0	2	0	1	0	1	0	0	0	0	0	0
Block3RTF	02-Jul-17	Block3	RTF	Shallow	RTFShallo	24	3	10	0	0	0	0	0	0	0	0	0	0	1	0	1	0
Block3RTF	02-Jul-17	Block3	RTF	Deep	RTFDeep	43	3	22	0	0	0	2	0	0	0	2	0	0	0	0	0	0
Block4CTF	02-Jul-17	Block4	CTF	Zero	CTFZero	80	3	30	0	0	0	0	0	0	0	0	0	0	2	2	0	0
Block4CTF	02-Jul-17	Block4	CTF	Shallow	CTFShallo	100	5	63	0	0	0	0	0	0	0	0	2	1	2	0	2	0
Block4CTF	02-Jul-17	Block4	CTF	Deep	CTFDeep	41	4	12	1	0	0	0	0	0	0	0	0	2	0	0	0	0
Block4LGP	02-Jul-17	Block4	LGP	Zero	LGPZero	8	3	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Block4LGP	02-Jul-17	Block4	LGP	Shallow	LGPShallo	58	5	33	1	0	0	1	1	0	0	0	1	0	0	0	0	0
Block4LGP	02-Jul-17	Block4	LGP	Deep	LGPDeep	101	4	36	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Block4RTF	02-Jul-17	Block4	RTF	Zero	RTFZero	39	3	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Block4RTF	02-Jul-17	Block4	RTF	Shallow	RTFShallo	36	5	10	0	0	0	1	1	0	0	0	0	2	2	0	2	0
Block4RTF	02-Jul-17	Block4	RTF	Deep	RTFDeep	35	3	4	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Block1CTF	########	Block1	CTF	Zero	CTFZero	16	2	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1CTF	########	Block1	CTF	Shallow	CTFShallo	33	3	8	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block1CTF	########	Block1	CTF	Deep	CTFDeep	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1LGP	########	Block1	LGP	Zero	LGPZero	8	4	1	1	0	0	0	0	0	0	0	5	0	0	0	0	0
Block1LGP	########	Block1	LGP	Shallow	LGPShallo	17	3	9	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block1LGP	########	Block1	LGP	Deep	LGPDeep	111	4	80	0	1	0	0	0	0	0	0	0	1	0	0	0	0
Block1RTF	########	Block1	RTF	Zero	RTFZero	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block1RTF	########	Block1	RTF	Shallow	RTFShallo	33	4	13	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Block1RTF	########	Block1	RTF	Deep	RTFDeep	60	4	18	0	0	0	1	0	1	0	0	0	1	0	0	0	0
Block2CTF	########	Block2	CTF	Zero	CTFZero	33	2	21	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2CTF	########	Block2	CTF	Shallow	CTFShallo	39	3	16	0	0	0	2	0	2	0	0	0	0	0	0	0	0
Block2CTF	########	Block2	CTF	Deep	CTFDeep	84	4	25	2	0	0	1	0	1	0	0	0	0	0	0	0	0
Block2LGP	########	Block2	LGP	Zero	LGPZero	132	2	117	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2LGP	########	Block2	LGP	Shallow	LGPShallo	97	3	50	0	0	0	3	0	2	0	1	0	0	0	0	0	0
Block2LGP	########	Block2	LGP	Deep	LGPDeep	48	2	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block2RTF	########	Block2	RTF	Zero	RTFZero	63	3	28	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block2RTF	########	Block2	RTF	Shallow	RTFShallo	47	4	21	0	0	0	1	0	1	0	0	0	1	0	0	0	0
Block2RTF	########	Block2	RTF	Deep	RTFDeep	125	2	109	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block3CTF	########	Block3	CTF	Zero	CTFZero	28	2	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block3CTF	########	Block3	CTF	Shallow	CTFShallo	39	4	14	0	0	0	1	0	1	0	0	0	0	2	0	2	0
Block3CTF	########	Block3	CTF	Deep	CTFDeep	29	4	17	0	0	0	1	1	0	0	0	0	0	1	0	1	0
Block3LGP	########	Block3	LGP	Zero	LGPZero	35	4	17	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Block3LGP	########	Block3	LGP	Shallow	LGPShallo	49	5	32	0	0	0	2	0	2	0	0	0	2	0	0	0	0
Block3LGP	########	Block3	LGP	Deep	LGPDeep	49	3	22	0	0	0	0	0	0	0	0	0	0	2	0	2	0
Block3RTF	########	Block3	RTF	Zero	RTFZero	15	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Block3RTF	########	Block3	RTF	Shallow	RTFShallo	139	6	109	2	0	0	0	0	0	0	0	0	1	1	0	1	0
Block3RTF	########	Block3	RTF	Deep	RTFDeep	73	4	45	0	0	0	0	0	0	0	0	0	2	1	0	1	0
Block4CTF	########	Block4	CTF	Zero	CTFZero	63	2	35	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block4CTF	########	Block4	CTF	Shallow	CTFShallo	146	4	112	0	0	0	0	0	0	0	0	0	3	0	0	0	0
Block4CTF	########	Block4	CTF	Deep	CTFDeep	145	5	87	0	0	0	1	0	1	0	0	1	2	0	0	0	0
Block4LGP	########	Block4	LGP	Zero	LGPZero	12	2	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Block4LGP	########	Block4	LGP	Shallow	LGPShallo	107	4	53	0	0	0	4	0	4	0	0	0	4	0	0	0	0
Block4LGP	########	Block4	LGP	Deep	LGPDeep	35	4	18	0	0	0	1	0	1	0	0	0	2	0	0	0	0
Block4RTF	########	Block4	RTF	Zero	RTFZero	20	3	11	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Block4RTF	########	Block4	RTF	Shallow	RTFShallo	34	4	14	1	0	0	0	0	0	0	0	1	0	0	0	0	0
Block4RTF	########	Block4	RTF	Deep	RTFDeep	112	4	69	0	0	0	0	0	0	0	0	4	8	0	0	0	0

SAMPLE	DATE	CENTIPED	MOLLUSC	Lepidopte	THYSANO	THYSANO	THYSANO	PSCOCOP	DIPLURA	COLLEMB	COLLEMB	Ceratophy	Cyphoder	Entomobr	Parisotom	Heteroms	Heterosm	Isotoma v	Isotoma a
Block1CTF	01-Jun-17	0	0	0	1	1	0	0	0	88	9	2	1	0	0	1	0	2	14
Block1CTF	01-Jun-17	0	0	0	0	0	0	0	0	80	7	0	0	0	0	1	0	4	53
Block1CTF	01-Jun-17	0	0	0	1	1	0	0	0	49	6	0	0	0	0	0	0	2	27
Block1LGP	01-Jun-17	0	0	0	0	0	0	0	0	58	9	4	1	0	0	0	0	10	13
Block1LGP	01-Jun-17	0	0	1	0	0	0	0	0	167	9	1	1	0	0	0	0	1	84
Block1LGP	01-Jun-17	0	0	2	0	0	0	0	0	103	7	1	2	0	0	0	0	2	31
Block1RTF	01-Jun-17	0	0	0	0	0	0	0	0	14	5	1	0	0	0	2	0	0	8
Block1RTF	01-Jun-17	0	0	0	0	0	0	0	0	103	6	0	2	0	0	0	0	2	43
Block1RTF	01-Jun-17	0	0	0	0	0	0	0	0	60	6	0	0	0	0	1	1	0	35
Block2CTF	01-Jun-17	0	0	0	0	0	0	0	0	114	10	3	0	0	0	0	5	3	37
Block2CTF	01-Jun-17	0	0	1	0	0	0	0	0	61	7	4	1	0	0	0	0	0	15
Block2CTF	01-Jun-17	0	0	0	1	0	1	0	0	39	5	0	1	0	0	0	0	0	18
Block2LGP	01-Jun-17	0	0	0	0	0	0	0	0	62	7	0	0	0	0	0	0	10	33
Block2LGP	01-Jun-17	0	0	0	0	0	0	0	0	120	6	0	2	0	0	0	0	4	99
Block2LGP	01-Jun-17	0	0	0	0	0	0	0	0	159	9	0	1	0	0	0	0	82	7
Block2RTF	01-Jun-17	0	0	0	0	0	0	0	0	130	8	2	0	0	0	0	0	6	93
Block2RTF	01-Jun-17	0	0	0	0	0	0	0	0	43	9	1	1	0	0	0	0	2	15
Block2RTF	01-Jun-17	0	0	1	0	0	0	0	0	110	7	1	0	0	0	0	0	4	32
Block3CTF	01-Jun-17	0	0	0	0	0	0	0	0	111	7	2	0	0	0	0	0	4	73
Block3CTF	01-Jun-17	0	0	0	0	0	0	0	0	81	9	1	1	0	0	1	0	2	25
Block3CTF	01-Jun-17	0	0	0	0	0	0	1	0	109	8	0	3	0	0	0	0	3	57
Block3LGP	01-Jun-17	0	0	0	0	0	0	0	0	51	7	1	0	1	0	0	0	4	21
Block3LGP	01-Jun-17	0	0	0	0	0	0	0	0	67	8	3	0	0	0	0	0	1	39
Block3LGP	01-Jun-17	0	0	0	0	0	0	0	0	127	5	0	0	0	0	0	0	1	69
Block3RFT	01-Jun-17	0	0	0	1	0	1	0	0	116	8	0	1	0	0	0	0	4	89
Block3RTF	01-Jun-17	0	0	1	0	0	0	0	0	61	6	0	0	0	0	0	0	1	50
Block3RTF	01-Jun-17	0	0	0	0	0	0	0	0	68	5	0	0	0	0	0	0	0	28
Block4CTF	01-Jun-17	0	0	0	0	0	0	0	0	48	6	0	0	0	0	1	0	4	18
Block4CTF	01-Jun-17	0	0	0	0	0	0	0	0	48	7	0	0	0	0	0	0	4	14
Block4CTF	01-Jun-17	0	0	0	0	0	0	0	0	132	7	0	2	0	0	2	0	4	41
Block4LGP	01-Jun-17	0	0	0	0	0	0	0	0	52	5	0	0	0	0	1	0	3	25
Block4LGP	01-Jun-17	0	0	0	0	0	0	0	0	102	7	0	0	0	0	3	0	3	50
Block4LGP	01-Jun-17	0	0	0	0	0	0	0	0	36	7	0	1	0	0	0	0	0	12
Block4RTF	01-Jun-17	0	0	0	0	0	0	0	0	33	8	0	0	0	0	1	0	3	10
Block4RTF	01-Jun-17	0	0	0	6	6	0	0	0	113	6	0	0	0	0	0	0	1	73
Block4RTF	01-Jun-17	0	0	0	5	4	1	0	0	133	7	0	0	0	0	0	0	4	51
Block1CTF	02-Jul-17	0	0	0	0	0	0	0	0	25	5	0	2	3	0	1	0	0	7
Block1CTF	02-Jul-17	0	0	0	0	0	0	0	0	30	6	0	0	0	0	1	0	1	5
Block1CTF	02-Jul-17	0	0	0	0	0	0	0	0	31	6	0	2	0	0	0	0	2	2
Block1LGP	02-Jul-17	0	0	0	0	0	0	0	0	17	4	0	0	0	0	1	0	3	0
Block1LGP	02-Jul-17	0	0	0	0	0	0	0	0	8	5	2	0	0	0	0	0	1	1
Block1LGP	02-Jul-17	0	0	0	0	0	0	0	0	30	4	0	0	0	0	0	0	2	2
Block1RTF	02-Jul-17	0	0	0	0	0	0	0	0	13	5	1	1	0	0	0	0	3	0
Block1RTF	02-Jul-17	0	0	0	0	0	0	0	0	57	8	4	0	1	0	0	0	3	2
Block1RTF	02-Jul-17	0	0	0	0	0	0	0	0	46	6	3	0	0	0	0	0	1	5
Block2CTF	02-Jul-17	0	0	0	0	0	0	0	0	44	5	0	0	3	0	0	0	1	2
Block2CTF	02-Jul-17	0	0	0	0	0	0	0	0	18	6	1	0	0	0	0	0	0	4
Block2CTF	02-Jul-17	0	0	0	0	0	0	0	0	54	5	2	0	0	0	0	0	0	0
Block2LGP	02-Jul-17	0	0	0	1	0	1	0	0	27	9	2	1	1	0	0	0	0	3
Block2LGP	02-Jul-17	0	0	0	0	0	0	0	0	12	3	0	0	0	0	0	0	0 1 10 0 1 0 0 0 0 0 0 0 11 2 0 0 1 1 0 0 0 0 0 0 0 0 slug slime	
Block2LGP	02-Jul-17	0	0	0	0	0	0	0	0	25	5	1	0	0	0	0	0	0	9
Block2RTF	02-Jul-17	0	0	0	0	0	0	0	0	13	4	0	0	0	0	0	0	1	0
Block2RTF	02-Jul-17	0	0	0	1	0	1	0	0	27	5	0	0	0	0	0	0	1	4
Block2RTF	02-Jul-17	0	0	0	0	0	0	0	0	38	5	0	4	0	0	0	0	2	0
Block3CTF	02-Jul-17	0	0	0	0	0	0	0	0	54	6	2	3	0	0	0	0	1	3
Block3CTF	02-Jul-17	0	0	0	0	0	0	0	0	60	5	3	1	0	0	0	0	0	0
Block3CTF	02-Jul-17	0	0	0	0	0	0	0	0	33	4	2	0	0	0	0	0	0	0
Block3LGP	02-Jul-17	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0
Block3LGP	02-Jul-17	0	0	0	0	0	0	0	0	23	4	0	0	1	0	0	0	0	0
Block3LGP	02-Jul-17	0	0	0	0	0	0	0	0	26	4	0	2	0	0	0	0	0	6
Block3RTF	02-Jul-17	0	0	0	0	0	0	0	1	29	5	4	0	0	0	0	0	1	1
Block3RTF	02-Jul-17	0	0	0	0	0	0	0	0	13	4	0	2	0	0	0	0	3	4
Block3RTF	02-Jul-17	0	0	0	0	0	0	0	0	15	4	4	0	0	0	0	0	1	0
Block4CTF	02-Jul-17	0	0	0	0	0	0	0	0	48	7	5	2	0	0	0	0	3	0
Block4CTF	02-Jul-17	0	0	0	0	0	0	0	0	32	7	4	1	0	0	0	0	0	2
Block4CTF	02-Jul-17	0	0	0	0	0	0	0	0	26	3	2	0	0	0	0	0	0	0
Block4LGP	02-Jul-17	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0
Block4LGP	02-Jul-17	0	0	0	0	0	0	0	0	20	8	1	3	1	0	0	1	2	3
Block4LGP	02-Jul-17	0	0	0	0	0	0	0	0	63	6	4	4	0	0	0	0	0	7
Block4RTF	02-Jul-17	0	0	0	0	0	0	0	0	27	5	0	0	0	0	0	0	0	1
Block4RTF	02-Jul-17	0	0	0	0	0	0	0	0	19	3	0	0	0	0	0	0	0	1
Block4RTF	02-Jul-17	0	0	0	0	0	0	0	0	29	6	2	2	0	0	0	1	0	0
Block1CTF	########	0	0	0	0	0	0	0	0	8	4	0	0	0	0	0	0	0	2
Block1CTF	########	0	0	0	0	0	0	0	0	24	4	0	0	0	0	0	0	11	0
Block1CTF	########	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
Block1LGP	########	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
Block1LGP	########	0	0	0	0	0	0	0	0	7	3	3	0	0	0	0	0	0	0
Block1LGP	########	0	0	0	0	0	0	0	0	29	4	0	0	0	0	0	0	12	1
Block1RTF	########	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	2
Block1RTF	########	0	0	0	0	0	0	0	0	18	5	0	0	0	0	0	0	4	8
Block1RTF	########	0	0	0	0	0	0	0	0	38	4	0	0	0	0	0	0	0	22
Block2CTF	########	0	0	0	0	0	0	0	0	12	3	1	0	0	0	0	0	0	0
Block2CTF	########	0	0	0	0	0	0	0	0	17	3	0	0	0	0	0	0	8	0
Block2CTF	########	0	0	0	0	0	0	0	0	54	5	1	0	0	0	0	0	4	18
Block2LGP	########	0	0	0	0	0	0	0	0	15	4	0	0	0	0	0	0	9	1
Block2LGP	########	0	0	0	0	0	0	0	0	38	4	0	0	0	0	0	0	9	4
Block2LGP	########	0	0	0	0	0	0	0	0	22	5	0	0	0	0	0	0	7	3
Block2RTF	########	0	0	0	0	0	0	0	0	34	3	0	0	0	0	0	0	23	0
Block2RTF	########	0	0	0	0	0	0	0	0	22	4	0	0	0	0	0	0	7	0
Block2RTF	########	0	0	0	0	0	0	0	0	16	5	0	0	0	0	1	0	4	6
Block3CTF	########	0	0	0	0	0	0	0	0	10	4	1	0	0	0	0	0	1	0
Block3CTF	########	0	0	0	0	0	0	0	0	20	4	0	0	0	0	0	0	6	1
Block3CTF	########	0	0	0	0	0	0	0	0	8	4	0	0	0	0	0	0	0	0
Block3LGP	########	0	0	0	0	0	0	0	0	16	5	0	0	0	0	0	0	1	4
Block3LGP	########	0	0	0	1	0	1	0	0	8	6	0	0	0	0	1	0	0	2
Block3LGP	########	0	0	0	0	0	0	0	0	25	3	0	0	0	0	0	0	0	9
Block3RTF	########	0	0	0	0	0	0	0	0	14	4	0	0	0	0	0	0	10	2
Block3RTF	########	0	0	0	2	0	2	0	0	24	3	0	0	0	0	0	0	4	0
Block3RTF	########	0	0	0	0	0	0	0	0	25	5	0	0	0	0	2	0	4	0
Block4CTF	########	0	0	0	0	0	0	0	0	28	3	1	0	0	0	0	0	0	0
Block4CTF	########	0	1	0	0	0	0	0	0	30	3	0	0	0	0	0	0	14	0
Block4CTF	########	0	0	0	0	0	0	0	0	52	6	0	0	0	0	0	0	17	0
Block4LGP	########	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0
Block4LGP	########	0	0	0	0	0	0	0	0	38	4	0	0	0	0	0	0	32	0
Block4LGP	########	0	0	0	0	0	0	0	0	12	4	0	0	0	0	1	0	7	0
Block4RTF	########	0	0	0	0	0	0	0	0	7	3	0	0	0	0	4	0	2	1
Block4RTF	########	0	0	0	0	0	0	0	0	18	4	0	0	0	0	1	0	7	2
Block4RTF	########	0	0	0	0	0	0	0	0	31	5	0	0	0	0	0	0	8	0

SAMPLE	DATE	Isotomiell	lepidocyrt	Lepidocyr	Megaloth	Neanura	Ochesella	Stenapho	Willemia	Hypogastu	Hypogastu	Isotomida	Isotomida	Bourletiel	Bourletiel	Entomobr	Entomobr	Neelidae	Neelidae	Neanurid	Neanurid	Paronellid	Paronellid	Tullbergii	Tullbergii	NOTES
Block1CTF	01-Jun-17	50	0	5	12	0	0	0	1	3	2	66	3	1	1	5	1	12	1	0	0	1	1	0	0	
Block1CTF	01-Jun-17	11	0	3	4	0	0	0	4	4	1	68	3	1	1	3	1	4	1	0	0	0	0	0	0	
Block1CTF	01-Jun-17	11	0	2	5	0	2	0	0	0	0	40	3	0	0	4	2	5	1	0	0	0	0	0	0	
Block1LGP	01-Jun-17	18	5	0	4	0	0	1	2	6	2	41	3	0	0	5	1	4	1	0	0	1	1	1	1	
Block1LGP	01-Jun-17	50	5	2	22	0	1	0	0	1	1	135	3	0	0	8	3	22	1	0	0	1	1	0	0	
Block1LGP	01-Jun-17	44	0	2	21	0	0	0	0	1	1	77	3	0	0	2	1	21	1	0	0	2	1	0	0	
Block1RTF	01-Jun-17	2	0	0	0	0	1	0	0	1	1	10	2	2	1	1	1	0	0	0	0	0	0	0	0	
Block1RTF	01-Jun-17	50	0	0	4	0	0	0	2	2	1	95	3	0	0	0	0	4	1	0	0	2	1	0	0	
Block1RTF	01-Jun-17	19	0	0	2	0	0	0	2	2	1	54	2	2	2	0	0	2	1	0	0	0	0	0	0	
Block2CTF	01-Jun-17	18	0	10	30	0	2	3	3	6	2	58	3	5	1	12	2	30	1	0	0	0	0	3	1	
Block2CTF	01-Jun-17	22	0	0	0	0	4	2	13	17	2	37	2	0	0	4	1	0	0	0	0	1	1	2	1	
Block2CTF	01-Jun-17	16	0	0	3	0	0	0	1	1	1	34	2	0	0	0	0	3	1	0	0	1	1	0	0	
Block2LGP	01-Jun-17	9	0	6	2	0	1	0	1	1	1	52	3	0	0	7	2	2	1	0	0	0	0	0	0	
Block2LGP	01-Jun-17	8	0	0	6	0	0	0	1	1	1	111	3	0	0	0	0	6	1	0	0	2	1	0	0	
Block2LGP	01-Jun-17	32	2	12	20	0	2	0	1	1	1	121	3	0	0	16	3	20	1	0	0	1	1	0	0	
Block2RTF	01-Jun-17	18	0	4	5	0	1	1	0	2	1	117	3	0	0	5	2	5	1	0	0	0	0	1	1	
Block2RTF	01-Jun-17	14	0	4	3	0	2	0	1	2	2	31	3	0	0	6	2	3	1	0	0	1	1	0	0	
Block2RTF	01-Jun-17	52	0	1	5	0	0	0	15	16	2	88	3	0	0	1	1	5	1	0	0	0	0	0	0	
Block3CTF	01-Jun-17	12	0	2	15	0	0	0	3	5	2	89	3	0	0	2	1	15	1	0	0	0	0	0	0	
Block3CTF	01-Jun-17	21	0	4	1	0	0	0	25	26	2	48	3	1	1	4	1	1	1	0	0	1	1	0	0	
Block3CTF	01-Jun-17	19	0	3	0	20	0	3	1	1	1	79	3	0	0	3	1	0	0	20	1	3	1	3	1	
Block3LGP	01-Jun-17	9	0	6	9	0	0	0	0	1	1	34	3	0	0	7	2	9	1	0	0	0	0	0	0	
Block3LGP	01-Jun-17	17	0	3	2	0	0	1	1	4	2	57	3	0	0	3	1	2	1	0	0	0	0	1	1	
Block3LGP	01-Jun-17	32	0	2	23	0	0	0	0	0	0	102	3	0	0	2	1	23	1	0	0	0	0	0	0	
Block3RFT	01-Jun-17	12	0	7	1	0	0	1	1	1	1	105	3	0	0	7	1	1	1	0	0	1	1	1	1	
Block3RTF	01-Jun-17	7	0	0	1	0	1	1	0	0	0	58	3	0	0	1	1	1	1	0	0	0	0	1	1	
Block3RTF	01-Jun-17	13	0	4	18	0	0	0	5	5	1	41	2	0	0	4	1	18	1	0	0	0	0	0	0	
Block4CTF	01-Jun-17	15	0	6	4	0	0	0	0	0	0	37	3	1	1	6	1	4	1	0	0	0	0	0	0	
Block4CTF	01-Jun-17	14	0	5	4	0	2	0	5	5	1	32	3	0	0	7	2	4	1	0	0	0	0	0	0	
Block4CTF	01-Jun-17	63	0	0	17	0	3	0	0	0	0	108	3	2	1	3	1	17	1	0	0	2	1	0	0	
Block4LGP	01-Jun-17	22	0	0	1	0	0	0	0	0	0	50	3	1	1	0	0	1	1	0	0	0	0	0	0	
Block4LGP	01-Jun-17	38	0	3	4	0	1	0	0	0	0	91	3	3	1	4	2	4	1	0	0	0	0	0	0	
Block4LGP	01-Jun-17	15	1	0	5	0	1	0	1	1	1	27	2	0	0	2	2	5	1	0	0	1	1	0	0	
Block4RTF	01-Jun-17	10	0	2	4	0	1	2	0	0	0	23	3	1	1	3	2	4	1	0	0	0	0	2	1	
Block4RTF	01-Jun-17	28	0	5	5	0	0	1	0	0	0	102	3	0	0	5	1	5	1	0	0	0	0	1	1	
Block4RTF	01-Jun-17	50	0	5	16	0	3	0	4	4	1	105	3	0	0	8	2	16	1	0	0	0	0	0	0	
Block1CTF	02-Jul-17	12	0	0	0	0	0	0	0	0	0	19	2	1	1	3	1	0	0	0	0	2	1	0	0	
Block1CTF	02-Jul-17	18	0	1	0	0	0	0	4	4	1	24	3	1	1	1	1	0	0	0	0	0	0	0	0	
Block1CTF	02-Jul-17	9	0	6	0	0	0	0	10	10	1	13	3	0	0	6	1	0	0	0	0	2	1	0	0	
Block1LGP	02-Jul-17	4	0	9	0	0	0	0	0	0	0	7	2	1	1	9	1	0	0	0	0	0	0	0	0	
Block1LGP	02-Jul-17	3	0	0	0	0	0	0	1	3	2	5	3	0	0	0	0	0	0	0	0	0	0	0	0	
Block1LGP	02-Jul-17	25	0	1	0	0	0	0	0	0	0	29	3	0	0	1	1	0	0	0	0	0	0	0	0	
Block1RTF	02-Jul-17	7	0	1	0	0	0	0	0	1	1	10	2	0	0	1	1	0	0	0	0	1	1	0	0	
Block1RTF	02-Jul-17	12	0	10	1	0	0	0	24	28	2	17	3	0	0	11	2	1	1	0	0	0	0	0	0	
Block1RTF	02-Jul-17	23	0	10	0	0	0	0	4	7	2	29	3	0	0	10	1	0	0	0	0	0	0	0	0	
Block2CTF	02-Jul-17	12	0	0	0	0	0	0	26	26	1	15	3	0	0	3	1	0	0	0	0	0	0	0	0	
Block2CTF	02-Jul-17	7	0	2	0	0	0	1	3	4	2	11	2	0	0	2	1	0	0	0	0	0	0	1	1	
Block2CTF	02-Jul-17	13	0	9	6	0	0	0	24	26	2	13	1	0	0	9	1	6	1	0	0	0	0	0	0	
Block2LGP	02-Jul-17	6	0	8	1	0	0	2	3	5	2	9	2	0	0	9	2	1	1	0	0	1	1	2	1	
Block2LGP	02-Jul-17																									
Block2LGP	02-Jul-17	7	0	2	0	0	0	0	6	7	2	16	2	0	0	2	1	0	0	0	0	0	0	0	0	
Block2RTF	02-Jul-17	10	0	1	0	0	0	0	1	1	1	11	2	0	0	1	1	0	0	0	0	0	0	0	0	
Block2RTF	02-Jul-17	4	0	4	0	0	0	0	14	14	1	9	3	0	0	4	1	0	0	0	0	0	0	0	0	
Block2RTF	02-Jul-17	18	0	10	0	0	0	0	4	4	1	20	2	0	0	10	1	0	0	0	0	4	1	0	0	
Block3CTF	02-Jul-17	21	0	24	0	0	0	0	0	2	1	25	3	0	0	24	1	0	0	0	0	3	1	0	0	
Block3CTF	02-Jul-17	26	0	7	0	0	0	0	23	26	2	26	1	0	0	7	1	0	0	0	0	1	1	0	0	
Block3CTF	02-Jul-17	21	0	9	0	0	0	0	1	3	2	21	1	0	0	9	1	0	0	0	0	0	0	0	0	
Block3LGP	02-Jul-17	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	
Block3LGP	02-Jul-17	9	0	3	0	0	0	0	10	10	1	9	1	0	0	4	2	0	0	0	0	0	0	0	0	
Block3LGP	02-Jul-17	15	0	3	0	0	0	0	0	0	0	21	2	0	0	3	1	0	0	0	0	2	1	0	0	
Block3RTF	02-Jul-17	19	0	4	0	0	0	0	0	4	1	21	3	0	0	4	1	0	0	0	0	0	0	0	0	
Block3RTF	02-Jul-17	0	0	4	0	0	0	0	0	0	0	7	2	0	0	4	1	0	0	0	0	2	1	0	0	
Block3RTF	02-Jul-17	4	0	6	0	0	0	0	0	4	1	5	2	0	0	6	1	0	0	0	0	0	0	0	0	
Block4CTF	02-Jul-17	15	0	8	8	0	0	0	7	12	2	18	2	0	0	8	1	8	1	0	0	2	1	0	0	
Block4CTF	02-Jul-17	6	0	12	0	0	1	0	6	10	2	8	2	0	0	13	2	0	0	0	0	1	1	0	0	
Block4CTF	02-Jul-17	22	0	2	0	0	0	0	0	2	1	22	1	0	0	2	1	0	0	0	0	0	0	0	0	
Block4LGP	02-Jul-17	1	0	1	0	0	0	0	0	0	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	
Block4LGP	02-Jul-17	6	0	3	0	0	0	0	0	1	1	11	3	1	1	4	2	0	0	0	0	3	1	0	0	
Block4LGP	02-Jul-17	34	0	12	0	0	0	0	2	6	2	41	2	0	0	12	1	0	0	0	0	4	1	0	0	
Block4RTF	02-Jul-17	13	0	4	0	0	0	2	7	7	1	14	2	0	0	4	1	0	0	0	0	0	0	2	1	
Block4RTF	02-Jul-17	17	0	1	0	0	0	0	0	0	0	18	2	0	0	1	1	0	0	0	0	0	0	0	0	
Block4RTF	02-Jul-17	15	0	4	0	0	0	0	5	7	2	15	1	1	1	4	1	0	0	0	0	2	1	0	0	
Block1CTF	########	4	0	0	1	0	1	0	0	0	0	6	2	0	0	1	1	1	1	0	0	0	0	0	0	
Block1CTF	########	10	0	1	0	0	0	0	2	2	1	21	2	0	0	1	1	0	0	0	0	0	0	0	0	
Block1CTF	########	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	
Block1LGP	########	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	
Block1LGP	########	2	0	2	0	0	0	0	0	3	1	2	1	0	0	2	1	0	0	0	0	0	0	0	0	
Block1LGP	########	12	0	0	0	0	0	0	4	4	1	25	3	0	0	0	0	0	0	0	0	0	0	0	0	
Block1RTF	########	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	
Block1RTF	########	3	0	1	2	0	0	0	0	0	0	15	3	0	0	1	1	2	1	0	0	0	0	0	0	
Block1RTF	########	13	0	2	1	0	0	0	0	0	0	35	2	0	0	2	1	1	1	0	0	0	0	0	0	
Block2CTF	########	9	0	2	0	0	0	0	0	1	1	9	1	0	0	2	1	0	0	0	0	0	0	0	0	
Block2CTF	########	4	0	5	0	0	0	0	0	0	0	12	2	0	0	5	1	0	0	0	0	0	0	0	0	
Block2CTF	########	15	0	16	0	0	0	0	0	1	1	37	3	0	0	16	1	0	0	0	0	0	0	0	0	
Block2LGP	########	3	0	2	0	0	0	0	0	0	0	13	3	0	0	2	1	0	0	0	0	0	0	0	0	
Block2LGP	########	13	0	12	0	0	0	0	0	0	0	26	3	0	0	12	1	0	0	0	0	0	0	0	0	
Block2LGP	########	8	0	3	1	0	0	0	0	0	0	18	3	0	0	3	1	1	1	0	0	0	0	0	0	
Block2RTF	########	10	0	1	0	0	0	0	0	0	0	33	2	0	0	1	1	0	0	0	0	0	0	0	0	
Block2RTF	########	6	0	8	0	0	0	0	1	1	1	13	2	0	0	8	1	0	0	0	0	0	0	0	0	
Block2RTF	########	4	0	0	0	0	0	0	1	1	1	14	3	1	1	0	0	0	0	0	0	0	0	0	0	
Block3CTF	########	3	0	5	0	0	0	0	0	1	1	4	2	0	0	5	1	0	0	0	0	0	0	0	0	
Block3CTF	########	8	0	5	0	0	0	0	0	0	0	15	3	0	0	5	1	0	0	0	0	0	0	0	0	
Block3CTF	########	3	0	2	1	0	0	0	2	2	1	3	1	0	0	2	1	1	1	0	0	0	0	0	0	
Block3LGP	########	1	0	9	0	0	1	0	0	0	0	6	3	0	0	10	2	0	0	0	0	0	0	0	0	
Block3LGP	########	2	0	1	0	0	1	0	1	1	1	4	2	1	1	2	2	0	0	0	0	0	0	0	0	
Block3LGP	########	8	0	8	0	0	0	0	0	0	0	17	2	0	0	8	1	0	0	0	0	0	0	0	0	
Block3RTF	########	1	0	0	0	0	0	0	1	1	1	13	3	0	0	0	0	0	0	0	0	0	0	0	0	
Block3RTF	########	2	0	18	0	0	0	0	0	0	0	6	2	0	0	18	1	0	0	0	0	0	0	0	0	
Block3RTF	########	6	0	10	3	0	0	0	0	0	0	10	2	2	1	10	1	3	1	0	0	0	0	0	0	
Block4CTF	########	26	0	1	0	0	0	0	0	1	1	26	1	0	0	1	1	0	0	0	0	0	0	0	0	
Block4CTF	########	11	0	5	0	0	0	0	0	0	0	25	2	0	0	5	1	0	0	0	0	0	0	0	0	
Block4CTF	########	22	0	1	6	0	1	0	5	5	1	39	2	0	0	2	2	6	1	0	0	0	0	0	0	
Block4LGP	########	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	
Block4LGP	########	3	0	2	0	0	0	0	1	1	1	35	2	0	0	2	1	0	0	0	0	0	0	0	0	
Block4LGP	########	1	0	3	0	0	0	0	0	0	0	8	2	1	1	3	1	0	0	0	0	0	0	0	0	
Block4RTF	########	0	0	0	0	0	0	0	0	0	0	3	2	4	1	0	0	0	0	0	0	0	0	0	0	
Block4RTF	########	0	0	8	0	0	0	0	0	0	0	9	2	1	1	8	1	0	0	0	0	0	0	0	0	
Block4RTF	########	5	0	16	1	0	0	0	1	1	1	13	2	0	0	16	1	1	1	0	0	0	0	0	0	

Raw datachapter 4

SAMPLE	DATE	PLOT	TREATMENT	TOTALAB	ORDERDI	ACARI	ANNELID	APHID	ARANEAE	NEMATOD	DIPTERAL	SYMPHYL	ACHILOP	ODGASTROP	COLLEMB	COLEOPTE	DIPLOPOD	CARABID	COLEOPTE	OTHER CO	STAPHYLI	MILLIPED	MILLIPEDE	COLLEMB	Ceratophy	Entomobr	Parisotom	Heteroms	Heterosm	Isotomav	Isotomaa	Isotomiell	lepidocyrt	Lepidocyr	Megaloth	Neanura	Orchesell	Stenapho	COLLEMB	Hypogastu	Hypogastu	Isotomida	Isotomida	Bourletiel	Bourletiel	Entomobr	Entomobr	Neelidae	Neelidae	Neanurid	Neanurid	Tullbergii	Tullbergii	NOTES
1	21-Sep-16	plot1	NOTCULTIVATED	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 0 DRIED OU																		
2	21-Sep-16	plot1	NOTCULTIVATED	91	5	9	1	0	0	2	0	0	0	0	77	2	0	1	1	0	0	0	0	5	0	4	3	0	0	59	0	2	0	0	0	0 0 9 5 4 1 64 3 0 0 0 0 0 0 0 0 9 1																		
3	21-Sep-16	plot1	NOTCULTIVATED	6	3	1	0	0	0	0	0	0	0	0	4	1	0	0	0	0	1	0	0	2	0	0	2	0	0	2	0	0	0	0	0	0	0	0	2	0	0	4	2	0	0	0	0	0	0	0	0	0	0	DRIED OU
4	21-Sep-16	plot1	NOTCULTIVATED	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NOTHING
5	21-Sep-16	plot1	NOTCULTIVATED	70	6	32	2	0	0	1	0	2	0	0	32	1	0	1	0	0	0	0	0	4	0	1	8	0	0	13	0	0	0	10	0	0 0 0 6 1 1 21 2 0 0 10 1 0 0 0 0 0 0																		
6	21-Sep-16	plot1	NOTCULTIVATED	3	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	DRIED OU
7	21-Sep-16	plot1	NOTCULTIVATED	4	2	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	4	1	1	1	1	0	0	0	0	0	0	0	0	0	0	DRIED OU
8	21-Sep-16	plot1	NOTCULTIVATED	47	5	23	2	0	0	5	0	0	0	0	16	1	0	1	0	0	0	0	0	7	2	0	3	0	0	3	0	1	0	4	0	0	2	1	5	0	0	7	3	0	0	6	2	0	0	0	0	1	1	lost part o
9	21-Sep-16	plot1	NOTCULTIVATED	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	
10	21-Sep-16	plot1	NOTCULTIVATED	81	6	10	3	0	0	7	1	0	0	0	58	2	0	0	1	0	1	0	0	5	3	0	8	0	0	23	0	0	0	7	0	0	0	17	5	0	0	31	2	0	0	7	1	0	0	0	0	17	1	
11	21-Sep-16	plot1	NOTCULTIVATED	75	4	14	1	0	0	26	0	0	0	0	34	0	0	0	0	0	0	0	0	7	4	2	3	0	0	4	0	0	0	1	0	0	1	19	7	2	1	7	2	0	0	2	2	0	0	0	0	19	1	
12	21-Sep-16	plot1	NOTCULTIVATED	46	5	5	2	0	0	1	0	0	0	0	37	1	0	1	0	0	0	0	0	6	1	0	1	0	0	23	0	0	0	4	0	1	0	7	7	0	0	24	2	0	0	4	1	0	0	1	1	7	1	
13	21-Sep-16	plot1	NOTCULTIVATED	55	3	21	0	0	0	6	0	0	0	0	28	0	0	0	0	0	0	0	0	4	9	6	0	0	0	9	0	0	0	4	0	0	0	0	6	6	1	9	1	0	0	4	1	0	0	0	0	0	0	
14	21-Sep-16	plot1	NOTCULTIVATED	31	5	11	2	0	0	1	0	0	0	0	16	1	0	0	0	0	1	0	0	4	0	1	1	0	0	6	0	0	0	8	0	0	0	0	6	1	1	7	2	0	0	8	1	0	0	0	0	0	0	
15	21-Sep-16	plot1	NOTCULTIVATED	21	5	7	0	0	0	6	0	1	0	0	5	2	0	0	1	1	0	0	0	3	0	3	0	0	0	1	0	0	0	1	0	0	0	0	6	3	1	1	1	0	0	1	1	0	0	0	0	0	0	
16	21-Sep-16	plot1	NOTCULTIVATED	43	3	22	0	0	0	3	0	0	0	0	18	0	0	0	0	0	0	0	0	3	0	0	0	0	0	14	0	0	0	2	0	0 0 2 5 0 0 14 1 0 0 2 1 0 0 0 0 2 1 LABEL?																		
17	21-Sep-16	plot1	NOTCULTIVATED	145	3	41	0	0	0	21	0	0	0	0	83	0	0	0	0	0	0	0	0	6	5	5	27	0	0	39	0	0	0	4	0	0	0	3	7	5	1	66	2	0	0	4	1	0	0	0	0	3	1	
18	21-Sep-16	plot1	NOTCULTIVATED	99	4	17	2	0	0	8	0	0	0	0	72	0	0	0	0	0	0	0	0	5	8	0	30	0	0	21	0	8	0	0	0	0	0	5	3	0	0	59	3	0	0	0	0	0	0	0	0	5	1	
19	21-Sep-16	plot1	NOTCULTIVATED	84	5	38	2	0	0	9	0	0	0	0	34	0	1	0	0	0	0	1	0	5	6	0	11	0	0	14	0	0	0	1	0	0	0	2	5	0	0	25	2	0	0	1	1	0	0	0	0	2	1	
20	21-Sep-16	plot1	NOTCULTIVATED	60	5	15	4	0	0	11	3	0	0	0	27	0	0	0	0	0	0	0	0	5	0	1	23	0	0	1	0	0	0	1	0	0	0	1	7	1	1	24	2	0	0	1	1	0	0	0	0	1	1	
21	21-Sep-16	plot1	NOTCULTIVATED	47	3	17	0	0	0	12	0	0	0	0	18	0	0	0	0	0	0	0	0	6	1	1	0	0	0	9	0	0	0	4	0	0	1	2	7	1	1	9	1	0	0	5	2	0	0	0	0	2	1	
22	21-Sep-16	plot1	NOTCULTIVATED	124	5	17	0	0	0	7	1	0	0	0	96	0	3	0	0	0	0	3	0	7	2	1	30	0	0	56	0	3	0	2	0	0	0	2	7	1	1	89	3	0	0	2	1	0	0	0	0	2	1	
23	21-Sep-16	plot1	NOTCULTIVATED	14	5	6	0	0	0	1	1	0	0	0	3	3	0	1	2	0	0	0	0	2	0	0	0	0	0	1	0	0	0	2	0	0	0	0	4	0	0	1	1	0	0	2	1	0	0	0	0	0	0	
24	21-Sep-16	plot1	NOTCULTIVATED	85	6	9	4	0	1	6	0	0	0	0	60	5	0	0	5	0	0	0	0	6	1	3	0	0	0	33	0	2	0	11	0	0	0	10	7	3	1	35	2	0	0	11	1	0	0	0	0	10	1	
25	21-Sep-16	plot1	NOTCULTIVATED	71	6	5	3	0	0	5	1	0	0	0	56	1	0	0	0	0	1	0	0	5	1	0	8	0	0	27	0	0	0	9	0	0	0	11	5	0	0	35	2	0	0	9	1	0	0	0	0	11	1	
26	21-Sep-16	plot1	NOTCULTIVATED	118	6	52	0	1	0	12	0	0	0	0	50	1	2	1	0	0	0	0	2	6	1	0	22	0	0	14	0	1	0	2	0	0 0 10 5 0 0 37 3 0 0 2 1 0 0 0 0 10 1 LOST PART																		
27	21-Sep-16	plot1	NOTCULTIVATED	77	4	11	6	0	0	5	0	0	0	0	55	0	0	0	0	0	0	0	0	6	1	0	12	0	0	31	0	1	0	4	0	0	0	6	5	0	0	44	3	0	0	4	1	0	0	0	0	6	1	
28	21-Sep-16	plot1	NOTCULTIVATED	128	5	11	1	0	0	6	1	0	0	0	109	0	0	0	0	0	0	0	0	6	3	0	44	1	0	43	0	0	0	6	0	0	0	12	7	0	0	87	2	1	1	6	1	0	0	0	0	12	1	
29	21-Sep-16	plot1	NOTCULTIVATED	72	4	22	0	0	0	5	0	0	0	0	44	1	0	0	1	0	0	0	0	6	2	0	7	0	0	21	0	0	1	2	0	0	0	11	5	0	0	28	2	0	0	3	2	0	0	0	0	11	1	
30	21-Sep-16	plot1	NOTCULTIVATED	189	6	134	1	0	0	16	2	0	0	0	33	3	0	1	0	0	2	0	0	7	4	3	0	1	0	15	0	5	0	3	0	0	0	2	9	3	1	20	2	1	1	3	1	0	0	0	0	2	1	
						1A		22-Nov-16	plot1	CULTIVATED		12	3	9	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0 0 0 0 0 2 0 0 1 1 0 0 0 0 0 0 0 0 0 1B?												
1B	22-Nov-16	plot1	CULTIVATED	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1C	22-Nov-16	plot1	CULTIVATED	7	2	4	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	3	1	
1D	22-Nov-16	plot1	CULTIVATED	15	1	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1E	22-Nov-16	plot1	CULTIVATED	42	3	28	0	0	0	0	0	0	0	0	12	2	0	0	2	0	0	0	0	4	1	0	4	0	0	6	0	0	0	1	0	0	0	0	4	0	0	10	2	0	0	1	1	0	0	0	0	0	0	
2A	22-Nov-16	plot2	NOTCULTIVATED	42	3	17	0	0	0	4	0	0	0	0	21	0	0	0	0	0	0	0	0	4	0	0	2	3	0	15	0	0	0	1	0	0	0	0	6	0	0	17	2	3	1	1	1	0	0	0	0	0	0	
2B	22-Nov-16	plot2	NOTCULTIVATED	57	6	16	2	0	0	4	1	0	0	0	33	1	0	0	1	0	0	0	0	3	1	0	15	0	0	17	0	0	0	0	0	0	0	0	2	0	0	32	2	0	0	0	0	0	0	0	0	0	0	
2C	22-Nov-16	plot2	NOTCULTIVATED	22	4	5	0	0	0	2	0	0	0	0	13	2	0	0	1	0	1	0	0	2	0	0	0	0	0	11	0	0	0	2	0 0 0 0 4 0 0 11 1 0 0 2 1 0 0 0 0 0 0 DRIED OU																			
2D	22-Nov-16	plot2	NOTCULTIVATED	78	4	50	0	0	0	5	0	0	0	0	21	2	0	0	2	0	0	0	0	4	0	0	13	1	0	5	0	0	0	2	0	0	0	0	6	0	0	18	2	1	1	2	1	0	0	0	0	0	0	
2E	22-Nov-16	plot2	NOTCULTIVATED	44	3	26	0	0	0	10	0	0	0	0	8	0	0	0	0	0	0	0	0	3	1	0	5	0	0	2	0	0	0	0	0	0	0	0	2	0	0	7	2	0	0	0	0	0	0	0	0	0	0	
3A	22-Nov-16	plot3	CULTIVATED	7	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3B	22-Nov-16	plot3	CULTIVATED	11	3	9	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3C	22-Nov-16	plot3	CULTIVATED	14	3	6	0	0	0	3	0	0	0	0	5	0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	1	0	3	0	0	0	0	4	0	0	2	2	0	0	3	1	0	0	0	0	0	0	
3D	22-Nov-16	plot3	CULTIVATED	16	2	10	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	1	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3E	22-Nov-16	plot3	CULTIVATED	45	4	36	0	0	0	2	2	0	0	0	5	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	4	0	0	0	0	4	0	0	1	1	0	0	4	1	0	0	0	0	0	0	
4A	22-Nov-16	plot4	CULTIVATED	8	1	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4B	22-Nov-16	plot4	CULTIVATED	5	2	4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	
4C	22-Nov-16	plot4	CULTIVATED	10	3	5	0	0	0	3	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	1	0	0	0	0	4	0	0	1	1	0	0	1	1	0	0	0	0	0	0	
4D	22-Nov-16	plot4	CULTIVATED	8	3	4	0	0	0	1	0	0	0	0	3	0	0	0	0	0	0	0	0	3	1	0	0	0	0	1	0	0	0	1	0	0	0	0	4	0	0	1	1	0	0	1	1	0	0	0	0	0	0	
4E	22-Nov-16	plot4	CULTIVATED	14	3	4	0	0	0	1	0	0	0	0	9	0	0	0	0	0	0	0	0	4	0	0	2	3	0	3	0	0	0	0	0	0	0	1	5	0	0	5	2	3	1	0	0	0	0	0	0	1	1	
5A	22-Nov-16	plot5	NOTCULTIVATED	61	3	48	0	0	0	3	0	0	0	0	10	0	0	0	0	0	0	0	0	2	0	0	0	0	0	6	0	0	0	4	0	0	0	0	4	0	0	6	1	0	0	4	1	0	0	0	0	0	0	
5B	22-Nov-16	plot5	NOTCULTIVATED	54	3	20	0	0	0	7	0	0	0	0	27	0	0	0	0	0	0	0	0	4	1	0	13	0	0	9	0	4	0	0	0	0	0	0	2	0	0	26	3	0	0	0	0	0	0	0	0	0	0	
5C	22-Nov-16	plot5	NOTCULTIVATED	45	3	24	0	0	0	7	0	0	0	0	14	0	0	0	0	0	0	0	0	2	0	0	9	0	0	5	0	0	0	0	0	0	0	0	2	0	0	14	2	0	0	0	0	0	0	0	0	0	0	
5D	22-Nov-16	plot5	NOTCULTIVATED	6	2	5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	
5E	22-Nov-16	plot5	NOTCULTIVATED	83	3	73	0	0	0	0	0	0	0	0	9	1	0	0	1	0	0	0	0	4	1	0	0	0	0	5	0	0	0	2	0	0	0	1	5	0	0	5	1	0	0	2	1	0	0	0	0	1	1	
6A	22-Nov-16	plot6	NOTCULTIVATED	96	3	55	0	0	0	3	0	0	0	0	38	0	0	0	0	0	0	0	0	5	0	0	3	0	0	28	0	0	0	1	3	0	0	3	7	0	0	31	2	0	0	1	1	3	1	0	0	3	1	
6B	22-Nov-16	plot6	NOTCULTIVATED	63	4	46	0	0	0	2	0	0	0	0	14	0	1	0	0	0	0	0	1	3	0	0	10	0	0	2	0	2	0	0	0	0	0	0	2	0	0	14	3	0	0	0	0	0	0	0	0	0	0	
6C	22-Nov-16	plot6	NOTCULTIVATED	386	7	114	1	0	0	2	2	0	0	0	265	1	1	0	1	0	0	0	1	5	6	0	131	0	0	76	0	47	0	5	0	0	0	0	4	0	0	254	3	0	0	5	1	0	0	0	0	0	0	
6D	22-Nov-16	plot6	NOTCULTIVATED	69	6	41	1	0	0	5	0	0	0	0	20	1	1	0	1	0	0	0	1	5	6	0	5	0	0	4	0	0	0	0	0	0	1	4	5	0	0	9	2	0	0	1	1	0	0	0	0	4	1	
6E	22-Nov-16	plot6	NOTCULTIVATED	52	5	19	1	0	1	3	0	0	0	0	28	0	0	0	0	0	0	0	0	6	1	0	9	0	0	13	0	1	0	0	0	0	1	3	5	0	0	23	3	0	0	1	1	0	0	0	0	3	1	
1A	23-May-17	plot1	CULTIVATED	115	7	33	1	0	1	2	2	0	0	0	75	1	0	0	1	0	0	0	0	8	0	0	30	1	1	16	15	8	3	0	0	0	0	1	7	0	0	69	4	2	2	3	1	0	0	0	0	1	1	
1B	23-May-17	plot1	CULTIVATED	156	5	23	0	1	0	1	0	0	0	0	130	1	0	0	1	0	0	0	0	7	0	5	36	9	0	57	11	11	0	1	0	0 0 0 8 5 1 115 4 9 1 1 1 0 0 0 0 0 0 0 stoney sm																		
1C	23-May-17	plot1	CULTIVATED	172	5	62	0	1	0	1	0	0	0	0	106	2	0	0	2	0	0	0	0	6	0	0	7	7	0	53	32	4	0	3	0	0	0	0	6	0	0	96	4	7	1	3	1	0	0	0	0	0	0	
1D	23-May-17	plot1	CULTIVATED	90	5	20	0	2	1	1	0	0	0	0	66	0	0	0	0	0	0	0	0	7	2	0	17	3	0	19	13	2	0	10	0	0	0	0	6	0	0	51	4	3	1	10	1	0	0	0	0	0	0	
1E	23-May-17	plot1	CULTIVATED	128	7	45	1	1	0	3	1	0	0	0	75	2	0	0	0	0	2	0	0	9	1	0	23	2	0	15	19	10	0	1	0	0	2	2	7	0	0	67	4	2	1	3	2	0	0	0	0	2	1	
2A	23-May-17	plot2	NOTCULTIVATED	59	5	21	0	0	0	2	1	0	0	0	34	1	0	0	1	0	0	0	0	7	3	0	6	2	0	6	10	2	0	0	0	0	0	5	5	0	0	24	4	2	1	0	0	0	0	0	0	5	1	
2B	23-May-17	plot2	NOTCULTIVATED	128	4	48	0	0	0	2	0	0	0	0	74	4	0	0	2	1	1	0	0	8	2	2	31	0	1	19	12	3	0	0	0	0	0	4	7	2	1	65	4	1	1	0	0	0	0	0	0	4	1	
2C	23-May-17	plot2	NOTCULTIVATED	140	6	21	1	0	0	7	1	0	0	0	109	1	0	0	1	0	0	0	0	10	0	7	15	11	1	47	17	2	1	5	0	0	0	3	9	7	1	81	4	12	2	6	2	0	0	0	0	3	1	
2D	23-May-17	plot2	NOTCULTIVATED	63	6	8	3	4	0	2	0	0	0	1	45	0	0	0	0	0	0	0	0	5	0	0	1	6	0	27	10	0	0	0	0	0	1	0	6	0	0	38	3	6	1	1	1	0	0	0	0	0	0	
2E	23-May-17	plot2	NOTCULTIVATED	119	4	16	1	0	0	5	0	0	0	0	97	0	0	0	0	0	0	0	0	7	8	0	17	10	1	27	31	0	0	0	0	0	0	3	5	0	0	75	3	11	2	0	0	0	0	0	0	3	1	
3A	23-May-17	plot3	CULTIVATED	115	5	60	0	0	1	3	0	0	0	0	50	1	0	0	1	0	0	0	0	8	1	2	0	8	0	11	19	4	0	0	1	0	0	4	9	2	1	34	3	8	1	0	0	1	1	0	0	4	1	
3B	23-May-17	plot3	CULTIVATED	163	6	65	0	2	0	5	1	0	0	0	87	3	0	1	1	0	1	0	0	5	7	0	0	1	0	63	12	0	0	4	0	0	0	0	6	0	0	75	2	1	1	4	1	0	0	0	0	0	0	
3C	23-May-17	plot3	CULTIVATED	130	3	39	0	1	0	0	0	0	0	0	90	0	0	0	0	0	0	0	0	6	2	0	0	3	0	45	28	0	0	10	0	0	0	2	7	0	0	73	2	3	1	10	1	0	0	0	0	2	1	
						3D		23-May-17	plot3	CULTIVATED		59	5	34	1	0	0	1	0	0	0	0	21	2	0	0	2	0	0	0	0	7	0	0	1	1	0	10	4	2	0	1 0 0 0 2 7 0 0 17 4 1 1 1 1 0 0 0 0 2 1 SPILT												
3E	23-May-17	plot3	CULTIVATED	223	5	128	0	0	1	4	0	0	0	0	89	1	0	0	1	0	0	0	0	7	1	0	2	5	0	24	45	0	0	11	0	0	0	1	7	0	0	71	3	5	1	11	1	0	0	0	0	1	1	
4A	23-May-17	plot4	CULTIVATED	234	4	164	0	0	1	0	0	0	0	0	64	5	0	1	4	0	0	0	0	8	0	3	6	6	0	29	11	2	0	4	0	0	0	3	9	3	1	48	4	6	1	4	1	0	0	0	0	3	1	
4B	23-May-17	plot4	CULTIVATED	128	4	58	0	0	2	0	1	0	0	0	67	0	0	0	0	0	0	0	0	6	0	0	28	1	0	14	19	0	0	4	0	0	0	1	7	0	0	61	3	1	1	4	1	0	0	0	0	1	1	
4C	23-May-17	plot4	CULTIVATED	94	6	33	1	0	1	5	0	0	0	0	52	2	0	0	2	0	0	0	0	10	1	3	5	3	0	25	2	4	0	5	1	0	0	3	11	3	1	36	4	3	1	5	1	1	1	0	0	3	1	
4D	23-May-17	plot4	CULTIVATED	278	6	128	1	0	0	0	0	0	1	0	133	3	12	1	1	0	1	12	0	9	0	1	103	3	1	10	4	1	0	7	0	0	0	3	9	1	1	118	4	4	2	7	1	0	0	0	0	3	1	
4E	23-May-17	plot4	CULTIVATED	547	8	318	3	0	1	30	7	1	1	0	186	0	0	0	0	0	0	0	0	8	5	9	68	0	0	45	25	24	0	0	0	0	1	9	7	9	1	162	4	0	0	1	1	0	0	0	0	9	1	
5A	23-May-17	plot5	NOTCULTIVATED	417	5	51	3	0	0	14	0	0	0	0	348	1	0	0	1	0	0	0	0	9	8	3	104	10	0	102	58	40	0	4	0	0	0	19	9	3	1	304	4	10	1	4	1	0	0	0	0	19	1	
5B	23-May-17	plot5	NOTCULTIVATED	100	5	26	2	0	0	2	0	0	0	0	68	2	0	0	1	0	1	0	0	9	4	0	14	1	1	13	15	12	0	2	0	0	0	6	7	0	0	54	4	2	2	2	1	0	0	0	0	6	1	
5C	23-May-17	plot5	NOTCULTIVATED	203	5	43	0	1	0	0	2	0	0	0	135	0	22	0	0	0	0	22	0	6	0	0	19	2	0	14	94	1	0	0	0	0	0	5	5	0	0	128	4	2	1	0	0	0	0	0	0	5	1	
5D	23-May-17	plot5	NOTCULTIVATED	140	6	14	1	0	0	14	2	0	0	0	108	1	0	0	1	0	0	0	0	8	7	1	48	4	0	18	7	9	0	0	0	0	0	14	7	1	1	82	4	4	1	0	0	0	0	0	0	14	1	
5E	23-May-17	plot5	NOTCULTIVATED	41	4	17	0	0	0	1	0	1	0	0	22	0	0	0	0	0	0	0	0	6	3	1	0	0	0	12	0	1	0	4	1 0 0 0 8 1 1 13 2 0 0 4 1 1 1 0 0 0 0 clay soil																			
6A	23-May-17	plot6	NOTCULTIVATED	131	5	45	0	0	2	6	0	0	0	0	75	3	0	0	3	0	0	0	0	6	4	0	37	2	0	9	19	4	0	0	0	0	0	0	4	0	0	69	4	2	1	0	0	0	0	0	0	0	0	
6B	23-May-17	plot6	NOTCULTIVATED	120	3	8	0	0	0	6	0	0	0	0	106	0	0	0	0	0	0	0	0	7	5	0	49	5	3	17	24	0	0	3	0	0	0	0	6	0	0	90	3	8	2	3	1	0	0	0	0	0	0	
6C	23-May-17	plot6	NOTCULTIVATED	259	5	46	1	0	0	14	0	0	0	0	188	10	0	0	10	0	0	0	0	7	0	1	99	0	0	67	6	9	0	5	0	0	0	1	7	1	1	181	4	0	0	5	1	0	0	0	0	1	1	
6D	23-May-17	plot6	NOTCULTIVATED	153	8	78	1	0	1	3	0	0	0	1	65	2	2	0	2	0	0	2	0	8	4	0	40	1	0	6	11	1	0	1	0	0	0	1	7	0	0	58	4	1	1	1	1	0	0	0	0	1	1	
6E	23-May-17	plot6	NOTCULTIVATED	274	6	91	5	0	0	8	0	0	0	0	162	2	6	0	2	0	0	6	0	7	3	0	74	1	0	64	16	2	0	2	0	0	0	0	6	0	0	156	4	1	1	2	1	0	0	0	0	0	0	

APPENDIX C

R code chapter2

```
##FIELD COMP

#load data
#change dir
rm(list=ls())
hau<-read.csv("HAUfield27092017.csv", header=T)
hau
attach(hau)
str(hau)
summary(DATE)

##water
meanwater<-tapply(water,list(MANAGEMENT,DATE),mean)
meanwater
centres<-barplot(meanwater,beside=T,ylim=c(0,1),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean soil moisture g g-1 ",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
sewater<-
(tapply(water,list(MANAGEMENT,DATE),sd)/sqrt(tapply(water,list(MANAGEMENT,DATE),length)))
sewater
arrows(centres,meanwater+sewater,centres,meanwater-sewater,code=3,angle=90,length=0.1)
legend(x=10, y=0.8, legend=c("arable","grass ley","pasture"), fill=c("gray15","gray40","gray70"),box.lty=0)
modwater<-lm(water~MANAGEMENT*DATE+Field)
summary(modwater)
modwater2<-update(modwater, ~. -MANAGEMENT:DATE:Field)
summary(modwater2)
modwater3<-update(modwater2, ~. -MANAGEMENT:Field)
summary(modwater3)
modwater3<-step(modwater)
modwater4<-lm(water ~ DATE + Field + DATE:Field)
summary(modwater4)

##SUMMARY MESOFAUNA GRAPHS
par(mfrow = c(1,1))

boxplot(TOTAL.ABUNDANCE~DATE, xlab="Sampling Date", ylab="Total mesofauna abundance",names=c("April 2014","May 2014", "July 2014", "August 2014"))
text(0.7,400, "a",cex=3)
boxplot(ORDER.DIVERSITY~DATE,xlab="Sampling Date", ylab="Total mesofauna order richness",names=c("April 2014","May 2014", "July 2014", "August 2014"))
text(0.7,8, "b",cex=3)
medianabund<-tapply(TOTAL.ABUNDANCE,DATE,median)
medianabund
medianorder<-tapply(ORDER.DIVERSITY,DATE,median)
medianorder

meanabun<-tapply(TOTAL.ABUNDANCE,list(MANAGEMENT,DATE),mean)
meanabun
centres<-barplot(meanabun,beside=T,ylim=c(0,250),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean abundance of total mesofauna",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
seabun<-
(tapply(TOTAL.ABUNDANCE,list(MANAGEMENT,DATE),sd)/sqrt(tapply(TOTAL.ABUNDANCE,list
(MANAGEMENT,DATE),length)))
seabun
arrows(centres,meanabun+seabun,centres,meanabun-seabun,code=3,angle=90,length=0.1)
```

```
legend(x=10, y=250, legend=c("arable","grass ley","pasture"), fill=c("gray15","gray40","gray70"),box.lty=0)
text(2,220, "a",cex=3)

modtotabun<-glm(TOTAL.ABUNDANCE~MANAGEMENT*DATE*water*Field, family=poisson)
summary(modtotabun)
modtotabun2<-step(modtotabun)
modtotabun2<-update(modtotabun, ~. -MANAGEMENT:DATE:water:Field)
summary(modtotabun2)
modtotabun3<-update(modtotabun2, ~. -DATE:water:Field)
summary(modtotabun3)
modtotabun4<-update(modtotabun3, ~. -MANAGEMENT:water:Field)
summary(modtotabun4)
modtotabun5<-update(modtotabun4, ~. -MANAGEMENT:DATE:Field)
summary(modtotabun5)
modtotabun6<-update(modtotabun5, ~. -MANAGEMENT:DATE:water)
summary(modtotabun6)
modtotabun7<-update(modtotabun6, ~. -water:Field)
summary(modtotabun7)
modtotabun8<-update(modtotabun7, ~. -DATE:Field)
summary(modtotabun8)
modtotabun9<-update(modtotabun8, ~. -MANAGEMENT:Field)
summary(modtotabun9)
modtotabun10<-update(modtotabun9, ~. -DATE:water)
summary(modtotabun10)
plot(modtotabun10)
modtotabun10<-glm(TOTAL.ABUNDANCE ~ MANAGEMENT + DATE + water + Field +
MANAGEMENT:DATE + MANAGEMENT:water, family = quasipoisson)

meandiv<-tapply(ORDER.DIVERSITY,list(MANAGEMENT,DATE),mean)
meandiv
centres<-barplot(meandiv,beside=T,ylim=c(0,8),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean order richness of total mesofauna",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
sediv<-
(tapply(ORDER.DIVERSITY,list(MANAGEMENT,DATE),sd)/sqrt(tapply(ORDER.DIVERSITY,list(M
ANAGEMENT,DATE),length)))
sediv
arrows(centres,meandiv+sediv,centres,meandiv-sediv,code=3,angle=90,length=0.1)
legend(x=10, y=8, legend=c("arable","grass ley","pasture"), fill=c("gray15","gray40","gray70"),box.lty=0)
text(2,7, "b",cex=3)
modtotdiv<-glm(ORDER.DIVERSITY~MANAGEMENT*DATE*water*Field, family=poisson)
summary(modtotdiv)
modtotdiv2<-update(modtotdiv, ~. -MANAGEMENT:DATE:water:Field)
summary(modtotdiv2)
modtotdiv3<-update(modtotdiv2, ~. -DATE:water:Field)
summary(modtotdiv3)
modtotdiv4<-update(modtotdiv3, ~. -MANAGEMENT:water:Field)
summary(modtotdiv4)
modtotdiv5<-update(modtotdiv4, ~. -MANAGEMENT:DATE:Field)
summary(modtotdiv5)
modtotdiv6<-update(modtotdiv5, ~. -MANAGEMENT:DATE:water)
summary(modtotdiv6)
modtotdiv<-step(modtotdiv)

meanacari<-tapply(ACARI,list(MANAGEMENT,DATE),mean)
meanacari
centres<-barplot(meanacari,beside=T,ylim=c(0,150),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean abundance of acari",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
```

```
seacari<-
(tapply(ACARI,list(MANAGEMENT,DATE),sd)/sqrt(tapply(ACARI,list(MANAGEMENT,DATE),lengt
h)))
seacari
arrows(centres,meanacari+seacari,centres,meanacari-seacari,code=3,angle=90,length=0.1)
legend(x=7, y=120, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
modtotacari<-glm(ACARI~MANAGEMENT*DATE*water*Field, family=poisson)
summary(modtotacari)
modtotacari1<-glm(ACARI~MANAGEMENT*DATE+water+Field, family=quasipoisson)
summary(modtotacari1)

##SUMMARY COLLEMBOLA GRAPHS
boxplot(COLLEMBOLA.ABUNDANCE ~DATE, xlab="Sampling Date", ylab="Total collembola
abundance",names=c("April 2014","May 2014", "July 2014", "August 2014"))
text(0.7,150, "a",cex=3)
boxplot(COLLEMBOLA.SPECIES.DIVERSITY ~DATE ,xlab="Sampling Date", ylab="Total
collembola species richness",names=c("April 2014","May 2014", "July 2014", "August 2014"))
text(0.7,10, "b",cex=3)
mediancolabund<-tapply(COLLEMBOLA.ABUNDANCE,DATE,median)
mediancolabund
mediancolorder<-tapply(COLLEMBOLA.SPECIES.DIVERSITY,DATE,median)
mediancolorder

meancolabun<-tapply(COLLEMBOLA.ABUNDANCE,list(MANAGEMENT,DATE),mean)
meancolabun
centres<-barplot(meancolabun
,beside=T,ylim=c(0,100),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"),
xlab="Sampling Date", ylab = "Mean abundance of total
collembola",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
secolabun<-
(tapply(COLLEMBOLA.ABUNDANCE,list(MANAGEMENT,DATE),sd)/sqrt(tapply(COLLEMBOLA.A
BUNDANCE,list(MANAGEMENT,DATE),length)))
secolabun
arrows(centres,meancolabun+secolabun,centres,meancolabun-
secolabun,code=3,angle=90,length=0.1)
legend(x=10, y=90, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,90, "a",cex=3)
modcolabun<-glm(COLLEMBOLA.ABUNDANCE~MANAGEMENT*DATE*water+Field,
family=quasipoisson)
summary(modcolabun)
modcolabun2<-update(modcolabun, ~. -MANAGEMENT:DATE:water)
summary(modcolabun2)
modcolabun3<-update(modcolabun2, ~. -DATE:water)
summary(modcolabun3)
modcolabun2<-step(modcolabun)

meancoldiv<-tapply(COLLEMBOLA.SPECIES.DIVERSITY,list(MANAGEMENT,DATE),mean)
meancoldiv
centres<-barplot(meancoldiv,beside=T,ylim=c(0,8),names.arg=c("April 2014","May 2014", "July
2014", "August 2014"), xlab="Sampling Date", ylab = "Mean species richness
collembola",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
secoldiv<-
(tapply(COLLEMBOLA.SPECIES.DIVERSITY,list(MANAGEMENT,DATE),sd)/sqrt(tapply(COLLEM
BOLA.SPECIES.DIVERSITY,list(MANAGEMENT,DATE),length)))
secoldiv
arrows(centres,meancoldiv+secoldiv,centres,meancoldiv-secoldiv,code=3,angle=90,length=0.1)
legend(x=10, y=7, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,7, "b",cex=3)
modcoldiv<-glm(COLLEMBOLA.SPECIES.DIVERSITY~MANAGEMENT*DATE*water+Field,
family=poisson)
```

```
summary(modcoldiv)
modcoldiv2<-update(modcoldiv, ~. -MANAGEMENT:DATE:water)
summary(modcoldiv2)
modcoldiv10<-step(modcoldiv)
summary(modcoldiv10)

###COLLEMBOLA FAMILY ABUNDANCE

meanisoabun<-tapply(Isotomidae.abundance,list(MANAGEMENT,DATE),mean)
meanisoabun
centres<-barplot(meanisoabun,beside=T,ylim=c(0,90),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean abundance of isotomidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
seisoabun<-(tapply(Isotomidae.abundance
,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Isotomidae.abundance,list(MANAGEMENT,DATE),leng
th)))
seisoabun
arrows(centres,meanisoabun+seisoabun,centres,meanisoabun-
seisoabun,code=3,angle=90,length=0.1)
legend(x=10, y=70, legend=c("arable","grass ley","pasture"), fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,70, "a",cex=3)
modisoabun<-glm(Isotomidae.abundance~MANAGEMENT*DATE*water+Field,
family=quasipoisson)
summary(modisoabun)
modisoabun2<-update(modisoabun, ~. -MANAGEMENT:DATE:water)
summary(modisoabun2)
modisoabun3<-update(modisoabun2, ~. -DATE:water)
summary(modisoabun3)

meanisodiv<-tapply(Isotomidae.diversity,list(MANAGEMENT,DATE),mean)
meanisodiv
centres<-barplot(meanisodiv,beside=T,ylim=c(0,3),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean species richness of isotomidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
seisodiv<-
(tapply(Isotomidae.diversity,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Isotomidae.diversity,list(MA
NAGEMENT,DATE),length)))
seisodiv
arrows(centres,meanisodiv+seisodiv,centres,meanisodiv-seisodiv,code=3,angle=90,length=0.1)
legend(x=10, y=2.9, legend=c("arable","grass ley","pasture"), fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,2.9, "a",cex=3)
modisodiv<-glm(Isotomidae.diversity~MANAGEMENT*DATE*water+Field, family=poisson)
summary(modisodiv)
modisodiv2<-update(modisodiv, ~. -MANAGEMENT:DATE:water)
summary(modisodiv2)
modisodiv3<-update(modisodiv2, ~. -DATE:water)
summary(modisodiv3)
modisodiv10<-step(modisodiv)
summary(modisodiv10)
glm(formula = Isotomidae.diversity ~ MANAGEMENT + DATE + water +
    MANAGEMENT:water + DATE:water, family = poisson)

meanhypoabun<-tapply(Hypogasturidae.abundance,list(MANAGEMENT,DATE),mean)
meanhypoabun
centres<-barplot(meanhypoabun,beside=T,ylim=c(0,15),names.arg=c("April 2014","May 2014", "July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean abundance of hypogasturidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
sehypoabun<-(tapply(Hypogasturidae.abundance
,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Hypogasturidae.abundance,list(MANAGEMENT,DATE)
,length)))
sehypoabun
```

```
arrows(centres,meanhypoabun+sehypoabun,centres,meanhypoabun-
sehypoabun,code=3,angle=90,length=0.1)
legend(x=9, y=13, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,12, "a",cex=3)
modhypoabun<-glm(Hypogasturidae.abundance~MANAGEMENT*DATE*water+Field,
family=quasipoisson)
summary(modhypoabun)
modhypoabun2<-update(modhypoabun, ~. -MANAGEMENT:DATE:water)
summary(modhypoabun2)

meanhypodiv<-tapply(Hypogasturidae.diversity,list(MANAGEMENT,DATE),mean)
meanhypodiv
centres<-barplot(meanhypodiv,beside=T,ylim=c(0,2),names.arg=c("April 2014","May 2014", "July
2014", "August 2014"), xlab="Sampling Date", ylab = "Mean species richness of
hypogasturidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
sehypodiv<-
(tapply(Hypogasturidae.diversity,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Hypogasturidae.diversi
ty,list(MANAGEMENT,DATE),length)))
sehypodiv
arrows(centres,meanhypodiv+sehypodiv,centres,meanhypodiv-
sehypodiv,code=3,angle=90,length=0.1)
legend(x=10, y=1.8, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,1.75, "b",cex=3)
modhypodiv<-glm(Hypogasturidae.diversity~MANAGEMENT*DATE*water+Field, family=poisson)
summary(modhypodiv)
modhypodiv2<-update(modhypodiv, ~. -MANAGEMENT:DATE:water)
summary(modhypodiv2)
modhypodiv10<-step(modhypodiv)
summary(modhypodiv10)
glm(formula = Hypogasturidae.diversity ~ MANAGEMENT + DATE +
   water, family = poisson)

meanbourabun<-tapply(Bourletiellidae.abundance,list(MANAGEMENT,DATE),mean)
meanbourabun
centres<-barplot(meanbourabun,beside=T,ylim=c(0,15),names.arg=c("April 2014","May 2014",
"July 2014", "August 2014"), xlab="Sampling Date", ylab = "Mean abundance of
bourletiellidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
sebourabun<-(tapply(Bourletiellidae.abundance
,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Bourletiellidae.abundance,list(MANAGEMENT,DATE),l
ength)))
sebourabun
arrows(centres,meanbourabun+sebourabun,centres,meanbourabun-
sebourabun,code=3,angle=90,length=0.1)
legend(x=12, y=14, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,12, "a",cex=3)
modbourabun<-glm(Bourletiellidae.abundance~MANAGEMENT*DATE*water+Field,
family=quasipoisson)
summary(modbourabun)
modbourabun2<-update(modhypoabun, ~. -MANAGEMENT:DATE:water)
summary(modbourabun2)
modbourabun3<-update(modbourabun2, ~. -DATE:water)
summary(modbourabun3)
modbourabun4<-update(modbourabun3, ~. -MANAGEMENT:DATE)
summary(modbourabun4)

meanbourdiv<-tapply(Bourletiellidae.diversity,list(MANAGEMENT,DATE),mean)
meanbourdiv
centres<-barplot(meanbourdiv,beside=T,ylim=c(0,3),names.arg=c("April 2014","May 2014", "July
2014", "August 2014"), xlab="Sampling Date", ylab = "Mean species richness of
bourletiellidae",col=c("gray15","gray40","gray70"),cex.lab=1.3,cex.names=1)
```

```
sebourdiv<-
(tapply(Bourletiellidae.diversity,list(MANAGEMENT,DATE),sd)/sqrt(tapply(Bourletiellidae.diversity,li
st(MANAGEMENT,DATE),length)))
sebourdiv
arrows(centres,meanbourdiv+sebourdiv,centres,meanbourdiv-
sebourdiv,code=3,angle=90,length=0.1)
legend(x=12, y=2.8, legend=c("arable","grass ley","pasture"),
fill=c("gray15","gray40","gray70"),box.lty=0)
text(1.5,2.8, "b",cex=3)
modbourdiv<-glm(Bourletiellidae.diversity~MANAGEMENT*DATE*water+Field,
family=quasipoisson)
summary(modbourdiv)
modbourdiv2<-update(modhypodiv, ~. -MANAGEMENT:DATE:water)
summary(modbourdiv2)
modbourdiv3<-update(modbourdiv2, ~. -DATE:water)
summary(modbourdiv3)
modbourdiv4<-update(modbourdiv3, ~. -MANAGEMENT:DATE)
summary(modbourdiv4)
glm(formula = Hypogasturidae.diversity ~ MANAGEMENT + DATE +
    water + Field + MANAGEMENT:water, family = poisson)
```

R code chapter3

```
#change dir
rm(list=ls())
ctf<-read.csv("CTFdata26092017.csv", header=T)
ctf
attach(ctf)
str(ctf)
summary(DATE)
install.packages("RColorBrewer")
library("RColorBrewer")

##SUMMARY MESOFAUNA GRAPHS
par(mfrow = c(1,1))
boxplot(TOTAL.ABUNDANCE~DATE, xlab="Sampling Date", ylab="Total mesofauna
abundance",names=c("June 2014", "July 2014", "November 2014"))
text(0.7,250, "a",cex=3)
boxplot(ORDER.DIVERSITY~DATE,xlab="Sampling Date", ylab="Total mesofauna order
richness",names=c("June 2014", "July 2014", "November 2014"))
text(0.7,5.7, "b",cex=3)
medianabund<-tapply(TOTAL.ABUNDANCE,DATE,median)
medianabund
medianorder<-tapply(ORDER.DIVERSITY,DATE,median)
medianorder
meanabun<-tapply(TOTAL.ABUNDANCE,list(COMBINED.TREATMENT,DATE),mean)
meanabun
centres<-barplot(meanabun,beside=T,ylim=c(0,250),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean abundance of total
mesofauna",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","san
dybrown"),cex.lab=1.3,cex.names=1)
seabun<-
(tapply(TOTAL.ABUNDANCE,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(TOTAL.ABUN
DANCE,list(COMBINED.TREATMENT,DATE),length)))
seabun
arrows(centres,meanabun+seabun,centres,meanabun-seabun,code=3,angle=90,length=0.1)
legend(x=15, y=250, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
```

```
modtotabun<-
glm(TOTAL.ABUNDANCE~TRAFFIC.TREATMENT*TILLAGE.TREATMENT*DATE*BLOCK,
family=quasipoisson)
summary(modtotabun)

meandiv<-tapply(ORDER.DIVERSITY,list(COMBINED.TREATMENT,DATE),mean)
meandiv
centres<-barplot(meandiv,beside=T,ylim=c(0,10),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean order richness of total
mesofauna",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","san
dybrown"),cex.lab=1.3,cex.names=1)
sediv<-
(tapply(ORDER.DIVERSITY,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(ORDER.DIVER
SITY,list(COMBINED.TREATMENT,DATE),length)))
sediv
arrows(centres,meandiv+sediv,centres,meandiv-sediv,code=3,angle=90,length=0.1)
legend(x=15, y=9, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modordabunseptnov<-
aov(sample(ORDER.DIVERSITY[1:30],15)~ORDER.DIVERSITY[c(36:40,51:60)])
summary(modordabunseptnov)
modtotdiv<-glm(ORDER.DIVERSITY~TILLAGE.TREATMENT*DATE+BLOCK,
family=quasipoisson)
summary(modtotdiv)

meanacari<-tapply(ACARI,list(COMBINED.TREATMENT,DATE),mean)
meanacari
centres<-barplot(meanacari,beside=T,ylim=c(0,100),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean abundance of
acari",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybro
wn"),cex.lab=1.3,cex.names=1)
seacari<-
(tapply(ACARI,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(ACARI,list(COMBINED.TREA
TMENT,DATE),length)))
seacari
arrows(centres,meanacari+seacari,centres,meanacari-seacari,code=3,angle=90,length=0.1)
legend(x=15, y=100, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modacari<-glm(ACARI~TILLAGE.TREATMENT+DATE+BLOCK, family=quasipoisson)
summary(modacari)

##SUMMARY COLLEMBOLA GRAPHS
par(mfrow = c(1,1))
str(ctf)
boxplot(COLLEMBOLA.ABUNDANCE ~DATE, xlab="Sampling Date", ylab="Total collembola
abundance",names=c("June 2014", "July 2014", "November 2014"))
text(0.7,150, "a",cex=3)
boxplot(COLLEMBOLA.DIVERSITY ~DATE ,xlab="Sampling Date", ylab="Total collembola species
richness",names=c("June 2014", "July 2014", "November 2014"))
text(0.7,9, "b",cex=3)
mediancolabund<-tapply(COLLEMBOLA.ABUNDANCE,DATE,median)
mediancolabund
mediancolorder<-tapply(COLLEMBOLA.DIVERSITY,DATE,median)
mediancolorder


meancolabun<-tapply(COLLEMBOLA.ABUNDANCE,list(COMBINED.TREATMENT,DATE),mean)
meancolabun
```

```
centres<-barplot(meancolabun,beside=T,ylim=c(0,150),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean abundance of total collembola",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),cex.lab=1.3,cex.names=1)
secolabun<-
(tapply(COLLEMBOLA.ABUNDANCE,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(COLLEMBOLA.ABUNDANCE,list(COMBINED.TREATMENT,DATE),length)))
secolabun
arrows(centres,meancolabun+secolabun,centres,meancolabun-secolabun,code=3,angle=90,length=0.1)
legend(x=15, y=150, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),box.lty=0)
modtotcolabun<-
glm(COLLEMBOLA.ABUNDANCE~TRAFFIC.TREATMENT*TILLAGE.TREATMENT*DATE*BLOCK, family=quasipoisson)
summary(modtotcolabun)

meancoldiv<-tapply(COLLEMBOLA.DIVERSITY,list(COMBINED.TREATMENT,DATE),mean)
meancoldiv
centres<-barplot(meancoldiv,beside=T,ylim=c(0,10),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean species richness of total collembola",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),cex.lab=1.3,cex.names=1)
legend(x=20, y=10, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),box.lty=0)
secoldiv<-
(tapply(COLLEMBOLA.DIVERSITY,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(COLLEMBOLA.DIVERSITY,list(COMBINED.TREATMENT,DATE),length)))
secoldiv
arrows(centres,meancoldiv+secoldiv,centres,meancoldiv-secoldiv,code=3,angle=90,length=0.1)
legend(x=1, y=9, legend=c("tilled plots", "no till plots"), fill=c("gray18","gray48"),box.lty=0)
modtotcoldiv<-
glm(COLLEMBOLA.DIVERSITY~TRAFFIC.TREATMENT+TILLAGE.TREATMENT+DATE+BLOCK, family=poisson)
summary(modtotcoldiv)

###EACH COLLEMBOLA FAMILY ABUNDANCE

meanhypoabun<-tapply(Hypogasturidae.abundance,list(COMBINED.TREATMENT,DATE),mean)
meanhypoabun
centres<-barplot(meanhypoabun,beside=T,ylim=c(0,20),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean abundance of hypogasturidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),cex.lab=1.3,cex.names=1)
sehypoabun<-(tapply(Hypogasturidae.abundance
,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Hypogasturidae.abundance,list(COMBINED.TREATMENT,DATE),length)))
sehypoabun
arrows(centres,meanhypoabun+sehypoabun,centres,meanhypoabun-sehypoabun,code=3,angle=90,length=0.1)
legend(x=20, y=15, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),box.lty=0)
modhypooabun<-
glm(Hypogasturidae.abundance~TRAFFIC.TREATMENT+TILLAGE.TREATMENT+DATE+BLOCK, family=quasipoisson)
summary(modtotcolabun)
```

```
meanhypodiv<-tapply(Hypogasturidae.diversity,list(COMBINED.TREATMENT,DATE),mean)
meanhypodiv
centres<-barplot(meanhypodiv,beside=T,ylim=c(0,3),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean species richness of hypogasturidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red", "sandybrown"),cex.lab=1.3,cex.names=1)
sehypodiv<-
(tapply(Hypogasturidae.diversity,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Hypogasturi
dae.diversity,list(COMBINED.TREATMENT,DATE),length)))
sehypodiv
arrows(centres,meanhypodiv+sehypodiv,centres,meanhypodiv-
sehypodiv,code=3,angle=90,length=0.1)
legend(x=20, y=3, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modhypoodiv<-
glm(Hypogasturidae.diversity~TRAFFIC.TREATMENT+TILLAGE.TREATMENT+DATE+BLOCK,
family=poisson)
summary(modhypoodiv)

meanisoabun<-tapply(Isotomidae.abundance,list(COMBINED.TREATMENT,DATE),mean)
meanisoabun
centres<-barplot(meanisoabun,beside=T,ylim=c(0,120),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean abundance of isotomidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","san
dybrown"),cex.lab=1.3,cex.names=1)
seisoabun<-(tapply(Isotomidae.abundance
,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Isotomidae.abundance,list(COMBINED.TRE
ATMENT,DATE),length)))
seisoabun
arrows(centres,meanisoabun+seisoabun,centres,meanisoabun-
seisoabun,code=3,angle=90,length=0.1)
legend(x=20, y=100, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modisoabun<-
glm(Isotomidae.abundance~TRAFFIC.TREATMENT*TILLAGE.TREATMENT+DATE+BLOCK,
family=quasipoisson)
summary(modisoabun)

meanisodiv<-tapply(Isotomidae.diversity,list(COMBINED.TREATMENT,DATE),mean)
meanisodiv
centres<-barplot(meanisodiv,beside=T,ylim=c(0,5),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean species richness of isotomidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","san
dybrown"),cex.lab=1.3,cex.names=1)
seisodiv<-
(tapply(Isotomidae.diversity,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Isotomidae.divers
ity,list(COMBINED.TREATMENT,DATE),length)))
seisodiv
arrows(centres,meanisodiv+seisodiv,centres,meanisodiv-seisodiv,code=3,angle=90,length=0.1)
legend(x=20, y=5.1, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modisodiv<-
glm(Isotomidae.diversity~TRAFFIC.TREATMENT+TILLAGE.TREATMENT+DATE+BLOCK,
family=poisson)
summary(modisodiv)

meanentoabun<-tapply(Entomobryidae.abundance,list(COMBINED.TREATMENT,DATE),mean)
```

```
meanentoabun
centres<-barplot(meanentoabun,beside=T,ylim=c(0,20),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean abundance of
entomobryidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red",
"sandybrown"),cex.lab=1.3,cex.names=1)
seentoabun<-(tapply(Entomobryidae.abundance
,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Entomobryidae.abundance,list(COMBINED.T
REATMENT,DATE),length)))
seentoabun
arrows(centres,meanentoabun+seentoabun,centres,meanentoabun-
seentoabun,code=3,angle=90,length=0.1)
legend(x=20, y=20, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modentoabun<-
glm(Entomobryidae.abundance~TRAFFIC.TREATMENT*TILLAGE.TREATMENT+DATE+BLOCK,
family=quasipoisson)
summary(modentoabun)

meanentodiv<-tapply(Entomobryidae.diversity,list(COMBINED.TREATMENT,DATE),mean)
meanentodiv
centres<-barplot(meanentodiv,beside=T,ylim=c(0,3),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean species richness of
entomobryidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red",
"sandybrown"),cex.lab=1.3,cex.names=1)
seentodiv<-
(tapply(Entomobryidae.diversity,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Entomobryid
ae.diversity,list(COMBINED.TREATMENT,DATE),length)))
seentodiv
arrows(centres,meanentodiv+seentodiv,centres,meanentodiv-
seentodiv,code=3,angle=90,length=0.1)
legend(x=20, y=3, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modentodiv<-
glm(Entomobryidae.diversity~TRAFFIC.TREATMENT+TILLAGE.TREATMENT+DATE+BLOCK,
family=poisson)
summary(modentodiv)

meanneelabun<-tapply(Neelidae.abundance,list(COMBINED.TREATMENT,DATE),mean)
meanneelabun
centres<-barplot(meanneelabun,beside=T,ylim=c(0,25),names.arg=c("June 2014", "July 2014",
"November 2014"), xlab="Sampling Date", ylab = "Mean abundance of
neelidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandy
brown"),cex.lab=1.3,cex.names=1)
seneelabun<-(tapply(Neelidae.abundance
,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Neelidae.abundance,list(COMBINED.TREAT
MENT,DATE),length)))
seneelabun
arrows(centres,meanneelabun+seneelabun,centres,meanneelabun-
seneelabun,code=3,angle=90,length=0.1)
legend(x=20, y=20, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep",
"LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"),
fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modneelabun<-
glm(Neelidae.abundance~TRAFFIC.TREATMENT+TILLAGE.TREATMENT*DATE+BLOCK,
family=quasipoisson)
summary(modentoabun)

meanneeldiv<-tapply(Neelidae.diversity,list(COMBINED.TREATMENT,DATE),mean)
```

```
meanneeldiv
centres<-barplot(meanneeldiv,beside=T,ylim=c(0,2),names.arg=c("June 2014", "July 2014", "November 2014"), xlab="Sampling Date", ylab = "Mean species richness of neelidae",col=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandy brown"),cex.lab=1.3,cex.names=1)
seneeldiv<-
(tapply(Neelidae.diversity,list(COMBINED.TREATMENT,DATE),sd)/sqrt(tapply(Neelidae.diversity,li
st(COMBINED.TREATMENT,DATE),length)))
seneeldiv
arrows(centres,meanneeldiv+seneeldiv,centres,meanneeldiv-
seneeldiv,code=3,angle=90,length=0.1)
legend(x=20, y=2, legend=c("CTFZero","CTFDeep", "CTFShallow", "LGPZero", "LGPDeep", "LGPShallow", "RTFZero", "RTFDeep", "RTFShallow"), fill=c("darkgreen","green","lightgreen","darkblue","blue","lightblue","darkred","red","sandybrown"),bo
x.lty=0)
modneeldiv<-
glm(Neelidae.diversity~TRAFFIC.TREATMENT*TILLAGE.TREATMENT+DATE+BLOCK,
family=poisson)
summary(modneeldiv)
```

R code chapter4

```
#change dir
rm(list=ls())
soulton<-read.csv("SoultonMesofauna19092017.csv", header=T)
soulton
attach(soulton)
str(soulton)
summary(DATE)

##SUMMARY MESOFAUNA GRAPHS
par(mfrow = c(1,1))

boxplot(TOTAL.ABUNDANCE~DATE, xlab="Sampling Date", ylab="Total mesofauna abundance",names=c("September 2016", "November 2016", "May 2017"))
text(1,450, "a",cex=3)
boxplot(ORDER.DIVERSITY~DATE,xlab="Sampling Date", ylab="Total mesofauna order richness",names=c("September 2016", "November 2016", "May 2017"))
text(1,7, "b",cex=3)
medianabund<-tapply(TOTAL.ABUNDANCE,DATE,median)
medianabund
medianorder<-tapply(ORDER.DIVERSITY,DATE,median)
medianorder

meanabun<-tapply(TOTAL.ABUNDANCE,list(TREATMENT,DATE),mean)
meanabun
centres<-barplot(meanabun,beside=T,ylim=c(0,250),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean abundance of total mesofauna",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seabun<-
(tapply(TOTAL.ABUNDANCE,list(TREATMENT,DATE),sd)/sqrt(tapply(TOTAL.ABUNDANCE,list(T
REATMENT,DATE),length)))
seabun
arrows(centres,meanabun+seabun,centres,meanabun-seabun,code=3,angle=90,length=0.1)
legend(x=1, y=200, legend=c("tilled plots", "no till plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,220, "a",cex=3)
modtotabunseptnovtill<-
t.test(sample(TOTAL.ABUNDANCE[1:30],15),TOTAL.ABUNDANCE[c(31:35,41:50)])
modtotabunseptnovtill
modtotabunseptnovnotill<-
t.test(sample(TOTAL.ABUNDANCE[1:30],15),TOTAL.ABUNDANCE[c(36:40,51:60)])
modtotabunseptnovnotill
text(2.5,80,"b",cex=1)
```

```
modtotabundnov<-aov(TOTAL.ABUNDANCE[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modtotabundnov)
text(4.5,25,"a",cex=1)
text(5.5,110,"b",cex=1
modtotabunnovmaytill<-
t.test(TOTAL.ABUNDANCE[c(31:35,41:50)],TOTAL.ABUNDANCE[c(61:65,71:80)])
modtotabunnovmaytill
modtotabunnovmaynotill<-
t.test(TOTAL.ABUNDANCE[c(36:40,51:60)],TOTAL.ABUNDANCE[c(66:70,81:90)])
modtotabunnovmaynotill
modtotabundmay<-aov(TOTAL.ABUNDANCE[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modtotabundmay)
text(7.5,215,"c",cex=1)
text(8.5,190,"c",cex=1)

meandiv<-tapply(ORDER.DIVERSITY,list(TREATMENT,DATE),mean)
meandiv
centres<-barplot(meandiv,beside=T,ylim=c(0,6),names.arg=c("September 2016", "November
2016", "May 2017"),xlab="Sampling Date", ylab = "Mean order richness of total
mesofauna",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
sediv<-
(tapply(ORDER.DIVERSITY,list(TREATMENT,DATE),sd)/sqrt(tapply(ORDER.DIVERSITY,list(TRE
ATMENT,DATE),length)))
sediv
arrows(centres,meandiv+sediv,centres,meandiv-sediv,code=3,angle=90,length=0.1)
legend(x=1, y=5.5, legend=c("tilled plots", "no till plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,5.7, "b",cex=3)
modordabunseptnov<-
aov(sample(ORDER.DIVERSITY[1:30],15)~ORDER.DIVERSITY[c(36:40,51:60)])
summary(modordabunseptnov)

modordabunseptnovtill<-
t.test(sample(ORDER.DIVERSITY[1:30],15),ORDER.DIVERSITY[c(31:35,41:50)])
modordabunseptnovtill
modordabunseptnovnotill<-
t.test(sample(ORDER.DIVERSITY[1:30],15),ORDER.DIVERSITY[c(36:40,51:60)])
modordabunseptnovnotill

text(2.5,4.6,"b",cex=1)
modordabundnov<-aov(ORDER.DIVERSITY[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modordabundnov)

modordabunnovmaytill<-
t.test(ORDER.DIVERSITY[c(31:35,41:50)],ORDER.DIVERSITY[c(61:65,71:80)])
modordabunnovmaytill
modordabunnovmaynotill<-
t.test(ORDER.DIVERSITY[c(36:40,51:60)],ORDER.DIVERSITY[c(66:70,81:90)])
modordabunnovmaynotill
modordabundmay<-aov(ORDER.DIVERSITY[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modordabundmay)




text(4.5,2.7,"a",cex=1)
text(5.5,4.5,"b",cex=1)
modordabundmay<-aov(ORDER.DIVERSITY[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
```

```
summary(modordabundmay)
text(7.5,5.9,"c",cex=1)
text(8.5,5.6,"c",cex=1)



##SUMMARY COLLEMBOLA GRAPHS
par(mfrow = c(1,1))
str(soulton)

boxplot(COLLEMBOLA.ABUNDANCE ~DATE, xlab="Sampling Date", ylab="Total collembola
abundance",names=c("September 2016", "November 2016", "May 2017"))
text(1,300, "a",cex=3)
boxplot(COLLEMBOLA.SPECIESDIVERSITY~DATE ,xlab="Sampling Date", ylab="Total
collembola species richness",names=c("September 2016", "November 2016", "May 2017"))
text(1,9, "b",cex=3)
mediancolabund<-tapply(COLLEMBOLA.ABUNDANCE,DATE,median)
mediancolabund
mediancolorder<-tapply(COLLEMBOLA.SPECIESDIVERSITY,DATE,median)
mediancolorder


meancolabun<-tapply(COLLEMBOLA.ABUNDANCE,list(TREATMENT,DATE),mean)
meancolabun
centres<-barplot(meancolabun,beside=T,ylim=c(0,140),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean abundance of
Collembola",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
secolabun<-
(tapply(COLLEMBOLA.ABUNDANCE,list(TREATMENT,DATE),sd)/sqrt(tapply(COLLEMBOLA.AB
UNDANCE,list(TREATMENT,DATE),length)))
secolabun
arrows(centres,meancolabun+secolabun,centres,meancolabun-
secolabun,code=3,angle=90,length=0.1)
legend(x=1, y=100, legend=c("tilled plots", "no till plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,120, "a",cex=3)
modcolabunseptnov<-
aov(sample(COLLEMBOLA.ABUNDANCE[1:30],15)~COLLEMBOLA.ABUNDANCE[c(36:40,51:60)
])
summary(modcolabunseptnov)

modcolabunseptnov<-
aov(sample(ORDER.DIVERSITY[1:30],15)~ORDER.DIVERSITY[c(36:40,51:60)])
summary(modordabunseptnov)

modcolabunseptnovtill<-
t.test(sample(COLLEMBOLA.ABUNDANCE[1:30],15),COLLEMBOLA.ABUNDANCE[c(31:35,41:50
)])
modcolabunseptnovtill
modcolabunseptnovnotill<-
t.test(sample(COLLEMBOLA.ABUNDANCE[1:30],15),COLLEMBOLA.ABUNDANCE[c(36:40,51:60
)])
modcolabunseptnovnotill



text(2.5,47,"b",cex=1)
modcolabundnov<-aov(COLLEMBOLA.ABUNDANCE[DATE=="22-Nov-
16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modcolabundnov)
```

```
modordabundnov<-aov(ORDER.DIVERSITY[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modordabundnov)

modcolabunnovmaytill<-
t.test(COLLEMBOLA.ABUNDANCE[c(31:35,41:50)],COLLEMBOLA.ABUNDANCE[c(61:65,71:80)])
modcolabunnovmaytill
modcolabunnovmaynotill<-
t.test(COLLEMBOLA.ABUNDANCE[c(36:40,51:60)],COLLEMBOLA.ABUNDANCE[c(66:70,81:90)])
modcolabunnovmaynotill
modcolabundmay<-aov(ORDER.DIVERSITY[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modcolabundmay)


text(4.5,9,"b",cex=1)
text(5.5,56,"b",cex=1)
modcolabundmay<-aov(COLLEMBOLA.ABUNDANCE[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modcolabundmay)
text(7.5,102,"c",cex=1)
text(8.5,135,"c",cex=1)


meancoldiv<-tapply(COLLEMBOLA.SPECIESDIVERSITY,list(TREATMENT,DATE),mean)
meancoldiv
centres<-barplot(meancoldiv,beside=T,ylim=c(0,9),names.arg=c("September 2016", "November
2016", "May 2017"), xlab="Sampling Date", ylab = "Mean richness of Collembola
species",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
secoldiv<-
(tapply(COLLEMBOLA.SPECIESDIVERSITY,list(TREATMENT,DATE),sd)/sqrt(tapply(COLLEMBO
LA.SPECIESDIVERSITY,list(TREATMENT,DATE),length)))
secoldiv
arrows(centres,meancoldiv+secoldiv,centres,meancoldiv-secoldiv,code=3,angle=90,length=0.1)
legend(x=1, y=7, legend=c("tilled plots", "no till plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,7.5, "b",cex=3)
modcoldivseptnov<-
aov(sample(COLLEMBOLA.SPECIESDIVERSITY[1:30],15)~COLLEMBOLA.SPECIESDIVERSITY[
c(36:40,51:60)])
summary(modcoldivseptnov)

modcoldivseptnovtill<-
t.test(sample(COLLEMBOLA.SPECIESDIVERSITY[1:30],15),COLLEMBOLA.SPECIESDIVERSITY
[c(31:35,41:50)])
modcoldivseptnovtill
modcoldivseptnovnotill<-
t.test(sample(COLLEMBOLA.SPECIESDIVERSITY[1:30],15),COLLEMBOLA.SPECIESDIVERSITY
[c(36:40,51:60)])
modcoldivseptnovnotill

text(2.5,5.1,"b",cex=1)
modcoldivnov<-aov(COLLEMBOLA.SPECIESDIVERSITY[DATE=="22-Nov-
16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modcoldivnov)
text(4.5,2.1,"a",cex=1)
text(5.5,4.2,"b",cex=1)
modcoldivdmay<-aov(COLLEMBOLA.SPECIESDIVERSITY[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modcoldivdmay)

modcoldivnovmaytill<-
t.test(COLLEMBOLA.SPECIESDIVERSITY[c(31:35,41:50)],COLLEMBOLA.SPECIESDIVERSITY[c
(61:65,71:80)])
```

```
modcoldivnovmaytill
modcoldivnovmaynotill<-
t.test(COLLEMBOLA.SPECIESDIVERSITY[c(36:40,51:60)],COLLEMBOLA.SPECIESDIVERSITY[c
(66:70,81:90)])
modcoldivnovmaynotill
modcoldivmay<-aov(COLLEMBOLA.SPECIESDIVERSITY[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modcoldivmay)



text(7.5,8,"c",cex=1)
text(8.5,7.9,"c",cex=1)

meancolfamdiv<-tapply(COLLEMBOLA.FAMILY.DIVERSITY,list(TREATMENT,DATE),mean)
meancolfamdiv
centres<-barplot(meancolfamdiv,beside=T,ylim=c(0,10),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean richness of Collembola
families",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
secolfamdiv<-
(tapply(COLLEMBOLA.FAMILY.DIVERSITY,list(TREATMENT,DATE),sd)/sqrt(tapply(COLLEMBOL
A.FAMILY.DIVERSITY,list(TREATMENT,DATE),length)))
secolfamdiv
arrows(centres,meancolfamdiv+secolfamdiv,centres,meancolfamdiv-
secolfamdiv,code=3,angle=90,length=0.1)
legend(x=1, y=8, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
modcolfamdivseptnov<-
aov(sample(COLLEMBOLA.FAMILY.DIVERSITY[1:30],15)~COLLEMBOLA.FAMILY.DIVERSITY[c(
36:40,51:60)])
summary(modcolfamdivseptnov)

modcolfamdivseptnovtill<-
t.test(sample(COLLEMBOLA.FAMILY.DIVERSITY[1:30],15),COLLEMBOLA.FAMILY.DIVERSITY[c
(31:35,41:50)])
modcolfamdivseptnovtill
modcolfamdivseptnovnotill<-
t.test(sample(COLLEMBOLA.FAMILY.DIVERSITY[1:30],15),COLLEMBOLA.FAMILY.DIVERSITY[c
(36:40,51:60)])
modcolfamdivseptnovnotill

text(2.5,5.8,"b",cex=1)

modcolfamdivnovmaytill<-
t.test(COLLEMBOLA.FAMILY.DIVERSITY[c(31:35,41:50)],COLLEMBOLA.FAMILY.DIVERSITY[c(6
1:65,71:80)])
modcolfamdivnovmaytill
modcolfamdivnovmaynotill<-
t.test(COLLEMBOLA.FAMILY.DIVERSITY[c(36:40,51:60)],COLLEMBOLA.FAMILY.DIVERSITY[c(6
6:70,81:90)])
modcolfamdivnovmaynotill
modcolfamdivmay<-aov(COLLEMBOLA.FAMILY.DIVERSITY[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modcolfamdivmay)


modcolfamdivnov<-aov(COLLEMBOLA.FAMILY.DIVERSITY[DATE=="22-Nov-
16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modcolfamdivnov)
text(4.5,2.9,"a",cex=1)
text(5.5,4.7,"b",cex=1)
modcolfamdivdmay<-aov(COLLEMBOLA.FAMILY.DIVERSITY[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
```

```
summary(modcolfamdivdmay)
text(7.5,8.2,"c",cex=1)
text(8.5,7.2,"c",cex=1)

###EACH COLLEMBOLA FAMILY ABUNDANCE / DIVERSITY

meanhypoabun<-tapply(Hypogasturidae.abundance,list(TREATMENT,DATE),mean)
meanhypoabun
centres<-barplot(meanhypoabun,beside=T,ylim=c(0,3),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Hypogasturidae
abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
sehypoabun<-
(tapply(Hypogasturidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Hypogasturidae.abund
ance,list(TREATMENT,DATE),length)))
sehypoabun
arrows(centres,meanhypoabun+sehypoabun,centres,meanhypoabun-
sehypoabun,code=3,angle=90,length=0.1)
legend(x=1, y=2.5, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,2.8, "a",cex=3)
modhypoabunseptnovtill<-
t.test(sample(Hypogasturidae.abundance[1:30],15),Hypogasturidae.abundance[c(31:35,41:50)])
modhypoabunseptnovtill
modhypoabunseptnovnotill<-
t.test(sample(Hypogasturidae.abundance[1:30],15),Hypogasturidae.abundance[c(36:40,51:60)])
modhypoabunseptnovnotill
text(2.5,1.5,"a",cex=1)
text(4.5,0.1,"b",cex=1)
text(5.5,0.1,"b",cex=1)
modhypoabunnovmaytill<-
t.test(Hypogasturidae.abundance[c(31:35,41:50)],Hypogasturidae.abundance[c(61:65,71:80)])
modhypoabunnovmaytill
modhypoabunnovmaynotill<-
t.test(Hypogasturidae.abundance[c(36:40,51:60)],Hypogasturidae.abundance[c(66:70,81:90)])
modhypoabunnovmaynotill
modhypoabunseptmaytill<-
t.test(sample(Hypogasturidae.abundance[1:30],15),Hypogasturidae.abundance[c(61:65,71:80)])
modhypoabunseptmaytill
modhypoabunseptmaynotill<-
t.test(sample(Hypogasturidae.abundance[1:30],15),Hypogasturidae.abundance[c(66:70,81:90)])
modhypoabunseptmaynotill
modhypoabunmay<-aov(Hypogasturidae.abundance[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modhypoabunmay)
text(7.5,2.3,"a",cex=1)
text(8.5,1.6,"a",cex=1)

meanhypodiv<-tapply(Hypogasturidae.diversity,list(TREATMENT,DATE),mean)
meanhypodiv
centres<-barplot(meanhypodiv,beside=T,ylim=c(0,0.8),names.arg=c("September 2016", "November
2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Hypogasturidae
diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
sehypodiv<-
(tapply(Hypogasturidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Hypogasturidae.diversity,l
ist(TREATMENT,DATE),length)))
sehypodiv
arrows(centres,meanhypodiv+sehypodiv,centres,meanhypodiv-
sehypodiv,code=3,angle=90,length=0.1)
legend(x=1, y=0.7, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,0.75, "b",cex=3)
modhypodivseptnovtill<-
t.test(sample(Hypogasturidae.diversity[1:30],15),Hypogasturidae.diversity[c(31:35,41:50)])
```

```
modhypodivseptnovtill
modhypodivseptnovnotill<-
t.test(sample(Hypogasturidae.diversity[1:30],15),Hypogasturidae.diversity[c(36:40,51:60)])
modhypodivseptnovnotill
text(2.5,0.55,"a",cex=1)
text(4.5,0.05,"b",cex=1)
text(5.5,0.05,"b",cex=1)
modhypodivnovmaytill<-
t.test(Hypogasturidae.diversity[c(31:35,41:50)],Hypogasturidae.diversity[c(61:65,71:80)])
modhypodivnovmaytill
modhypodivnovmaynotill<-
t.test(Hypogasturidae.diversity[c(36:40,51:60)],Hypogasturidae.diversity[c(66:70,81:90)])
modhypodivnovmaynotill
modhypodivseptmaytill<-
t.test(sample(Hypogasturidae.diversity[1:30],15),Hypogasturidae.diversity[c(61:65,71:80)])
modhypodivseptmaytill
modhypodivseptmaynotill<-
t.test(sample(Hypogasturidae.diversity[1:30],15),Hypogasturidae.diversity[c(66:70,81:90)])
modhypodivseptmaynotill
modhypodivmay<-aov(Hypogasturidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modhypodivmay)
text(7.5,0.55,"a",cex=1)
text(8.5,0.55,"a",cex=1)

meanisoabun<-tapply(Isotomidae.abundance,list(TREATMENT,DATE),mean)
meanisoabun
centres<-barplot(meanisoabun,beside=T,ylim=c(0,120),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Isotomidae
abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seisoabun<-
(tapply(Isotomidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Isotomidae.abundance,list(
TREATMENT,DATE),length)))
seisoabun
arrows(centres,meanisoabun+seisoabun,centres,meanisoabun-
seisoabun,code=3,angle=90,length=0.1)
legend(x=1, y=100, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,110, "a",cex=3)
modisoabunseptnovtill<-
t.test(sample(Isotomidae.abundance[1:30],15),Isotomidae.abundance[c(31:35,41:50)])
modisoabunseptnovtill
modisoabunseptnovnotill<-
t.test(sample(Isotomidae.abundance[1:30],15),Isotomidae.abundance[c(36:40,51:60)])
modisoabunseptnovnotill
text(2.5,33,"a",cex=1)
text(4.5,5,"b",cex=1)
text(5.5,51,"a",cex=1)
modisoabunnovmaytill<-
t.test(Isotomidae.abundance[c(31:35,41:50)],Isotomidae.abundance[c(61:65,71:80)])
modisoabunnovmaytill
modisoabunnovmaynotill<-
t.test(Isotomidae.abundance[c(36:40,51:60)],Isotomidae.abundance[c(66:70,81:90)])
modisoabunnovmaynotill
modisoabunmay<-aov(Isotomidae.abundance[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modhypoabunmay)
text(7.5,86,"c",cex=1)
text(8.5,117,"c",cex=1)

meanisodiv<-tapply(Isotomidae.diversity,list(TREATMENT,DATE),mean)
meanisodiv
```

```
centres<-barplot(meanisodiv,beside=T,ylim=c(0,4),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Isotomidae diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seisodiv<-
(tapply(Isotomidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Isotomidae.diversity,list(TREA
TMENT,DATE),length)))
seisodiv
arrows(centres,meanisodiv+seisodiv,centres,meanisodiv-seisodiv,code=3,angle=90,length=0.1)
legend(x=1, y=3, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,3.5, "b",cex=3)
modisodivseptnovtill<-
t.test(sample(Isotomidae.diversity[1:30],15),Isotomidae.diversity[c(31:35,41:50)])
modisodivseptnovtill
modisodivseptnovnotill<-
t.test(sample(Isotomidae.diversity[1:30],15),Isotomidae.diversity[c(36:40,51:60)])
modisodivseptnovnotill
text(2.5,2.1,"a",cex=1)
text(4.5,1.1,"b",cex=1)
text(5.5,2.3,"a",cex=1)
modisodivnovmaytill<-
t.test(Isotomidae.diversity[c(31:35,41:50)],Isotomidae.diversity[c(61:65,71:80)])
modisodivnovmaytill
modisodivnovmaynotill<-
t.test(Isotomidae.diversity[c(36:40,51:60)],Isotomidae.diversity[c(66:70,81:90)])
modisodivnovmaynotill
modisodivmay<-aov(Isotomidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-May-
17"],DATE[DATE=="23-May-17"])
summary(modhypoabunmay)
text(7.5,3.85,"c",cex=1)
text(8.5,3.95,"c",cex=1)

meanbourabun<-tapply(Bourletiellidae.abundance,list(TREATMENT,DATE),mean)
meanbourabun
centres<-barplot(meanbourabun,beside=T,ylim=c(0,6),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Bourletiellidae abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
sebourabun<-
(tapply(Bourletiellidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Bourletiellidae.abundan
ce,list(TREATMENT,DATE),length)))
sebourabun
arrows(centres,meanbourabun+sebourabun,centres,meanbourabun-
sebourabun,code=3,angle=90,length=0.1)
legend(x=1, y=5, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,5.5, "a",cex=3)
modbourabunseptnovtill<-
t.test(sample(Bourletiellidae.abundance[1:30],15),Bourletiellidae.abundance[c(31:35,41:50)])
modbourabunseptnovtill
modbourabunseptnovnotill<-
t.test(sample(Bourletiellidae.abundance[1:30],15),Bourletiellidae.abundance[c(36:40,51:60)])
modbourabunseptnovnotill
text(2.5,0.3,"a",cex=1)
text(4.5,0.6,"a",cex=1)
text(5.5,0.7,"a",cex=1)
modbourabunnovmaytill<-
t.test(Bourletiellidae.abundance[c(31:35,41:50)],Bourletiellidae.abundance[c(61:65,71:80)])
modbourabunnovmaytill
modbourabunnovmaynotill<-
t.test(Bourletiellidae.abundance[c(36:40,51:60)],Bourletiellidae.abundance[c(66:70,81:90)])
modbourabunnovmaynotill
modbourabunmay<-aov(Bourletiellidae.abundance[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
```

```
summary(modbourabunmay)
text(7.5,4.6,"b",cex=1)
text(8.5,5.4,"b",cex=1)


meanbourdiv<-tapply(Bourletiellidae.diversity,list(TREATMENT,DATE),mean)
meanbourdiv
centres<-barplot(meanbourdiv,beside=T,ylim=c(0,1.5),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Bourletiellidae diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
sebourdiv<-
(tapply(Bourletiellidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Bourletiellidae.diversity,list(
TREATMENT,DATE),length)))
sebourdiv
arrows(centres,meanbourdiv+sebourdiv,centres,meanbourdiv-
sebourdiv,code=3,angle=90,length=0.1)
legend(x=1, y=1.2, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,1.3, "b",cex=3)
modbourdivseptnovtill<-
t.test(sample(Bourletiellidae.diversity[1:30],15),Bourletiellidae.diversity[c(31:35,41:50)])
modbourdivseptnovtill
modbourdivseptnovnotill<-
t.test(sample(Bourletiellidae.diversity[1:30],15),Bourletiellidae.diversity[c(36:40,51:60)])
modbourdivseptnovnotill
text(2.5,0.16,"a",cex=1)
text(4.5,0.19,"a",cex=1)
text(5.5,0.27,"a",cex=1)
modbourdivnovmaytill<-
t.test(Bourletiellidae.diversity[c(31:35,41:50)],Bourletiellidae.diversity[c(61:65,71:80)])
modbourdivnovmaytill
modbourdivnovmaynotill<-
t.test(Bourletiellidae.diversity[c(36:40,51:60)],Bourletiellidae.diversity[c(66:70,81:90)])
modbourdivnovmaynotill
modbourdivmay<-aov(Bourletiellidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modbourdivmay)
text(7.5,1.23,"b",cex=1)
text(8.5,1.35,"b",cex=1)

meanentoabun<-tapply(Entomobryidae.abundance ,list(TREATMENT,DATE),mean)
meanentoabun
centres<-barplot(meanentoabun,beside=T,ylim=c(0,6),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Entomobryidae abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seentoabun<-
(tapply(Entomobryidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Entomobryidae.abunda
nce,list(TREATMENT,DATE),length)))
seentoabun
arrows(centres,meanentoabun+seentoabun,centres,meanentoabun-
seentoabun,code=3,angle=90,length=0.1)
legend(x=1, y=5, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,5.5, "a",cex=3)
modentoabunseptnovtill<-
t.test(sample(Entomobryidae.abundance[1:30],15),Entomobryidae.abundance[c(31:35,41:50)])
modentoabunseptnovtill
modentoabunseptnovnotill<-
t.test(sample(Entomobryidae.abundance[1:30],15),Entomobryidae.abundance[c(36:40,51:60)])
modentoabunseptnovnotill
modentoabunnov<-aov(Entomobryidae.abundance[DATE=="22-Nov-
16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modentoabunnov)
```

```
text(2.5,4,"a",cex=1)
text(4.5,1.2,"b",cex=1)
text(5.5,1.9,"b",cex=1)
modentoabunnovmaytill<-
t.test(Entomobryidae.abundance[c(31:35,41:50)],Entomobryidae.abundance[c(61:65,71:80)])
modentoabunnovmaytill
modentoabunnovmaynotill<-
t.test(Entomobryidae.abundance[c(36:40,51:60)],Entomobryidae.abundance[c(66:70,81:90)])
modentoabunnovmaynotill
modentoabunmay<-aov(Entomobryidae.abundance[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modentoabunmay)
text(7.5,5.6,"a",cex=1)
text(8.5,2.6,"b",cex=1)
modentoabunseptmaytill<-
t.test(sample(Entomobryidae.abundance[1:30],15),Entomobryidae.abundance[c(61:65,71:80)])
modentoabunseptmaytill
modentoabunseptmaynotill<-
t.test(sample(Entomobryidae.abundance[1:30],15),Entomobryidae.abundance[c(66:70,81:90)])
modentoabunseptmaynotill

meanentodiv<-tapply(Entomobryidae.diversity,list(TREATMENT,DATE),mean)
meanentodiv
centres<-barplot(meanentodiv,beside=T,ylim=c(0,1.5),names.arg=c("September 2016", "November
2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Entomobryidae
diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seentodiv<-
(tapply(Entomobryidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Entomobryidae.diversity,li
st(TREATMENT,DATE),length)))
seentodiv
arrows(centres,meanentodiv+seentodiv,centres,meanentodiv-
seentodiv,code=3,angle=90,length=0.1)
legend(x=1, y=1.3, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,1.4, "b",cex=3)
modentodivseptnovtill<-
t.test(sample(Entomobryidae.diversity[1:30],15),Entomobryidae.diversity[c(31:35,41:50)])
modentodivseptnovtill
modentodivseptnovnotill<-
t.test(sample(Entomobryidae.diversity[1:30],15),Entomobryidae.diversity[c(36:40,51:60)])
modentodivseptnovnotill
modentodivnov<-aov(Entomobryidae.diversity[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modentodivnov)
text(2.5,1.03,"a",cex=1)
text(4.5,0.5,"b",cex=1)
text(5.5,0.77,"a",cex=1)
modentodivnovmaytill<-
t.test(Entomobryidae.diversity[c(31:35,41:50)],Entomobryidae.diversity[c(61:65,71:80)])
modentodivnovmaytill
modentodivnovmaynotill<-
t.test(Entomobryidae.diversity[c(36:40,51:60)],Entomobryidae.diversity[c(66:70,81:90)])
modentodivnovmaynotill
modentodivmay<-aov(Entomobryidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modentodivmay)
text(7.5,1.15,"a",cex=1)
text(8.5,0.9,"a",cex=1)
modentodivseptmaytill<-
t.test(sample(Entomobryidae.diversity[1:30],15),Entomobryidae.diversity[c(61:65,71:80)])
modentodivseptmaytill
modentodivseptmaynotill<-
t.test(sample(Entomobryidae.diversity[1:30],15),Entomobryidae.diversity[c(66:70,81:90)])
```

```
modentodivseptmaynotill

meanneelabun<-tapply(Neelidae.abundance,list(TREATMENT,DATE),mean)
meanneelabun
centres<-barplot(meanneelabun,beside=T,ylim=c(0,1),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Neelidae abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seneelabun<-
(tapply(Neelidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Neelidae.abundance,list(TREATMENT,DATE),length)))
seneelabun
arrows(centres,meanneelabun+seneelabun,centres,meanneelabun-seneelabun,code=3,angle=90,length=0.1)
legend(x=1, y=0.8, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,0.9, "a",cex=3)
modneelabunseptnovtill<-
t.test(sample(Neelidae.abundance[1:30],15),Neelidae.abundance[c(31:35,41:50)])
modneelabunseptnovtill
modneelabunseptnovnotill<-
t.test(sample(Neelidae.abundance[1:30],15),Neelidae.abundance[c(36:40,51:60)])
modneelabunseptnovnotill
modneelabunnov<-aov(Neelidae.abundance[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modneelabunnov)
text(2.5,0.03,"a",cex=1)
text(4.5,0.03,"a",cex=1)
text(5.5,0.43,"a",cex=1)
modneelabunnovmaytill<-
t.test(Neelidae.abundance[c(31:35,41:50)],Neelidae.abundance[c(61:65,71:80)])
modneelabunnovmaytill
modneelabunnovmaynotill<-
t.test(Neelidae.diversity[c(36:40,51:60)],Neelidae.abundance[c(66:70,81:90)])
modneelabunnovmaynotill
modneelabunmay<-aov(Neelidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modneelabunmay)
text(7.5,0.25,"a",cex=1)
text(8.5,0.16,"a",cex=1)
modneelabunseptmaytill<-
t.test(sample(Neelidae.abundance[1:30],15),Neelidae.abundance[c(61:65,71:80)])
modneelabunseptmaytill
modneelabunseptmaynotill<-
t.test(sample(Neelidae.abundance[1:30],15),Neelidae.abundance[c(66:70,81:90)])
modneelabunseptmaynotill

meanneeldiv<-tapply(Neelidae.diversity,list(TREATMENT,DATE),mean)
meanneeldiv
centres<-barplot(meanneeldiv,beside=T,ylim=c(0,0.3),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Neelidae diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seneeldiv<-
(tapply(Neelidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Neelidae.diversity,list(TREATMENT,DATE),length)))
seneeldiv
arrows(centres,meanneeldiv+seneeldiv,centres,meanneeldiv-seneeldiv,code=3,angle=90,length=0.1)
legend(x=1, y=0.25, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,0.27, "b",cex=3)
modneeldivseptnovtill<-
t.test(sample(Neelidae.diversity[1:30],15),Neelidae.diversity[c(31:35,41:50)])
modneeldivseptnovtill
```

```
modneeldivseptnovnotill<-
t.test(sample(Neelidae.diversity[1:30],15),Neelidae.diversity[c(36:40,51:60)])
modneeldivseptnovnotill
modneeldivnov<-aov(Neelidae.diversity[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-Nov-
16"],DATE[DATE=="22-Nov-16"])
summary(modneeldivnov)
text(2.5,0.01,"a",cex=1)
text(4.5,0.01,"a",cex=1)
text(5.5,0.14,"a",cex=1)
modneeldivnovmaytill<-t.test(Neelidae.diversity[c(31:35,41:50)],Neelidae.diversity[c(61:65,71:80)])
modneeldivnovmaytill
modneeldivnovmaynotill<-
t.test(Neelidae.diversity[c(36:40,51:60)],Neelidae.diversity[c(66:70,81:90)])
modneeldivnovmaynotill
modneeldivmay<-aov(Entomobryidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-
May-17"],DATE[DATE=="23-May-17"])
summary(modneelabunmay)
text(7.5,0.235,"a",cex=1)
text(8.5,0.14,"a",cex=1)
modneeldivseptmaytill<-
t.test(sample(Neelidae.diversity[1:30],15),Neelidae.diversity[c(61:65,71:80)])
modneeldivseptmaytill
modneeldivseptmaynotill<-
t.test(sample(Neelidae.diversity[1:30],15),Neelidae.diversity[c(66:70,81:90)])
modneeldivseptmaynotill

meanneanabun<-tapply(Neanuridae.abundance,list(TREATMENT,DATE),mean)
meanneanabun
centres<-barplot(meanneanabun,beside=T,ylim=c(0,0.25),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Neanuridae
abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seneanabun<-
(tapply(Neanuridae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Neanuridae.abundance,list
(TREATMENT,DATE),length)))
seneanabun
arrows(centres,meanneanabun+seneanabun,centres,meanneanabun-
seneanabun,code=3,angle=90,length=0.1)
legend(x=1, y=0.2, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,0.22, "a",cex=3)
modneanabunseptnovtill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(31:35,41:50)])
modneanabunseptnovtill
modneanabunseptnovnotill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(36:40,51:60)])
modneanabunseptnovnotill
modneanabunnov<-aov(Neanuridae.abundance[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modneanabunnov)
text(2.5,0.075,"a",cex=1)
text(4.5,0.01,"a",cex=1)
text(5.5,0.01,"a",cex=1)
modneanabunnovmaytill<-
t.test(Neanuridae.abundance[c(31:35,41:50)],Neanuridae.abundance[c(61:65,71:80)])
modneanabunnovmaytill
modneanabunnovmaynotill<-
t.test(Neanuridae.abundance[c(36:40,51:60)],Neanuridae.abundance[c(66:70,81:90)])
modneanabunnovmaynotill
modneanabunmay<-aov(Neanuridae.abundance[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modneelabunmay)
text(7.5,0.01,"a",cex=1)
text(8.5,0.01,"a",cex=1)
```

```
modneanabunseptmaytill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(61:65,71:80)])
modneanabunseptmaytill
modneanabunseptmaynotill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(66:70,81:90)])
modneanabunseptmaynotill

meanneandiv<-tapply(Neanuridae.diversity,list(TREATMENT,DATE),mean)
meanneandiv
centres<-barplot(meanneandiv,beside=T,ylim=c(0,0.25),names.arg=c("September 2016",
"November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Neanuridae
diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
seneandiv<-
(tapply(Neanuridae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Neanuridae.diversity,list(TRE
ATMENT,DATE),length)))
seneandiv
arrows(centres,meanneandiv+seneandiv,centres,meanneandiv-
seneandiv,code=3,angle=90,length=0.1)
legend(x=1, y=0.2, legend=c("Cultivated plots", "Uncultivated plots"),
fill=c("gray18","gray48"),box.lty=0)
text(2,0.22, "b",cex=3)
modneanabunseptnovtill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(31:35,41:50)])
modneanabunseptnovtill
modneanabunseptnovnotill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(36:40,51:60)])
modneanabunseptnovnotill
modneanabunnov<-aov(Neanuridae.abundance[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-
Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modneanabunnov)
text(2.5,0.075,"a",cex=1)
text(4.5,0.01,"a",cex=1)
text(5.5,0.01,"a",cex=1)
modneanabunnovmaytill<-
t.test(Neanuridae.abundance[c(31:35,41:50)],Neanuridae.abundance[c(61:65,71:80)])
modneanabunnovmaytill
modneanabunnovmaynotill<-
t.test(Neanuridae.abundance[c(36:40,51:60)],Neanuridae.abundance[c(66:70,81:90)])
modneanabunnovmaynotill
modneanabunmay<-aov(Neanuridae.abundance[DATE=="23-May-
17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modneelabunmay)
text(7.5,0.01,"a",cex=1)
text(8.5,0.01,"a",cex=1)
modneanabunseptmaytill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(61:65,71:80)])
modneanabunseptmaytill
modneanabunseptmaynotill<-
t.test(sample(Neanuridae.abundance[1:30],15),Neanuridae.abundance[c(66:70,81:90)])
modneanabunseptmaynotill

meantullabun<-tapply(Tullbergiidae.abundance,list(TREATMENT,DATE),mean)
meantullabun
centres<-barplot(meantullabun,beside=T,ylim=c(0,7),names.arg=c("September 2016", "November
2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Tullbergiidae
abundance",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
setullabun<-
(tapply(Tullbergiidae.abundance,list(TREATMENT,DATE),sd)/sqrt(tapply(Tullbergiidae.abundance,l
ist(TREATMENT,DATE),length)))
setullabun
arrows(centres,meantullabun+setullabun,centres,meantullabun-
setullabun,code=3,angle=90,length=0.1)
```

```
legend(x=1, y=6.5, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,6.75, "a",cex=3)
modtullabunseptnovtill<-
t.test(sample(Tullbergiidae.abundance[1:30],15),Tullbergiidae.abundance[c(31:35,41:50)])
modtullabunseptnovtill
modtullabunseptnovnotill<-
t.test(sample(Tullbergiidae.abundance[1:30],15),Tullbergiidae.abundance[c(36:40,51:60)])
modtullabunseptnovnotill
modtullabunnov<-aov(Tullbergiidae.abundance[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modtullabunnov)
text(2.5,5.6,"a",cex=1)
text(4.5,0.7,"b",cex=1)
text(5.5,1.3,"b",cex=1)
modtullabunnovmaytill<-
t.test(Tullbergiidae.abundance[c(31:35,41:50)],Tullbergiidae.abundance[c(61:65,71:80)])
modtullabunnovmaytill
modtullabunnovmaynotill<-
t.test(Tullbergiidae.abundance[c(36:40,51:60)],Tullbergiidae.abundance[c(66:70,81:90)])
modtullabunnovmaynotill
modtullabunmay<-aov(Tullbergiidae.abundance[DATE=="23-May-17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modtullabunmay)
text(7.5,2.9,"c",cex=1)
text(8.5,5.7,"ac",cex=1)
modtullabunseptmaytill<-
t.test(sample(Tullbergiidae.abundance[1:30],15),Tullbergiidae.abundance[c(61:65,71:80)])
modtullabunseptmaytill
modtullabunseptmaynotill<-
t.test(sample(Tullbergiidae.abundance[1:30],15),Tullbergiidae.abundance[c(66:70,81:90)])
modtullabunseptmaynotill

meantulldiv<-tapply(Tullbergiidae.diversity,list(TREATMENT,DATE),mean)
meantulldiv
centres<-barplot(meantulldiv,beside=T,ylim=c(0,1),names.arg=c("September 2016", "November 2016", "May 2017"), xlab="Sampling Date", ylab = "Mean Tullbergiidae diversity",col=c("gray18","gray48"),cex.lab=1.3,cex.names=1)
setulldiv<-
(tapply(Tullbergiidae.diversity,list(TREATMENT,DATE),sd)/sqrt(tapply(Tullbergiidae.diversity,list(TREATMENT,DATE),length)))
setulldiv
arrows(centres,meantulldiv+setulldiv,centres,meantulldiv-setulldiv,code=3,angle=90,length=0.1)
legend(x=1, y=0.9, legend=c("Cultivated plots", "Uncultivated plots"), fill=c("gray18","gray48"),box.lty=0)
text(2,0.95, "b",cex=3)
modtulldivseptnovtill<-
t.test(sample(Tullbergiidae.diversity[1:30],15),Tullbergiidae.diversity[c(31:35,41:50)])
modtulldivseptnovtill
modtulldivseptnovnotill<-
t.test(sample(Tullbergiidae.diversity[1:30],15),Tullbergiidae.diversity[c(36:40,51:60)])
modtulldivseptnovnotill
modtulldivnov<-aov(Tullbergiidae.diversity[DATE=="22-Nov-16"]~TREATMENT[DATE=="22-Nov-16"],DATE[DATE=="22-Nov-16"])
summary(modtulldivnov)
text(2.5,0.75,"a",cex=1)
text(4.5,0.25,"b",cex=1)
text(5.5,0.41,"b",cex=1)
modtulldivnovmaytill<-
t.test(Tullbergiidae.diversity[c(31:35,41:50)],Tullbergiidae.diversity[c(61:65,71:80)])
modtulldivnovmaytill
modtulldivnovmaynotill<-
t.test(Tullbergiidae.diversity[c(36:40,51:60)],Tullbergiidae.diversity[c(66:70,81:90)])
```

```
modtulldivnovmaynotill
modtulldivmay<-aov(Tullbergiidae.diversity[DATE=="23-May-17"]~TREATMENT[DATE=="23-May-17"],DATE[DATE=="23-May-17"])
summary(modtulldivmay)
text(7.5,0.88,"c",cex=1)
text(8.5,0.82,"c",cex=1)
modtulldivseptmaytill<-
t.test(sample(Tullbergiidae.diversity[1:30],15),Tullbergiidae.diversity[c(61:65,71:80)])
modtulldivseptmaytill
modtulldivseptmaynotill<-
t.test(sample(Tullbergiidae.diversity[1:30],15),Tullbergiidae.diversity[c(66:70,81:90)])
modtulldivseptmaynotill
```