



# **Succession of nematodes during composting processes and their potential as indicators of compost maturity**

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## Table of contents

<b>1. General Introduction</b>	<b>15</b>
1.1 Concept of composting and practical use	16
1.2 Parameters affecting composting processes	17
1.3. Compost maturity vs. stability	18
1.4. Compost biology and its potential as an indicator of the composting process status	19
1.4.1. State of the art	19
1.4.2. Mesofauna in compost	20
1.4.3. Potential of mesofauna as ecological indicator in compost	23
1.4.4 Nematode feeding types	26
1.5. Aims	27
1.6. Outline of this study	28
1.7. References	29
<b>2. Pilot study on the nematode community during composting</b>	<b>37</b>
2.1. Abstract	38
2.2. Introduction	38
2.3. Materials and methods	40
2.3.1. Study site and sampling	40
2.3.2. Data collection: environmental variables	41
2.3.3. Nematode community analyses	41
2.3.4. Statistical analyses	42
2.4. Results	43
2.4.1. Environmental variables	43
2.4.2. Nematode community analyses	44
2.5. Discussion	50
2.6 References	53
<b>3. The nematode fauna in compost</b>	<b>59</b>
<b>Part 1: Non-marine nematodes in Belgium: an updated list with special emphasis on compost nematodes.</b>	<b>60</b>
3.1 Abstract	60
3.2. Introduction	60
3.3. Materials & Methods	60

3.4 Results & Discussion	61
3.5. Conclusion	63
<b>Part 2: <i>Mononchoides composticola</i> n. sp. (Nematoda: Diplogasteridae) associated with composting processes: morphological, molecular and autoecological characterization.</b>	<b>78</b>
3.6 Abstract	78
3.7. Introduction	78
3.8. Materials and methods	80
3.9. Results	84
3.10. Discussion	96
3.11. References	99
<b>4. <i>The nematode community as a proxy of the microbial community in a rapidly changing compost environment</i></b>	<b>105</b>
<b>4.1 Abstract</b>	<b>106</b>
<b>4.2 Introduction</b>	<b>106</b>
<b>4.3. Materials and methods</b>	<b>108</b>
4.3.1 Study site and sampling	108
4.3.2 Abiotic data	109
4.3.3 Nematode community	109
4.3.4 Microbial community	110
4.3.5 Statistical analysis	111
<b>4.4. Results</b>	<b>112</b>
4.4.1 Abiotic variables	112
4.4.2 Nematode population dynamics	114
4.4.3. Microbial community dynamics	119
4.4.4. Relationships between microbial and nematode communities	122
<b>4.5. Discussion</b>	<b>122</b>
<b>4.6. References</b>	<b>125</b>
<b>5. <i>Survival and colonization of nematodes in a compost process</i></b>	<b>129</b>
<b>5.1 Abstract</b>	<b>130</b>
<b>5.2 Introduction</b>	<b>130</b>
<b>5.3 Materials and methods</b>	<b>131</b>
5.3.1 Closed vs. non-closed compost processes and its influence on nematode succession	131
5.3.2 Nematode survival	134
5.3.3 Insect phoresy	135

<b>5.4 Results</b>	<b>136</b>
5.4.1 Closed vs. non-closed compost processes and its influence on nematode succession	136
5.4.2 Nematode survival	142
5.4.3 Insect phoresy	142
<b>5.5 Discussion</b>	<b>144</b>
<b>5.6 Supplementary Material</b>	<b>148</b>
<b>5.7 References</b>	<b>150</b>
<b>6. <i>Factors influencing the nematode community during composting: comparison between experimental farm compost and industrial green waste compost</i></b>	<b>153</b>
<b>6.1 Abstract</b>	<b>154</b>
<b>6.2 Introduction</b>	<b>155</b>
<b>6.3 Materials and methods</b>	<b>156</b>
6.3.1 Composting sites and sampling	156
6.3.2 Abiotic variables	158
6.3.3 Nematode community analyses	158
6.3.4 Microbial community analyses	158
6.3.5 Statistical analysis	158
<b>6.4 Results</b>	<b>160</b>
6.4.1 Abiotic variables	160
6.4.2 Nematode community	163
6.4.3 Microbial community	173
<b>6.5 Discussion</b>	<b>177</b>
6.5.1 Microbial succession	177
6.5.2 Nematode succession	177
6.5.3 Green waste compost versus farm compost	179
6.5.4 Conclusion	180
<b>6.6 Supplementary material</b>	<b>181</b>
<b>6.7 References</b>	<b>184</b>
<b>7. <i>Nematode communities and macronutrients in composts and compost-amended soils as affected by feedstock composition</i></b>	<b>187</b>
<b>7.1. Abstract</b>	<b>188</b>
<b>7.2. Introduction</b>	<b>188</b>
<b>7.3. Materials and methods</b>	<b>190</b>

7.3.1. Compost trials	190
7.3.2. Incubation experiments	192
7.3.3. Nematode community analyses	194
7.3.4. Chemical analyses of compost, blank soil and incubated soil	195
7.3.5. Statistical analyses	196
<b>7.4. Results</b>	<b>198</b>
7.4.1. Chemical compost properties	198
7.4.2. Nematode community in composts	201
7.4.3. Effect of compost on soil chemical properties	204
7.4.4. Nematode community after 12 weeks of incubation	204
<b>7.5. Discussion</b>	<b>209</b>
7.5.1. Omnipresence of nematodes in composts and their potential to reflect compost status	209
7.5.2. Effects of compost addition: compost nematodes vs. existent soil-nematode communities	211
<b>7.6 References</b>	<b>213</b>
<b>8. General Discussion</b>	<b>219</b>
<b>8.1 Microbial communities as indicators of compost maturity: methodological considerations</b>	<b>220</b>
<b>8.2 Nematode succession in compost, a newly explored habitat</b>	<b>222</b>
<b>8.3 Nematodes as indicators of compost maturity</b>	<b>226</b>
8.3.1 Chemical versus biological maturity	226
8.3.2 Nematode-based criteria for compost maturity	227
<b>8.4 The importance of nematofauna in compost and its potential benefits</b>	<b>230</b>
<b>8.5 Future prospects: where to go from here?</b>	<b>231</b>
<b>8.6 Conclusion</b>	<b>232</b>
<b>8.7 References</b>	<b>233</b>
<b>9. Summary / Samenvatting</b>	<b>237</b>
9.1 Summary	238
9.2 Samenvatting	241
<b>List of publications</b>	<b>245</b>

# 1. General Introduction

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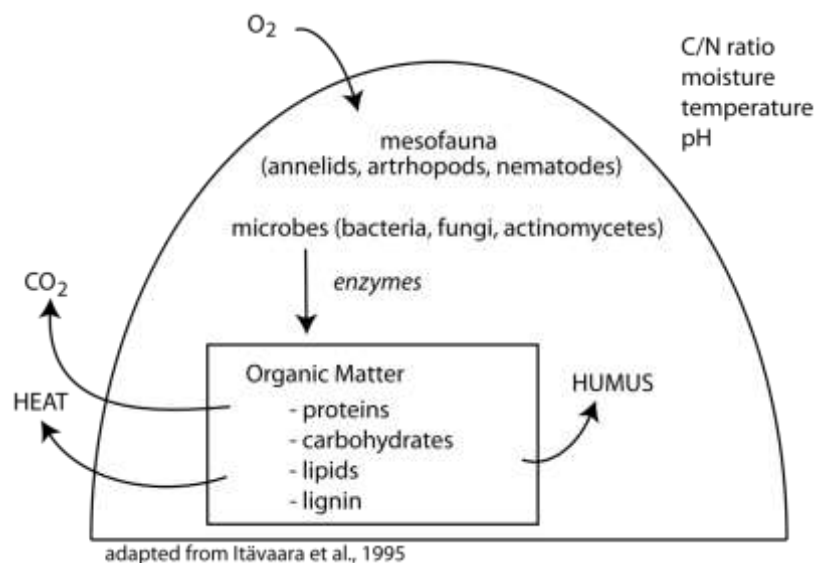
## 1.1 CONCEPT OF COMPOSTING AND PRACTICAL USE

Composting is an aerobic, heat-producing, and controlled process by which a wide spectrum of organisms converts a mixed organic substrate into water; carbon dioxide (CO<sub>2</sub>); inorganic nutrients; and stabilized sanitized organic matter (humus) (Figure 1.1). In contrast to natural rotting or decomposition, the environmental conditions during composting (e.g., moisture, temperature, substrate composition, and oxygenation) remain controllable (Zucconi and de Bertoldi 1987; Sharma et al. 1997; Baldwin and Greenfield 2009) and the process produces a recognizable heat peak (Kutzner 2000) (see also 1.2). Composting is considered important for sustainable agriculture and partly solves the problem of organic waste treatment (Sharma et al. 1997; López et al. 2008). It is an effective tool for the management of municipal and agro-industrial wastes by converting raw organic materials into a stabilized form, destroying human and animal pathogens and recycling valuable plant nutrients (Naidu et al. 2004). Multiple benefits of compost addition to the soil's physical and chemical characteristics have been reported and include increased soil organic matter content (Termorshuizen et al. 2004) and the subsequent improvement of soil aeration, soil porosity, drainage, and water holding capacity (Cogger 2005; Kuo et al. 2004; Termorshuizen et al. 2004). Furthermore, compost can provide an important source of nutrients for plants by providing readily available nitrogen and by promoting mineralization of compost nitrogen in the soil (Cogger 2005; D'Hose et al. 2012; Zvomuya et al. 2008). Composts are also known for their disease-suppressive activity based on both physicochemical and biological mechanisms (Akhtar and Malik 2000; Bailey and Lazarovit, 2003; Kuo et al, 2004; Oka 2010; Reuveni et al. 2002). Another benefit of compost application is the suppression of weed seeds (De Cauwer et al. 2010, 2011). Therefore, truly functional compost should meet criteria for stability and maturity (see 1.3) before application (Zorpas 2009).

The use of compost significantly impacts the soil fauna and flora (Pfozter and Schüler 1997). Application of compost enhanced the biological activity of the soil (i.e. higher microbial activity and higher numbers of protozoa and bacterial-feeding nematodes), resulting in enhanced turnover of organic matter and release of plant available nutrients (Forge et al. 2003). In translocating and transforming litter and soil organic matter and in changing the supply of nutrients to plant roots, soil fauna fulfill crucial roles in the nutrient supply and the conservation of the soil structure (Brussaard et al. 2004). Hence, compost application can strengthen the role of the living soil. However, current insight into the consequences of compost addition for the complex interactions in the soil is limited. In addition, soil biota can be considered important soil



quality indicators. The nematode community in particular is strongly influenced by soil physical and chemical properties (Boag and Yeates 1998; Goralczyk 1998). Furthermore, there is considerable evidence that organic amendments cause changes to the whole soil nematode community, affecting the presence and abundance of different nematode groups (Bulluck et al. 2002; Nahar et al. 2006; Renčo et al. 2010). The soil nematode community, in turn, plays an important role in nutrient cycling because of its abundance, rapid life cycle and intricate interactions with soil microbes and predators (Ingham et al. 1985).



**Figure 1.1**  
Schematic overview of the composting process.

## 1.2 PARAMETERS AFFECTING COMPOSTING PROCESSES

Under optimal conditions the composting process can be divided into temperature-related phases (Tuomela et al. 2000; Ishii et al. 2000; Ryckeboer et al. 2003b): within a few hours or a couple of days after mixing of the feedstock materials, the thermophilic phase (45-70°C) starts, lasting a few days, several weeks or even months (particularly in food wastes). Afterwards there is a mesophilic or cooling phase with temperatures below 45°C, during which mesophile organisms (often different from those of the feedstock materials) recolonize the substrate. The maturation (or curing) phase is a stabilization phase which can last for several weeks to several months. Temperature is very often not uniform throughout the composting mass with the center tending to be hotter than the peripheral edge. Heat production during composting is almost completely due to heat liberation from microbial metabolisms and is mainly determined by the degradability and energy content of the substrates, the availability of moisture and

oxygen, and the mode of energy conservation (Kutzner 2000; Ryckeboer et al. 2003). An adequate supply of oxygen is needed for aerobic microbial activity and to avoid offensive odours primarily produced by the anaerobic microbial community. Since decomposition predominantly occurs in the thin liquid films on the surface of the organic material, moisture plays an essential role (Kutzner, 2000). If moisture levels drop below a critical level (< 30%) microbial activity will decrease, while a moisture content that is too high (>65%) can cause oxygen depletion and losses of nutrients through leaching (Ryckeboer et al. 2003b). Nitrogen and carbon are the primary nutrients required by the microbial community in composting (Xu 2012). Optimal C/N ratio for active composting has been reported to range between 25 and 35 (Tuomela et al. 2000). If N is limiting during the process, decomposition of plant carbohydrates such as hemicellulose and cellulose will be reduced (Eiland et al. 2001). During composting the C/N ratio decreases due to the release of CO<sub>2</sub> as organic substrates are decomposed and due to the incorporation of N-rich microbial/fungal biomass into the organic substrata. Ammonium (NH<sub>4</sub><sup>+</sup>) is released during the rapid degradation of readily available substrates in the beginning of the process and causes the compost pH to increase, generally to above 8 (Wichuk and McCarthney 2010).

### **1.3. COMPOST MATURITY VS. STABILITY**

In order to be considered beneficial for the soil (see also 1.1) compost must be of high quality. Maturity and stability measures are used to evaluate or analyze the composting process and are important parameters for compost quality assessment. Maturity is a general term describing the fitness of the compost for a particular end use, while stability can be defined as the extent to which readily biodegradable material has decomposed (Sullivan and Miller 2001; Gómez et al. 2006). In other words mature compost is ready to use and will not cause adverse effects when used as, or applied to, plant-growing media while stable compost only refers to the resistance of the compost organic matter to further degradation. One of the key issues in compost research is to assess compost maturity as the status of the compost ultimately determines the quality of the product and the associated advantages as mentioned above (Tognetti et al. 2007; Moral et al. 2009). Nevertheless, compost maturity is often loosely defined as the state when compost is dominated by humic substances (Dinel et al. 1996) or as the state where the temperature reaches a near-ambient level (Cooperband 2000). For the past decade, researchers have proposed multiple chemical and physical variables (Zmora-Nahum et al. 2005; Sellami et al. 2008) to assess maturity as well as biological parameters (Gómez et al. 2006). At present and to the best of our knowledge, none of the proposed tests reliably, consistently, and unequivocally

quantifies compost maturity and stability as a stand-alone measure (Rynk 2003; Wichuk and McCartney 2010). Other important characteristics that need to be considered for evaluation of proposed maturity tests are required expertise, necessary lab equipment, time, and costs.

## **1.4. COMPOST BIOLOGY AND ITS POTENTIAL AS AN INDICATOR OF THE COMPOSTING**

### **PROCESS STATUS**

#### **1.4.1. State of the art**

Despite the fact that the compost fauna is not well known, interest in the ecological effects of composting has been growing and recently soil fauna is proposed as a potential tool to evaluate the ecotoxicology of compost (Kapanen and Itavaara 2001). However, the compost is comprised of fauna that can be used in assessing the maturity and quality of the compost. In general, biological parameters have enormous advantages for monitoring a given system, i.e., they are well correlated with ecosystem functioning, they respond sensitively to management practices and climate, and they illustrate the chain of cause and effect (Doran and Zeiss 2000). The surplus value of biological parameters in system monitoring holds true, especially for compost being the direct result of a biological process.

Compost supports a diversity of microbes (e.g., fungi, bacteria, actinomycetes, and algae), micro-fauna<sup>1</sup> (protozoa), and mesofauna<sup>1</sup> (mainly annelids, arthropods, and nematodes) (Cooperband 2000; Young et al. 2005). The microbes and microfauna are the chemical decomposers responsible for the organic matter decomposition through aerobic respiration, while the larger organisms (mesofauna) are the physical decomposers important for the (initial) mechanical breakdown of organic materials into smaller particles, thereby increasing surface area for microbial action (Cooperband 2000; Young et al. 2005) and/or mesofauna, and occupying key positions in the compost food chain.

Although microbes execute the major share of the primary decomposition, mesofauna have multiple advantages over soil microbes and micro-fauna as indicators for the quality and status of the compost. In general, mesofauna are more integrated in the food web by being one or two steps higher and their response to changes in the environment are more significant on a stable temporal scale because of their longer generation time, this way making it possible to

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<sup>1</sup> According to a generalized classification of soil fauna based on body length, microfauna ranges from 0.02 to 0.16 mm while mesofauna ranges from 0.16 to 10.4 mm (from Wallwork, 1970 in Coleman et al. 2004). As such, mesofauna is not synonymous to meiofauna, a term used to describe aquatic benthos retained on sieves with a mesh size of 44 µm but passing through a mesh size of 0.5 mm (Giere 2009), nevertheless both comprise largely the same major taxa, including nematodes.

distinguish between “real” environmental changes and transient nutrient flushes. In addition, some mesofauna groups (e.g., nematodes and mites) occur at more than one level in the energy pyramid and are representative of several levels of consumers.

In this chapter, we provide an overview of the mesofauna found in compost and discuss the potential for each taxon to be an indicator of compost quality and process status. In the second step, the use of effective indicators is further elaborated, based on nematodes as the most promising group.

#### **1.4.2. Mesofauna in compost**

Together with bacteria, fungi, and other microbes (e.g., actinomycetes), the mesofauna in compost form a complex food web or energy pyramid with primary, secondary, and tertiary levels of consumers. Obviously, the base of the pyramid or the energy source is made up of organic matter. All the levels above are populated, though not exclusively, by mesofauna. The mesofauna of compost includes Isopoda, Myriapoda, Acari, Collembola, Oligochaeta<sup>2</sup>, Tardigrada, Hexapoda and Nematoda. This wide spectrum of organisms forms a complex and rapidly changing community that is not limited to a specific compost but can be found from vermicompost to mushroom compost and from small- to large- scale controlled or open-air composting processes. However, the available information on mesofauna from compost is limited and mainly only present in “grey” literature or from non-scientific works. Information on their presence relative to the stage of a compost process (thermophilic phase, cooling phase, and maturation phase) is virtually absent. This limited information on compost mesofauna, ranging from structuring or natural compost inhabitants to more accidental taxa, will be listed in the following text. The known compost taxa can hereby be roughly classified according to the following main focuses: 1) their direct and visible influence on the compost process (i.e., mainly Oligochaeta) and 2) merely accidental records from general biodiversity studies. According to Coleman et al. (2004) earthworms are strictly macrofauna but for the sake of simplicity they are included in this overview of mesofauna.

Within the phylum Annelida, earthworms occur in diverse habitats with a lot of organic material like manure, litter, and compost (Sharma et al. 2005). Earthworms are very important physical decomposers in the composting process because they maintain the aerobic condition in the compost by tunneling, and therefore mechanically partitioning the organic matter while feeding on this material. As a consequence, they facilitate the transformation of nutrients into available

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<sup>2</sup> According to Coleman et al. (2004) some Oligochaeta such as Lumbricidae should be considered as macrofauna but for the sake of simplicity they are here included within the mesofauna.

forms and increase microbial activity (Devliegher and Verstraete 1995; Yakushev et al. 2009). When earthworms are artificially added to a composting process, the process is called vermicomposting. Many recent studies focus on this inoculation with epigeic earthworms and their potential to recycle organic waste materials into value-added products is well documented (e.g., Suthar and Singh 2008). Inoculation with earthworms accelerated the decomposition process (Manna et al. 2003), though the composting potential of different species in diverse compost situations remains to be investigated (Suthar and Singh 2008). In a study on forest litter decomposition by Manna et al. (2003), the composting potential of *Eisenia fetida* was clearly superior compared to other species (i.e., *Perionyx excavatus* and *Dicogaster bolau*). At present, *E. fetida* is the most popular compost earthworm and is known under various common names, including redworms, brandling worms, and tiger worms. Owing to its recognized function in a compost process, *E. fetida* specimens are widely commercially available in temperate regions for use in vermiculture. Domínguez et al. (2001) investigated the biology and ecology of the earthworm *Eudrilus eugeniae*, which is indigenous in Africa but bred extensively internationally for the fish bait market. These researchers concluded that this earthworm species might be a good candidate for vermicomposting in tropical climates. Thus, earthworms have a well-known positive effect on compost, but they usually only reach high densities after inoculation and/or within specific controlled circumstances. Furthermore, they are not present in all stages of the composting process.

Mites (Acari) are commonly found in compost (Ødegaard and Tømmerås 2000). Smith et al. (1998) and Skoracka et al. (2002) provided an overview of the species found in the investigated composts (respectively in Canada and in Central Europe). Clift and Terras (1995) associated bio-indicator value with mites based on a reported range of mite fauna in most of their investigated mushroom composts. This study reported the presence of either red pepper mites (*Siteroptes mesembrinae*) and/or bacterial feeding mites (*Histiostoma feroniarum*) and associated these mites with the reduced mushroom yield. Clift and Terras (1995) believe these species can serve as an indicator species for poor pasteurization or conditioning in mushroom compost processes. Other encounters with mites (i.e., *Pygmephorus* sp., *Histiostoma* sp., and *Parasitus bituberosus*) in mushroom compost were reported by Al-Amidi (1995). Although the contributions of mites in the compost food web are not known, mites cover multiple levels of the food web, ranging from scavenging on organic debris to fungal-feeding, bacterial-feeding, and predators, and most likely can have a certain structuring effect on the compost process, but this is not yet studied.

Within the arthropods, beetles (Coleoptera) are the most diverse animal group and they can

be found in almost all habitats, including compost (Ødegaard and Tømmerås 2000). Beetles might act as decomposers, fungivores, or as predators on other insects present in the compost (Ødegaard and Tømmerås 2000). Compost heaps can be very rich in beetle species: 273 species were found in compost from Lulea in northeastern Sweden (Lundberg and Persson 1973), >260 species in different composts from Uppsala in central Sweden (Palm 1979), and 225 species in seed-composts from Skane in southern Sweden (Baranowski 1978). A number of exotic beetle species (34) have been established in compost heaps in the Nordic countries during the 20th century. Ødegaard and Tømmerås (2000) hypothesized that the successful establishment of exotic species in compost habitats results from the increased frequency of introductions and warm, thermal stability in large compost heaps during the Nordic winter.

Woodlice (Isopoda) are saprophages that generally live in moist soil, but some species such as *Porcellionides pruinosus* and *P. sexfasciatus* live aggregated in compost and manure heaps (Achouri et al. 2008). Terrestrial isopods are principally consumers of organic debris in an ecosystem. However, according to Messelink and Bloemhard (2007), extreme populations of woodlice may cause serious damage to vegetables. But whereas populations of woodlice increased strongly in fresh compost, in mature compost they barely survived. Therefore, Messelink and Bloemhard (2007) stressed the importance of a complete compost process in order to manage woodlice populations at an acceptable level.

Centipedes (Chilopoda) and millipedes (Myriapoda) are another group of more accidental compost mesofauna. Centipedes are mainly carnivores (Wallwork 1976; Lewis 1981), while millipedes (Diplopoda) feed on plant materials and fragments of decaying organic material, though both groups are found in similar habitats. In urban areas, their common microhabitat is often extended by building stacks of materials like compost and garbage piles (Riedel et al. 2009). The distribution of *Oxidus gracilis* (millipedes) is connected with greenhouses and gardens with compost heaps in higher altitudes (Bergersen et al. 2006). Identified centipedes collected from compost heaps include *Geophilus proximus* and *Haplophilus subterraneus* (Rosenberg and Seifert 1977; Bergersen et al. 2006).

Gutiérrez and Mazo (2004) reported springtails (Collembola) from compost processed at the Corporación Universitaria Lasallista, Colombia. More specific recordings were done by Fjelberg (1998) and Gisin (1960), who found *Hypogastrura manubrialis* and *H. purpurascens* in compost. Nowadays, springtail reproductions in compost products are often used to develop ecotoxicological tests (e.g., *Folsomia candida* (Crouau et al. 2002)) or to investigate the survival of potential biocontrol species after the addition in composts (e.g., *Protaphorura*

*armata* (Sabatini et al. 2006)).

There also have been more isolated recordings of other Arthropoda taxa in compost. Gutiérrez and Vera (2004) found five different families of ants in the compost of the Corporación Univeristaria. Lasallista and Buddle (2010) reported compost heaps as typical habitats for pseudoscorpions. Goulson et al. (1999) found very large calyptrate fly populations associated with composting sites in the United Kingdom, probably caused by the abundance of warm decaying organic matter. Flies are, however, not involved in the decomposition process itself but use the compost heap as a breeding site.

Tardigrades or water bears, exhibit a high tolerance to extreme environmental conditions such as temperature, making them a likely group to appear in compost. However, published recordings of Tardigrada in compost are scarce. Vargha (1995) described *Hexapodibius reginae* from compost and Hatamoto et al. (2008) recorded tardigrades in rice straw compost using DGGE analysis. Our own observations indicate the accidental presence of tardigrades in compost (observations in the framework of this study).

Finally, recordings of nematodes in isolated compost samples were made by several authors, including Andrassy (1983), Anderson (1983), Gagarin (2000), Nadler et al. (2003), and Manso (2004). These primarily bacterivorous nematodes were recorded in general biodiversity studies, but their function within the compost process was not discussed. All the above mesofauna groups can be found in compost, but except nematodes none of them has been consistently found in all investigated compost types. Furthermore none of these groups is hitherto reported to be found throughout all successive compost stages. Considering the population dynamics in relation to the composting process, none of the above taxa have been thoroughly investigated.

### **1.4.3. Potential of mesofauna as ecological indicator in compost**

Several authors have used microbial communities (bacteria and fungi) to evaluate compost maturity. For example, Eiland et al. (2001) analyzed phospholipid fatty acid (PLFA) profiles of compost microbial communities but concluded that there was no correlation with compost maturity. Conversely, Steger et al. (2003, 2005, and 2007) and Ryckeboer et al. (2003a) found typical changes in the microbial community but stressed the need for more studies on different composts. An elaborate overview of bacteria and fungi occurring during composting and self-heating processes is given in Ryckeboer et al. (2003b). However, mesofauna has multiple advantages over microbial communities as indicators for the quality and status of compost. Firstly, it is very difficult and time-consuming to identify all bacteria, fungi, and protozoa in a sample and databases of biochemical profiles are either incomplete or inadequate, especially

for free-living taxa. Secondly, by being one or two steps higher in the food chain, mesofauna serve as integrators of physical, chemical, and biological properties related to their food resources. Third, their generation time (days to years) is longer than that of metabolically active microbes (hours to days), making them more stable temporally and not simply fluctuating with ephemeral nutrient flushes (Neher 2001).

A successful indicator must be able to reflect a past ecological process or predict a future ecological process (Neher and Darby 2009). Therefore, an indicator should have as many as possible of the following characters. For soil condition, the indicator should 1) reflect the structure and/or function of ecological processes in the soil no matter what geographical location is sampled, 2) respond to changes in soil condition, 3) have available methodologies, 4) be comprehensible, and 5) be inexpensive to measure (Neher et al. 2005; Doran and Zeiss 2000). Obviously, a thorough knowledge of the fauna used as an indicator is necessary; however, from the overview, it is clear that the knowledge of compost fauna is only fragmentary. Nevertheless, some mesofaunal taxa present in compost, such as Collembola, mites, earthworms and nematodes, have already proven their potential as bio-indicators (Table 1.1).

Collembola and mites have been widely used to assess the impact of agricultural management practices and disturbances. For example, Barbercheck et al. (2009) reported differences in richness, evenness, and abundances of mites and proportions of collembolans among agricultural sites. Other examples for mites as a bio-indicator include Koehler (1999), Gulvik (2007), and Bedano and Ruf (2010) and for Collembola include Fiera (2009), Chagnon et al. (2000) and Baretta et al. (2008). Despite their potential as bio-indicators, the evaluation of their community assemblages is often limited (O'Neill et al. 2010), due to the high proportion of undescribed species (Coleman and Whitman 2005) and insufficient information on general biology, distribution, and functional roles (Bolger 2001; Greenslade 2007). Geissen and Kampichler (2004) also questioned the suitability of collembolan communities as indicators to determine the influence of amelioration measures on soil ecosystems in European forests because they could not find a relationship after five years of study. This limited literature review shows that there is no univocal consensus about the use of mites and Collembola as bio-indicators in terrestrial ecosystems. Hence, an extrapolation to compost is not evident.

Conversely, the potential of earthworms as indicators of environmental changes is more generally accepted. Their possibilities as bio-indicators are based on community changes (Tondoh et al. 2007) or on a quantifiable bioaccumulation of metals in their tissues (Suthar et al. 2008). However, earthworms do not occur in every composting stage and process and



the accumulation of contaminations is not the main or only focus in assessing the compost status.

Unlike earthworms, Collembola, or mites, nematodes are ubiquitous, even in disturbed or polluted areas (Neher et al. 2005). Nematodes live beside the most diverse and abundant soil organisms and are the most important secondary consumers within soil mesofauna (Mulder et al. 2005). They have been extensively used as indicators of soil biodiversity and functioning (Neher 2001; Mulder et al. 2005) and as indicators of environmental disturbances in soil (Bongers and Ferris 1999; Ferris et al. 2001; Yeates 2003; Cerevková and Renč o 2009). They occupy key positions in the food web because they interact with the species providing their food (e.g., bacteria, fungi, etc.) and other organisms using the same food resources. They are also involved in predator-prey interactions (e.g., protozoa, fungi, and mites as well as nematodes) (Yeates et al. 2009). In these ways, changes in the food web are mirrored in shifts among nematode feeding groups (Yeates et al. 2009). Most importantly, nematodes show a rapid response, translated into proportions of functional (feeding) groups, to changes in the microbial decomposition pathway and the availability of food sources (Yeates et al. 1999; Brimecombe et al. 2001; Zelenev et al. 2004; Sánchez-Moreno et al. 2008), due to their relatively short generation time (Bongers 1990). In addition, the transparent nature of nematodes allows easy observation of the clear relationship between structure and function: their feeding behavior (see 1.4.4) is easily deduced from the structure of the mouth cavity and pharynx (Bongers and Ferris 1999). Furthermore, the relative abundance and small size of nematodes makes sampling relatively easy and cheap. Neher et al. (2005) and Sánchez-Moreno et al. (2009) validated the hypotheses that nematode-based soil food web indices are useful indicators of other soil organisms such as mites. Hence, nematode faunal assemblages theoretically have all of the properties needed to enable an optimal *in situ* assessment of the compost process, based on evaluation and interpretation of their abundance and function.

**Table 1.1°**

Overview of the mesofauna groups with potential use as bio-indicator and their characteristics.

	Mites	Collembola	Earthworms	Nematodes
<b>OCCURENCE</b>				
- Cosmopolitan/ ubiquitous				X
- Large population size			X*	X
- Present on more than 1 level in food web	X	X		X
<b>FUNCTION &amp; SERVICES IN ECOSYSTEM</b>				
- Important role in N-mineralization				X
- Potential to regulate even suppress magnitude of resources	X		X	X
- Variable sensitivity to stress factors, from extremely sensitive to extremely tolerant			X	X
<b>PRACTICAL APPLICABILITY</b>				
- Easily extracted and cultured				X
- Easy observation				X
- Identification up to species level not needed	X			X
- Inexpensive techniques and methodologies	X	X	X	X

\*When artificially added to the process.

°For references see text 1.4.3.

#### 1.4.4 Nematode feeding types

Assignment of nematodes to feeding groups provides insight into the functional role of nematodes in the ecosystem and into the effect of environmental changes on the nematode fauna (Yeates et al. 1993). Although it is clear that nematode feeding types are linked to stoma morphology, inferred feeding strategies without any empirical evidence can be misleading (Yeates et al. 1993). For example similar stoma structures may be used for different feeding behaviours. This is the case within the aphelenchid nematodes where *Aphelenchoides* may be classified as hyphal feeders and ecto- or endoparasites of plants, while the related genus *Seinura* is a predator (Moens et al. 2004). In other cases, species are allocated to one feeding type while they have developmental stages or generations that fit another feeding type (Neher 2001). In addition, the relevance of the (usually non-feeding) free-living stages of animal parasites and of the omnivores (which can be easily allocated to feeding types 3 to 6) for trophic studies has been questioned (Moens et al. 2004). The trophic classification of nematodes in Yeates et al. (1993), which is broadly used and has also been adopted in this study, heavily relies on stoma morphology but has been supplemented to a certain extent with experimental evidence. Yeates et al. (1993) distinguished 8 main feeding types; (1) plant-feeding, (2) hyphal- or fungal-feeding, (3) bacterial-feeding, (4) substrate ingesters, (5) carnivores, (6) unicellular eukaryote feeders, (7) dispersal stages of animal parasites, and (8) omnivores. Not all these feeding types are expected to occur in compost. For example in the absence of living plant tissue, plant feeding nematodes are expected to be absent, which substantially simplifies feeding type allocation of nematodes with stylet or spear.

## 1.5. AIMS

The overall aim of this study is to contribute to a better understanding of the compost biology during the composting process. Given its potential as bio-indicator for compost, as described above, we especially address the nematode community.

The main objectives of this study are to describe the nematode fauna of a virtually unexplored habitat, to provide the first insights in the nematode succession in a rapidly changing compost environment, to examine the effect of the compost comprising nematodes on the nematodes that are already present in the soil and finally to evaluate the potential of the nematode community as an indicator of compost maturity and quality. These main objectives translate into the following specific objectives:

- (i) To acquire fundamental knowledge on the nematode diversity in compost based on morphological analyses of the nematode community, complemented with sequence data. Compare the diversity of compost nematodes with the terrestrial nematofauna in Belgium. Assess whether the same nematode taxa can be found in disparate composting processes using different feedstock materials (Chapter 3).
- (ii) To obtain an integrated insight into the succession and the trophic structure of the nematode community during the composting process and link this to a selection of relevant biotic (microbial community) and abiotic factors (time of composting, temperature, pH, moisture content and C/N ratio) (Chapters 2, 4 & 6). This is complemented with experiments to reveal the feeding behavior of one of the dominant nematodes found in most of our composting trials (Chapter 3).
- (iii) To assess the survival and colonization capacity of nematodes in compost, by analyzing temperature tolerance and evaluating the importance of insect phoresy<sup>3</sup> for nematode arrival at the composting process (Chapter 5).
- (iv) To test the bio-control potential of compost with its associated nematodes by assessing the (short term) development of a soil nematode community after application of mature compost – comprising nematodes – to this soil. Does the species composition of the compost affect the nematode community in the soil? For instance, will the number of plant-parasitic nematodes in the soil decrease and the number of predators and fungal-feeding nematodes increase? (Chapter 7).

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<sup>3</sup> Insect phoresy or vectoring is a form of commensalism; a relationship where nematodes use mostly Arthropoda for dispersal or shelter but have no direct trophic relationship with them (Timper and Davies 2004; Dillman et al. 2012).

## 1.6. OUTLINE OF THIS STUDY

This thesis is divided into 8 chapters.

Chapter 1 is a general introduction, illustrating the context in which this study is situated and explaining the main aims of this work and their logical flow.

Chapters 2-7 contain the effective results, each with their respective specific introduction, material and methods, results and discussion. These chapters have been drafted according to requirements for manuscripts in SCI-indexed journals.

- Chapter 2, **Pilot study on the nematode community during composting**, presents the first detailed data on nematodes during composting.
- Chapter 3, **The nematode fauna in compost**, includes the species description of *Mononchoides composticola* n. sp. isolated from compost, and contains an updated checklist of free-living and plant-parasitic nematodes in Belgium.
- Chapter 4, **The nematode community as a proxy of the microbial community in a rapidly changing compost environment**, describes the temporal succession of both the microbial and the nematode community and their link during a composting process.
- Chapter 5, **Survival and colonization of nematodes in a compost process**, presents the results of experiments on temperature tolerance and on different colonization routes of compost by nematodes, including vectoring by insects.
- Chapter 6, **Factors influencing the nematode community during composting**, describes the relation of the nematode community dynamics with potentially important variables, i.e. temperature, time of composting and the microbial community.
- Chapter 7, **Nematode communities and macronutrients in composts and compost-amended soils as affected by feedstock composition**, presents the short term effect of compost and its associated nematodes on the soil chemical properties and the existing nematode community.

Chapter 8 contains the general discussion, which integrates the principal findings of Chapters 2-7.

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## 2. Pilot study on the nematode community during composting

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Modified from:

Steel H, de la Peña E, Fonderie P, Willkens K, Borgonie G and Bert W (2010). Nematode succession during composting and the potential of the nematode community as an indicator of compost maturity. *Pedobiologia* 53: 181-190.

## 2.1. ABSTRACT

One of the key issues in compost research is to assess when the compost has reached a mature stage. The maturity status of the compost determines the quality of the final soil amendment product. The nematode community occurring in a Controlled Microbial Composting (CMC) process was analyzed with the objective of assessing whether the species composition could be used as a bio-indicator of the compost maturity status. The results obtained here describe the major shifts in species composition that occur during the composting process. Compared to terrestrial ecosystems, nematode succession in compost differs mainly in the absence of K-strategists and numerical importance of diplogastrids. At the beginning of the composting process (thermophilic phase), immediately after the heat peak, the nematode population is primarily built by bacterial feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogastridae) followed by the bacterial-feeding general opportunists (cp-2) (Cephalobidae) and the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, during the cooling and maturation stage, the bacterial-feeding/predator opportunistic nematodes (*Mononchoides* sp.) became dominant. Finally, at the most mature stage, the fungal-feeding Anguinidae (mainly *Ditylenchus filiformis*) were most present. Both, the Maturity Index (MI) and the fungivorous/bacterivorous ratio (f/b ratio), increase as the compost becomes more mature (ranging, respectively, from 1 to 1.86 and from 0 to 11.90). Based on these results, both indices are suggested as potential suitable tools to assess compost maturity.

## 2.2. INTRODUCTION

Composting is an aerobic, heat-producing and controlled process by which microorganisms convert a mixed organic substrate into carbon dioxide (CO<sub>2</sub>), water, inorganic nutrients and stabilized organic matter. Control of the environmental conditions (moisture, temperature, substrate composition and oxygenation) during the process distinguishes composting from natural rotting or decomposition (Zucconi and de Bertoldi 1987; Baldwin and Greenfield 2006). The application of compost to soil has several benefits. The stabilized organic matter in compost improves soil structure. Consequently, soil aeration, soil porosity, water holding capacity and drainage increase (Kuo et al. 2004; Cogger 2005; Baldwin and Greenfield 2006). Furthermore, compost can provide an important source of nutrients for plants (for reviews see Cogger 2005; Zvomuya et al. 2008), especially the compost nitrogen that becomes available for plants after mineralization in the soil (Hadas and Portnoy 1997). In addition, composts are known to

suppress plant diseases through a combination of physiochemical and biological mechanisms (Akhtar and Malik 2000; Gamliel et al. 2000; Reuveni et al. 2002; Bailey and Lazarovits 2003; Vallad et al. 2003; Kuo et al. 2004).

Controlled Microbial Compost (commonly known as CMC or “Leubke compost”) is a premium grade and well-humified compost. The CMC method was developed through on-farm and laboratory research by the Leubke family (Diver 2004). The composting is carried out in windrows and during the process abiotic parameters such as CO<sub>2</sub> and temperature are intensively monitored. A microbial starter is usually added to inoculate the compost (Diver 2004). This method ensures process control by appropriate aerating through turning, prevention of nutrient leaching and/or reduction of gaseous emissions and heat losses through covering the heap (Rees 2007).

During composting, organic materials are disintegrated by processes associated with several organisms. The taxa that are most important to the composting process are Bacteria, Algae, Fungi, Isopoda, Acari, Nematoda and Protozoa. This wide spectrum of organisms forms a complex and rapidly changing community. Up to the present, only the dynamics of the bacterial community have been thoroughly investigated in relation to composting processes (e.g. Herrmann and Shann 1997; Ishii et al. 2000; Alfreider et al. 2002; Tiquia et al. 2002; Ryckeboer et al. 2003; Tiquia 2005; Fracchia et al. 2006; Halet et al. 2006). Research concerning the role of nematodes in decomposition processes tends to focus on specific natural processes in the soil (Ingham et al. 1985; Ruess 2003; Ruess and Ferris 2004; Wang et al. 2004; Georgieva et al. 2005; Postma-Blaauw et al. 2005) or on laboratory microcosm experiments with bacterial-feeding nematodes and their influence on the decomposition rate of organic material of marine environments (De Mesel et al. 2003, 2004, 2006). Although nematodes appear to be numerically important in the composting process, and their diversity and density in mature compost are considered crucial to constructing a robust soil food web (Ingham 2001, 2006; Ingham and Slaughter 2004), knowledge of the diversity and succession of the nematode community during the composting process is completely lacking. Moreover, nematodes show several characteristics which make them ideal bio-indicators of the ecosystem quality. Nematode community analyses are very useful in assessing ecosystem status and functions since nematodes are ubiquitous and easy to sample (Bongers and Ferris 1999; Ritz and Trudgill 1999; Yeates and Bongers 1999; Neher 2001; Yeates 2003). Furthermore, the species composition of the samples reflects a wide range of abiotic parameters such as substrate texture, climate, biogeography, organic inputs and both natural and anthropogenic disturbances (Yeates 1984; Neher 2001; Yeates 2003). The use of nematodes as functional indicators relies on the allocation

of nematodes to feeding groups (Yeates et al. 1993) and reproductive strategies (cp values) (Bongers 1990; Yeates 2003). Nematode genera with the same cp value are adapted to specific environmental conditions and food sources through anatomical and physiological commonalities (Ferris et al. 2001) and are similar in their responses to disturbance (Bongers 1999; Bongers and Ferris 1999).

One of the key issues in compost research is to assess when the compost has reached a mature stage. The maturity status of the compost determines ultimately the quality of the product. So far numerous tests, based on both physical and chemical parameters, have been proposed (e.g. Butler et al. 2001; Tiquia 2005; Chikae et al. 2006; Castaldi et al. 2008) but unfortunately, many of these have not been proven rigorous, reliable or consistent enough to be used in standard protocols, and those that are would require such a substantial investment in laboratory equipment and staff training that their use in regular composting laboratories is not feasible (Kuo et al. 2004; Baldwin and Greenfield 2006).

Since information on nematode populations in compost is virtually lacking, the first objective of this study was to analyze the structure and succession of the nematode community during a composting process. Secondly, we explored the possibilities of relating the observed structure of the nematode community structure to compost maturity.

## **2.3. MATERIALS AND METHODS**

### **2.3.1. Study site and sampling**

The examined compost heap was located at the Institute for Agricultural and Fisheries Research in Merelbeke, Belgium (Plant Science Unit, Growth and Development research area). The heap was composed of three different feedstock materials: 43% on a volume to volume base (% v/v) fine wood chips, 43% (v/v) dry hay and 14% (v/v) fresh grass. The C/N ratios of the feedstock materials were respectively approximately 90/1, 30/1 and 15/1. The heap was 50 m long, 3 m wide and 1.5 m high, and consisted of 3 m<sup>3</sup> feedstock materials per lineal meter. The compost was prepared according to the CMC method (Diver 2004), but no microbial starter was added.

A total of 45 composite samples on 15 different sampling moments were taken during the entire composting process. The entire monitored process lasted six months, from September 2006 to March 2007. During the first three weeks of the process, samples were taken twice a week (6 samples), after which sampling was reduced to once a week for seven weeks (7 samples). At the end of the process the heap was sampled once after one month and again after two months. By following this sampling pattern the complete process was observed and the changes in species



composition throughout could be investigated. Each sample was composed of 20 randomly picked samples of 50 ml of compost each. The samples were mixed to make a total volume of 1 L, from which a subsample of 100 ml was taken for nematode extraction. This sampling procedure was repeated 3 times per sampling event. Hence, replicate samples were taken from a single compost heap and are thus essentially pseudoreplicates.

### **2.3.2. Data collection: environmental variables**

The following abiotic variables were measured at every sampling: temperature (°C), moisture content, pH and percent carbon dioxide (CO<sub>2</sub>). Temperature and CO<sub>2</sub> content were measured in 3 locations on the heap using specialized equipment (respectively, Digital Thermometer GTH 1150 and Brigon Messtechnik D-63110 Rodgau). For the pH measurements, extractions of 20 g compost in 100 ml distilled water were made. The extractions were shaken by hand 3 times every 2 h and pH was measured with standard electrodes (Consort P400). The moisture content was determined by weighing 50 ml of compost before and after incubation for 48 h at 102 °C.

### **2.3.3. Nematode community analyses**

The existing nematodes in the subsample (100 ml) were extracted from the compost using a modified Baermann funnel method (tray 49 cm x 37.5 cm, basket 38.5 cm x 19.5 cm) (Hooper 1986). Nematodes were counted and 100 individuals were randomly picked out using a stereomicroscope (Leica MZ95). For light microscopical observations, half of the specimens were collected in a very small drop of water in an embryo dish. Formaldehyde (4% with 1% glycerol) was heated to 70 °C and an excess (4-5 ml) was quickly added to the specimens to fix and kill the nematodes (Seinhorst 1966). The fixed nematodes were processed to anhydrous glycerol following the glycerol-ethanol method (Seinhorst 1959, as modified by De Grisse 1969) and mounted on aluminium slides with double cover slips (Cobb 1917). As a supplement to this standard evaluation method, the remaining nematodes were mounted on mass slides (slide 40 mm x 76 mm; cover glass 34 mm x 60 mm). Measurements were prepared manually with a camera lucida on an Olympus BX 51 DIC microscope (Olympus Optical, Tokyo, Japan), which was equipped with an Olympus C5060WZ camera for photographs. Nematodes were identified to genus and species whenever possible. The abundance (individuals/gram dry weight compost) of each genus or species in each sample was determined. Dauer larvae were not included in the total counts and species analysis because accurate identification is often impossible and their immobility hampers a quantitative estimation using a mobility-based nematode extraction. In order to test whether dauer stages or eggs were able to survive the heat peak, additional samples from day 3, 6 and 9 were incubated on agar plates (1% nutrient agar plates containing

2.7 g bacteriological agar, 1.3 g nutrient agar and 80 ml cholesterol (5 mg ml<sup>-1</sup>) in 400 ml medium and 1% bacteriological agar plates containing cholesterol (80 ml 5 mg ml<sup>-1</sup> in 400 ml medium)). These plate incubations could facilitate reactivation of survival stages possibly present in the samples taken during the heat peak. The resulting data were also not further incorporated in the analysis since incubation experiments impede quantitative analysis and results were not available for all replicates.

Nematode genera were assigned to the 1-5 “coloniser-persister” cp scale according to their r and K life-strategy characteristics (Bongers 1990, 1999) and were classified according to their feeding type. These allocations were, respectively, used to calculate the Maturity Index (MI) (Bongers 1990, 1999) and the Trophic diversity Index (TI) (Heip et al. 1985). Additionally, the Structure Index (SI), Enrichment Index (EI) (Ferris et al. 2001) and the fungivorous/bacterivorous ratio (f/b ratio), also providing an indication of the ecosystem condition, were determined. The calculation of the SI and EI is based on guilds, which combine feeding type and cp value to cluster nematode taxa. The EI is based on the expected reaction of non-herbivore, opportunistic nematodes to the increase in food and gives the abundance and activity of primary detritus-feeding nematodes. The SI indicates the sensitivity to disturbances. The EI and SI can be used to construct a faunal profile, which indicates whether the nematode community is basal, enriched or structured (Ferris et al. 2001). The f/b ratio was used as an indicator of the dominant decomposition pathway (Ferris et al. 2001; Ruess 2003; Ruess and Ferris 2004). The Shannon-Wiener index (H'), with log base 2, and the Simpson index ( $\lambda$ ) were calculated to measure diversity. The Shannon-Wiener index is more appropriate for rare taxa (Heip et al. 1998) while the Simpson index gives more weight to the predominant taxa (Neher 2001).

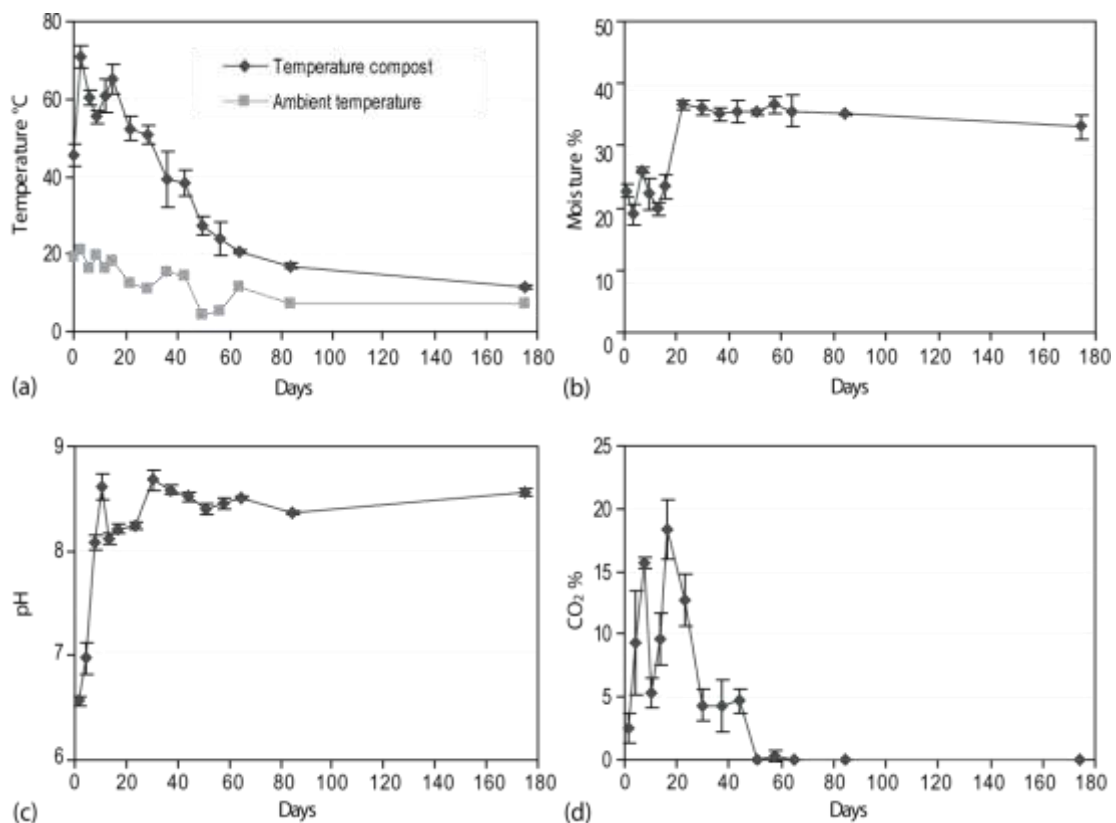
#### **2.3.4. Statistical analyses**

First, a correlation matrix was performed to unravel possible colinearity among abiotic variables. Subsequently, in order to reduce the redundancy between the different abiotic factors measured during the composting process, a Principal Component Analysis (PCA) was performed, by which the different abiotic variables were related to each other in a single principal component. Due to strong linear dependency in the data set, differences in the MI and f/b ratio during the composting process were addressed by categorizing the data into the different composting phases (thermophilic, cooling and maturing) and performing pair-wise Mann-Whitney tests using composting phase as a factor. All analyses were conducted with the statistical software Statistica 7.0.

## 2.4. RESULTS

### 2.4.1. Environmental variables

The abiotic conditions of the compost heap changed dramatically during the composting process (Figure 2.1). The temperature showed two distinct heat peaks; one on day 3 with an average temperature of 71 °C and another on day 15 with an average temperature of 65 °C. After the second peak, the temperature gradually decreased until it reached approximately 10 °C (Figure 2.1A). Although the moisture content and the pH of the compost heap fluctuated during the first 25 days of the process, both parameters stabilized after reaching their maxima (38% and 8.67%, respectively) (Figure 2.1B and C). The CO<sub>2</sub> concentration (Figure 2.1D) also showed two maxima during the first 29 days (15% on day 18, and 18% on day 6) and decreased afterwards in two stages (from 4.5% to 0%). Correlation analysis revealed that temperature was positively correlated with CO<sub>2</sub> concentration, moisture content and ambient temperature (Table 2.1). Ambient temperature also correlated positively with CO<sub>2</sub> concentration and negatively with both moisture content and pH. The PCA performed using heap temperature, pH, CO<sub>2</sub> and humidity reduced the variation to only one principal component which accounted for 67% of the variation within the data matrix and to which heap temperature and humidity contributed the most (see vector loadings, Table 2.1).



**Figure 2.1**

Environmental variables measured during the composting process including (a) temperature of the compost (°C) and the ambient temperature (°C), (b) moisture content (%), (c) pH values and (d) CO<sub>2</sub> concentration (%). Error bars indicate SD.

**Table 2.1**

Pearson correlation coefficients and product moment correlation coefficients among continuous environmental variables (Temperature, CO<sub>2</sub>, Moisture, pH, ambient temperature) measured during the composting process and the vector loadings of the Principal Component Analysis (PCA).

	Temperature	CO <sub>2</sub>	Moisture content	pH	Env. Temp.	Vector Loadings PCA
Temperature	1					-0.91
CO <sub>2</sub>	0.83 <sup>***</sup>	1				-0.76
Moisture content	-0.67 <sup>**</sup>	-0.5	1			0.86
pH	-0.43	-0.20 <sup>*</sup>	0.62 <sup>*</sup>	1		0.64
Ambient Temp.	0.86 <sup>***</sup>	0.61 <sup>*</sup>	-0.73 <sup>**</sup>	-0.55 <sup>**</sup>	1	-

(\*p<0.05; \*\*p<0.01; \*\*\*p≤0.001)

## 2.4.2. Nematode community analyses

### Species composition and number of nematodes

In total 18 genera belonging to 12 families were identified from the 15 sampling occasions during the complete process. The individual samples were generally characterized by relatively few taxa (maximum 9 different species). The most common taxa were *Aphelenchoides* sp., *Diploscapter coronatus*, *Mononchoides* sp., *Cephalobus* sp. and *Panagrolaimus labiatus*. Other taxa, e.g. *Diplogastrellus* sp., *Diplogaster* sp., *Halicephalobus gingivalis* and *Ditylenchus filimus*, were rare and were detected only at very specific periods during the process. Table 2.2 provides an overview of the species detected at every sampling occasion. For more detailed information about the species observed during the composting process, see <http://www.nematology.ugent.be/vce.html>. Also survival stages could be isolated with the modified Baermann funnel method (Table 2.2). The number of nematodes gradually increased with decrease in temperature (Figure 2.2A). Immediately after the heat peak, on day 3 until day 9, nematodes could not be detected using the Baermann funnel method. However, incubation of these compost samples on agar plates provided cultures of *H. gingivalis* and *D. coronatus* (Table 2.2). Most likely these were reactivated dauer stages or temperature resistant eggs. Thereafter, the number of nematodes increased gradually until the final sampling event. The highest numbers of nematodes were found in the first and in the last samples (respectively, 1234 and 933 nematodes per 100 g dry weight compost).

**Table 2.2**

Nematode species list with presence of the species during the composting process and information on the dauer larvae found during the process. The feeding type of each species is also provided (3=bacterial-feeding, 2=fungal-feeding, 3-5a=bacterial-feeding/predator, 8=omnivorous). All species were isolated using the modified Baermann funnel method except for the species with an asterisk, which were isolated after incubation of compost on agar plates.

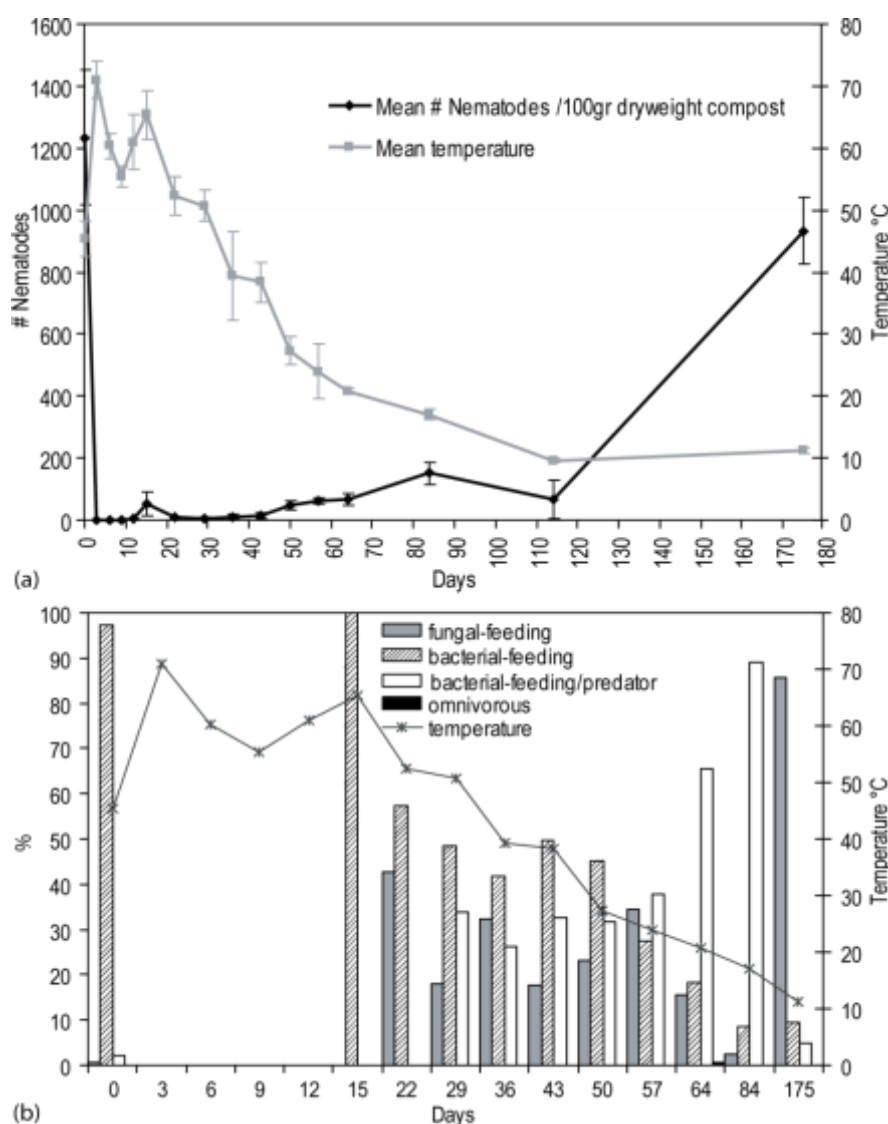
TAXA	Feeding-type	Day														
		0	3	6	9	12	15	22	29	36	43	50	57	64	84	175
<i>Rhabditis</i> sp.1	3	■														
<i>Rhabditis</i> sp.2	3															
<i>Rhabditis</i> sp.3	3															
<i>Diplogastrellus</i> sp.	3															
<i>Diplogasteritus</i> sp.	3						■		■			■	■	■		■
<i>Panagrolaimus labiatus</i>	3	■						■			■	■	■	■		
Rhabditidae sp.	3									■	■	■	■	■	■	■
Cephalobidae sp.	3															
<i>Cephalobus</i> sp.1	3									■	■	■	■	■	■	■
New genus Ordo Rhabditina	3															
<i>Diploscapter coronatus</i>	3															
<i>Cephaloboides</i> sp.1	3															
<i>Poikilolaimus</i> sp.1	3															
<i>Halicephalobus gingivalis</i>	3															
<i>Rhabditophanes cobbi</i>	3															
<i>Mesorhabditis</i> sp.1	3															
<i>Aphelenchoididae</i> sp.1	2	■														
<i>Aphelenchoides</i> sp.1	2															
<i>Aphelenchoides</i> sp.2	2															
<i>Paratylenchus</i> sp.	2															
<i>Ditylenchus filiformis</i>	2															
<i>Diplogaster</i> sp.	3-5a	■														
<i>Mononchoides</i> sp.	3-5a															
Qudsianematidae sp.	8															
SURVIVAL STAGE RECORD																
Rhabditidae dauer																
Diplogastriidae dauer																
Unknown dauer																
<i>Halicephalobus gingivalis</i> *		■	■	■												
<i>Diploscapter coronatus</i> *																

#### Functional groups: feeding type and cp value

The composition of nematode feeding types showed a clear dominance of bacterial feeders (16 species or 55% of the total abundance), followed by the subdominant fungal-feeders (5 species or 33.3% of the total abundance) and the bacterial-feeding and predatory (of nematodes) nematodes (2 species or 11.7% of the total abundance) (Table 2.3). Figure 2.2B displays the feeding-type compositions per sample based on the 3 replicas. Bacterial-feeding nematodes were present in all nematode-containing samples, but most samples included fungal-feeders and bacterial-feeding/predator nematodes as well as bacterial-feeders (days 36, 43, 50, 57, 64, 84 and 175). For the first 50 days of the process, bacterial-feeding nematodes were clearly dominant. From day 22 onwards, the fungal-feeding nematodes were also detected in the

samples. The density of the bacterial-feeding/predator nematodes increased gradually from day 29 onwards, and this type dominated the samples of days 64 and 84. In the most mature sample the fungal-feeders were clearly dominant.

The distribution of the nematode genera from the composting process along the cp scale was uneven. The enrichment opportunists (cp-1 value) were dominant (16 species or 66.7% of the total abundance) while the general opportunists (cp-2 value) were subdominant (7 species or 33.3% of the total abundance). One genus with a cp-4 value was present on day 64 but genera with a cp-3 value were completely absent (Table 2.3). The most mature stage (day 175) was dominated by cp-2 genera, unlike the other samples, wherein the genera with a cp-1 value were dominant (Table 2.3).



**Figure 2.2**

(a) The number of nematodes and the temperature of the compost during the process. (b) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator, omnivorous nematodes) and the temperature of the compost at every sampling occasion.

### Indices and integration of the abiotic data

At the beginning of the process and immediately after the heat peak, the TI, based on the defined feeding types, was relatively high, due to the dominance of a single feeding type (i.e. bacterial-feeding) (Table 2.3). The lowest TI values, due to the more equal distribution of the feeding types in the samples, appear from day 29 onwards, in the first half of the composting process when the temperature is still relatively high (40-50 °C). At the most mature stage, when the temperature of the heap most closely approximated the ambient temperature, the TI increased again as a result of the dominance of one feeding group (i.e. fungal-feeding). The f/b ratio showed a distinct change during the process (Table 2.3). The f/b ratio fluctuated between 0 and 2.68 with a maximal peak ( $11.90 \pm 8.15$ ) on day 175, in line with the enhancement of fungal-feeding nematodes (Table 2.3). The cp values of the genera were used to calculate the MI (Table 2.3). For the first 84 days of the process, the MI varied between 0.68 and 1.58 (Table 2.3). The pair-wise Mann-Whitney test revealed differences in the MI and f/b ratios between the different phases of the composting process (thermophilic phase: days 3-29, cooling phase: days 36-64, maturing phase: days 84-175) (Table 2.4). The mean MI and f/b ratio during the three composting phases are given in Table 2.4. The MI and the f/b ratio both showed a significant difference between the maturing and the two previous phases ( $p$  values, respectively, 0.001 and 0.05) (Table 2.4). Mark that especially the f/b ratio and maturity index trend are strongly influenced by the results of one single divergent sampling point (day 175). This limitation necessitates caution in the further interpretation of the statistical results. The diversity was highest on days 36 and 57, and slightly lower at the end of the process (Table 2.3). However, the observed fluctuations in diversity were not statistically significant. Neither the EI nor the SI showed a clear trend during the process, nor could they be linked to nematode succession. This could be attributed to the fact that these indices are designed for more complex, larger scale and longer lasting processes.

In summary, the taxonomic analysis of the nematode community revealed three clear successional phases after the heat peak. At the beginning of the process, just after the temperature peak observed on day 3, the nematode population was made up primarily of bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogastridae) followed by the bacterial-feeding general opportunists (cp-2) (Cephalobidae) and the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, the opportunistic bacterial-feeding/predator nematodes (*Mononchoides* sp.) became the dominant species. Finally, at the most mature stage, the fungal-feeding Anguinidae (e.g. *D. filimus*) was the most abundant group.

**Table 2.4**

Mean Maturity Index and f/b ratio during the three different phases of the composting process.

Index	Composting phase			P
	Thermophilic	Cooling	Maturing	
MI	0.81±0.59*	1.24±0.12*	1.34±0.34	0.001
f/b	0.30±0.56	1.50±1.72	3.58±6.13*	0.05



**Table 2.3**

Overview of the means  $\pm$ SD of the abundance of nematodes (per 100 g DW compost), number of genera, percent contribution to the functional groups (trophic groups: type 2 (fungal-feeding nematodes), type 3 (bacterial-feeding nematodes), type 3-5a (bacterial-feeding/predator nematodes), type 8 (omnivorous nematodes) and cp-groups: cp-1 (enrichment opportunists), cp-2 (general opportunists), cp-4 (persisters)) and the values of the indices: TI (Trophic Index), f/b (fungivorous/bacterivorous ratio), MI (maturity index), EI (enrichment index), SI (structure index), H' (Shannon-Wiener index) and  $\lambda$  (Simpson Index)) at every sampling event.

	DAY														
	0	3	6	9	12	15	22	29	36	43	50	57	64	84	175
<b>Abundance</b>	1234 $\pm$ 217.65	0	0	0	0	53 $\pm$ 37.64	8 $\pm$ 1.04	6 $\pm$ 2.35	13 $\pm$ 7.44	25 $\pm$ 13.25	49 $\pm$ 13.43	64 $\pm$ 9.68	68 $\pm$ 18.77	151 $\pm$ 35.09	933 $\pm$ 106.78
<b># Genera</b>	4 $\pm$ 1	0	0	0	0	3 $\pm$ 1	3 $\pm$ 1	3 $\pm$ 2	3 $\pm$ 1	3 $\pm$ 1	6 $\pm$ 1	6 $\pm$ 1	7 $\pm$ 2	5 $\pm$ 1	5 $\pm$ 1
<b>Functional groups %</b>															
<b>Trophic groups %</b>															
<b>type 2</b>	1 $\pm$ 0.8	0	0	0	0	0	43 $\pm$ 20.1	18 $\pm$ 21.7	32 $\pm$ 14.3	18 $\pm$ 17.0	23 $\pm$ 7.5	35 $\pm$ 19.1	15 $\pm$ 9.4	3 $\pm$ 1.5	86 $\pm$ 7.1
<b>type 3</b>	97 $\pm$ 1.7	0	0	0	0	100 $\pm$ 0.0	57 $\pm$ 20.1	48 $\pm$ 38.2	42 $\pm$ 30.3	50 $\pm$ 53.0	45 $\pm$ 12.2	28 $\pm$ 3.4	18 $\pm$ 8.6	8 $\pm$ 2.5	10 $\pm$ 5.2
<b>type 3-5a</b>	2 $\pm$ 2.3	0	0	0	0	0	0	34 $\pm$ 26.0	26 $\pm$ 34.7	33 $\pm$ 37.8	32 $\pm$ 19.6	38 $\pm$ 17.3	66 $\pm$ 2.5	89 $\pm$ 3.9	5 $\pm$ 1.9
<b>type 8</b>	0	0	0	0	0	0	0	0	0	0	0	0	1 $\pm$ 0.9	0	0
<b>Cp-groups %</b>															
<b>cp-1</b>	99 $\pm$ 0.8	0	0	0	0	100 $\pm$ 0.0	57 $\pm$ 20.1	82 $\pm$ 21.7	68 $\pm$ 14.3	82 $\pm$ 17.0	77 $\pm$ 7.5	65 $\pm$ 19.1	84 $\pm$ 9.8	97 $\pm$ 1.5	14 $\pm$ 7.1
<b>cp-2</b>	1 $\pm$ 0.8	0	0	0	0	0	43 $\pm$ 20.1	18 $\pm$ 21.7	32 $\pm$ 14.3	18 $\pm$ 17.0	23 $\pm$ 7.5	35 $\pm$ 19.1	15 $\pm$ 9.4	3 $\pm$ 1.5	86 $\pm$ 7.1
<b>cp-4</b>	0	0	0	0	0	0	0	0	0	0	0	0	1 $\pm$ 1.0	0	0
<b>Indices</b>															
<b>TI</b>	0.94 $\pm$ 0.03	0	0	0	0	1.00 $\pm$ 0.00	0.76 $\pm$ 0.21	0.61 $\pm$ 0.34	0.48 $\pm$ 0.06	0.64 $\pm$ 0.24	0.40 $\pm$ 0.07	0.39 $\pm$ 0.03	0.50 $\pm$ 0.04	0.80 $\pm$ 0.06	0.75 $\pm$ 0.11
<b>f/b</b>	0.00 $\pm$ 0.01	0	0	0	0	0	0.83 $\pm$ 0.63	0.50 $\pm$ 0.87	1.33 $\pm$ 1.45	2.68 $\pm$ 2.50	0.52 $\pm$ 0.04	1.24 $\pm$ 0.83	0.92 $\pm$ 0.74	0.28 $\pm$ 0.12	11.90 $\pm$ 8.15
<b>MI</b>	1.00 $\pm$ 0.01	0	0	0	0	1.00 $\pm$ 0.00	1.41 $\pm$ 0.20	1.13 $\pm$ 0.22	1.29 $\pm$ 0.14	1.21 $\pm$ 0.17	1.24 $\pm$ 0.08	1.33 $\pm$ 0.19	1.15 $\pm$ 0.11	1.03 $\pm$ 0.01	1.86 $\pm$ 0.07
<b>EI</b>	100.00 $\pm$ 0.19	0	0	0	0	100.00 $\pm$ 0.00	84.94 $\pm$ 9.58	96.00 $\pm$ 6.93	91.27 $\pm$ 4.79	93.45 $\pm$ 5.56	93.14 $\pm$ 2.52	98.41 $\pm$ 7.36	96.18 $\pm$ 2.86	99.37 $\pm$ 0.35	62.25 $\pm$ 5.39
<b>SI</b>	0	0	0	0	0	0	0	0	0	0	0	0	8.45 $\pm$ 14.63	0	0
<b>H'</b>	1.21 $\pm$ 0.34	0	0	0	0	0.85 $\pm$ 0.19	1.12 $\pm$ 0.21	0.84 $\pm$ 0.76	1.05 $\pm$ 0.19	0.69 $\pm$ 0.45	1.32 $\pm$ 0.25	1.38 $\pm$ 0.10	1.15 $\pm$ 0.17	0.48 $\pm$ 0.13	0.57 $\pm$ 0.22
<b><math>\lambda</math></b>	0.37 $\pm$ 0.16	0	0	0	0	0.47 $\pm$ 0.06	0.36 $\pm$ 0.09	0.55 $\pm$ 0.40	0.40 $\pm$ 0.09	0.63 $\pm$ 0.26	0.33 $\pm$ 0.08	0.31 $\pm$ 0.04	0.47 $\pm$ 0.04	0.79 $\pm$ 0.07	0.75 $\pm$ 0.11

## 2.5. DISCUSSION

The nematode community in compost has hitherto never been thoroughly investigated. The results obtained in this study describe major shifts in species composition during the composting process, and moreover, link these structural community changes with the shifts in abiotic conditions that take place during the process.

Several authors have already proposed the use of nematode assemblages as powerful tools to analyze ecosystem processes and quality (e.g. Bongers and Ferris 1999; Ritz and Trudgill 1999; Ferris et al. 2001; Neher 2001; Ferris and Bongers 2009; Yeates et al. 2009). The calculation of nematode-based indices is based on the allocation to functional groups and basic insights into the successional changes within a given studied system. A composting process is most likely an outstanding example of an ecosystem in transition that can be evaluated by the succession of nematodes.

In our case, the maturity index and the f/b ratio showed a clear pattern during the process and therefore seem to be suitable indices to evaluate the composting process. The MI and the f/b ratio both increase as the compost becomes more mature. According to Bongers (1999), a rapidly changing environment with an abundance of food is typically inhabited by opportunistic nematodes, starting with enrichment opportunists (cp-1), which are gradually replaced by general opportunists (cp-2). This trophic situation results in relatively low MI values at the beginning of the process and, by contrast, significantly higher MI values at the end of the process. The f/b ratio clearly reflects the shift in prevalence of bacterial-feeding nematodes in the thermophilic and cooling phases, to fungal-feeding nematodes in the maturation phase. This ratio can also be used to indicate the dominating decomposing pathway in a decomposing environment (Bongers and Bongers 1998; Ruess 2003; Ruess and Ferris 2004). From our analysis we could see that the first 84 days of the process, during which the f/b ratio is typically relatively low, decomposition occurred mainly through the bacterial-dominating pathway. However, in the final stage of the process (day 175), when the ratio is typically highest, the decomposition mainly occurred through the fungi-dominated pathway. This pattern may be an indication of a retardation of the decomposition rate due to the fungal-associated decomposition of more complex organic materials (Ruess and Ferris 2004).

A more detailed analysis of the successional changes of the nematode community revealed that the composting process actually undergoes a meticulous succession of r-strategists. According to Wharton (1986), habitats subject to environmental extremes do not favor K-strategists. This is most likely the main reason for their absence during the composting process. The first

nematodes capable of colonizing the compost during the last phase of the heat peak (= thermophilic phase,  $T \geq 45$  °C) belonged to the genera *Diplogasteritus*, *Panagrolaimus* and *Rhabditis*. This first population (on day 15) of early colonizers in a nutrient-rich environment was 100% bacterial-feeding and enrichment opportunistic nematodes, as proposed by Bongers (1990) and confirmed by many others (e.g. Ettema and Bongers 1993; Bardgett et al. 1998; Wasilewska 1998). At the very beginning of the cooling phase, from days 22-29, this first population was subverted by a population dominated by the genera *Cephalobus* and *Aphelenchoides*, both general opportunists (cp-2) and respectively bacterial and fungal-feeding. The replacement of the enrichment opportunists belonging to the Rhabditidae family (cp-1) by general opportunists from the family Cephalobidae (cp-2) and the occurrence of fungal-feeding nematodes has also been observed by Ferris and Matute (2003), Wang et al. (2004) and Georgieva et al. (2005) during the decomposition of several plant residues in soil. During the cooling phase (45 °C- ambient temperatures), occurring from day 36 onwards, the dominance of the former nematodes started to decrease and other species started to inhabit the compost: e.g. *D. coronatus*, *Rhabditis* (*Cephaloboides*) sp. and *Mononchoides* sp. Since bacterial-feeding fauna mirrors previous bacterial production (Georgieva et al. 2005; Ferris and Bongers 2006), this shift in nematode species composition and increase in the number of nematodes can be linked to increase in bacterial activity in the cooling phase and to the presence of completely different bacterial populations in the thermophilic and cooling phases as described by Ishii et al. (2000), Ryckeboer et al. (2003) and Halet et al. (2006). The cooling phase environment ( $\leq 45$  °C), with bacteria, fungi and various nematode species in abundance, gave *Mononchoides* sp. the opportunity to start blooming. This differs from decomposition in soil where Neodiplogasteridae (including *Mononchoides*) dominate from the beginning (Georgieva et al. 2005). This retardation might possibly be explained by the relatively high and lethal temperatures in the beginning of the cooling phase ( $\pm 40$  °C). During maturation at the end of the process, from days 84-175, a shift in prevalence of bacterivorous to fungivorous nematodes took place, which can be associated with the transition from mainly bacterial activity during the thermophilic and early cooling stages to an increase in activity of fungi in late cooling and maturation stages (Ryckeboer et al. 2003). Moreover, it is known that fungal energy channels predominate when the organic material is of a high C/N ratio and, conversely, bacterial decomposition channels predominate when the organic material is of a low C/N ratio (Ruess 2003; Ruess and Ferris 2004) (cfr. high C/N ratios of feedstock materials). In a study by Ferris and Matute (2003), the rate of succession from bacterivorous to fungivorous nematodes increased in plots receiving high C/N materials (Ferris and Matute 2003). Most likely, when looking at the whole process, during the

thermophilic phase the extreme environmental circumstances (i.e. temperature) are the limiting factors for nematode succession, whereas during the mesophilic and maturation phases, food resources might be the most important selective force for successional events.

According to the scanty literature, remarkably similar taxa to those observed in this study have been described from compost (Gagarin 2000; <http://www.soilfoodweb.com>). The majority of species described from other compost heaps also belonged to the rhabditids and the diplogasterids and nearly always the same genera (i.e. *Cephalobus*, *Rhabditis*, *Diploscapter*, *Aphelenchoides* and *Ditylenchus*) (Gagarin 2000; <http://www.soilfoodweb.com>). More specific similarities with other observations from compost include *P. labiatus* (China; Andrassy 1984), *D. filimus* (West Canada; Anderson 1983), *H. gingivalis* (USA, Riverside; Nadler et al. 2003) and *Rhabditis (Poikilolaimus) sp.* (mushroom compost, Russia; Gagarin 2000). Remarkably, notwithstanding the nematode destructive heat peak, the geographic disparity and different feedstock materials, the same genera and even the same species were found in these studies, including this one. Where do these “compost” nematodes come from? The composting process is an “open” process and the ability to arrive in a new habitat does not necessarily mean that the nematodes also become established. As a result it makes little difference whether the species come from “immigrations” by movement of air, water and tillage machinery or from awakened dauer stages or eggs, the surrounding soil or by insect phoresy, because the typical compost environment will ultimately serve as the fundamental selective force regardless of origin (for overview on nematode dispersal see Hodda et al. 2009). Hence, the nematode indices proposed herein for assessing compost maturity might be of universal relevance, although further research is required to clarify the ways in which nematodes can arrive at a compost heap.

Unlike Manso (2004), who only found bacterial-feeding Rhabditidae in mature compost, diplogasterids appeared to be numerically important (4 different genera were found). In particular, *Mononchoides sp.* was numerically important from days 29-84. According to Yeates et al. (1993), 2 of the recorded diplogasterid genera (*Diplogastrellus* and *Diplogasteritus*) are strictly bacterial-feeding nematodes (feeding type 3). The 2 other genera (*Mononchoides* and *Diplogaster*) could belong to the bacterial-feeding nematodes as well as to the predator nematodes (feeding type 5a) and to the omnivorous nematodes (feeding type 8) (Yeates et al. 1993). Because species within the same feeding group may vary in their food resources and some species can feed on several food resources, the allocation of nematodes to a specific feeding type is often uncertain (Yeates et al. 1993; Yeates 2003). The herein numerically very important *Mononchoides sp.* appeared to have a biphasic feeding ability (as described earlier by

Yeates 1969, 1970), namely on bacteria and other nematode species (Chapter 3, part 2). The neodiplogasterids *Mononchoides* sp. and the diplogasterid *Diplogaster* sp. were therefore allocated to a combined feeding group “bacterial-feeding/predator” (feeding type 3-5a) (see also Georgieva et al. 2005). However, most terrestrial nematode indices (e.g. EI, CI and TI) do not incorporate this new feeding type and thus are not usable for compost. Diplogasterids are known to be prey-selective to plant-parasitic nematodes (Khan and Kim 2007), and therefore, are very promising biological control agents (Bilgrami and Jairajpuri 1988; Bilgrami et al. 2005 ; Bilgrami 2008). This study shows that a composting process can provide a great range of potential predator nematodes. This is particularly an important factor in the suppressive capacity of compost against plant diseases.

In conclusion, this study produced some promising results. The successional changes of the nematode community during the process demonstrated opportunities to describe and evaluate the condition of the composting process. Although further research needs to be performed in order to strengthen these findings, the nematode-based indices maturity index and fungivorous/bacterivorous ratio are probably the most suitable tools to assess compost maturity. Thus, the next step should be to analyze different composting processes and more time frames in order to correlate particular maturity index and fungivorous/bacterivorous ranges to the state and maturity of the compost process. Finally, further work is required to assess the effectiveness and importance of the remarkably high number of bacterial-feeding/predator nematodes during certain compost stages on the potential suppressive effect of compost.

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### 3. The nematode fauna in compost

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Modified from:

- Steel H, Moens T, Scholaert A, Boshoff M, Houthoofd W and Bert W (2011).

*Mononchoides composticola* n. sp. (Nematoda: Diplogasteridae) associated with composting processes: morphological, molecular and autoecological characterization.

Nematology 13(3): 347-363.

- Steel H, Coomans A, Moens T and Bert W. Non-marine nematodes in Belgium: an updated list with special emphasis on compost nematodes. Submitted to Zootaxa.

## **PART 1: NON-MARINE NEMATODES IN BELGIUM: AN UPDATED LIST WITH SPECIAL EMPHASIS ON COMPOST NEMATODES.**

### **3.1 Abstract**

A study of the semi-artificial and controlled composting process in Eastern Flanders revealed 35 different taxa of which 21 were new records Belgium. An updated checklist of terrestrial, fresh- and brackish water nematodes in Belgium is presented. The Belgian non-marine nematofauna comprises 414 taxa, representing 4 subclasses, 14 orders, and 76 families. In total 124 new taxa were added: i.e. 21 from the newly explored compost habitat, 7 from freshwater samples and 96 from published data in literature.

### **3.2. Introduction**

The Belgian nematofauna has been relatively well studied. Coomans (1989) reviewed the nematofauna from Belgium, with exclusion of the animal parasitic nematodes. However, this list was published in the proceedings of the symposium "Invertebrates from Belgium" which is, to modern standards, an inaccessible national publication. More recently, Bert et al. (2003) published an updated list of the Tylenchomorpha from Belgium, with the addition of 42 species, based on new data together with data from Bert and Geraert (2000) and Coosemans (2002). However, for the free-living Belgian nematofauna the list of Coomans (1989) was never updated or revised to reflect recent taxonomical changes. Next to the newly explored compost habitat, as presented in this PhD, and new data from freshwater samples, a literature review on both free-living (terrestrial, freshwater, brackish water and brackish soil) and plant-parasitic nematodes has given a better insight into the diversity of the Belgian nematofauna. This resulted in a list of 414 taxa, 124 taxa of which are new compared to the list of Coomans (1989) combined with Bert et al. (2003). 21 records from compost are new to the Belgian fauna.

### **3.3. Materials & Methods**

The species list is mainly compiled based on compost samples, on a limited number of freshwater samples and on literature data. For compost, nine composting processes were sampled at different time points, these include five processes according to the Controlled Microbial Composting method (=farm composting), three small scale processes in barrels and one industrial green waste composting process. Seven additional samples of mature composts were analyzed from a green waste process and six farm composting processes executed at the experimental farm of the Institute for Agricultural and Fisheries Research (ILVO, Merelbeke,

Belgium). For more detailed information on the used method of sampling and processing of the samples see Chapters 2, 4 & 7. The included new records of freshwater nematodes are the result of about thirty randomly taken samples from freshwater habitats (ponds, lakes, canals, etc.).

The presented list includes the main characteristic of the site where the taxa were first recorded in Belgium, T= terrestrial, C= compost, Fw= freshwater, Bw= brackish water and Bs= brackish soil. This habitat indication is not exhaustive, presence in other habitats in- or outside Belgium is not provided. However, although this list only contains non-marine nematodes, taxa known to have also a marine distribution in- or outside Belgium are indicated with (M). Generally, the classification of De Ley and Blaxter (2004) is followed up to family level, unless stated otherwise. For the orders Triplonchida and Plectida, classifications of Holovachov and Shoshin (in press) and Holovachov (in press), respectively, were used. For the Dorylaimida the classifications of Peña-Santiago (2006) and Vinciguerra (2006) were applied while for the Mononchida the classification of Zullini and Peneva (2006) was applied. For classification of the infraorder Tylenchomorpha Decraemer and Hunt (2006) was used. On subfamily level more specialized classifications were followed for the following taxa: Rhabditidae (Sudhaus 2011); Diplogasteridae s.l. (Sudhaus and Fürst von Lieven 2003); Criconematidae (Geraert 2010) and Dolichodoridae and Psilenchidae (Hunt, Bert & Siddiqi, in press).

### 3.4 Results & Discussion

#### Compost nematodes

The study of the hitherto completely unexplored compost biotope resulted in 35 different taxa 21 of which were new records for Belgium (7 species, 13 genera and 1 family) (Table 1): Neotylenchidae unidentified sp., *Nygolaimoides* sp.; *Ektaphelenchoides* sp.; *Ditylenchus filimus*; 8 rhabditids: *Crustorhabditis* sp. *Cruznema* sp., *Diploscapter coronatus*, *Parasitorhabditis* sp., *Pelodera cylindrica*, *Pelodera terres*, *Rhabditophanes cobbi*, *Teratorhabditis* sp.; 6 diplogasterids: *Acrostichus* sp., *Diplogaster* sp., *Diplogasteritus* sp., *Diplogasterioides* sp., *Fictor* sp., *Mononchoides composticola* and 3 panagrolaimids: *Panagrellus* sp., *Panagrolaimus labiatus*, *Procephalobus* sp. Other genera recorded from compost but not new for Belgium were: *Cephalobus*, *Eucephalobus*, *Aphelenchoides*, *Seinura*, *Filenchus*, *Butlerius*, *Bunonema*, *Cephaloboides*, *Choriorhabditis*, *Mesorhabditis*, *Poikilolaimus* and *Protorhabditis*. Also *Rhabditella axei* and *Halicephalobus* cfr.<sup>4</sup> *gingivalis* were found in compost however their recording was not new for Belgium. By far the most widespread taxa in the examined compost samples (based on presence or absence) were *Pelodera terres*, *Pelodera cylindrica*,

<sup>4</sup> Unpublished results indicated considerable molecular differences between species that are morphologically identified as *Halicephalobus gingivalis*.

*Aphelenchoides* sp., *Halicephalobus* cfr. *gingivalis*, *Poikilolaimus* sp., *Diploscapter coronatus*, *Acrostichus* sp., *Fictor* sp. and *Mononchoides composticola*. For a detailed description of the latter see Part 2 of this chapter. Remarkably, the same genera and even the same species were recorded from the very limited compost samples studied by other authors. The majority of species found were also rhabditids, panagrolaimids and diplogasterids, and with even the same genera or species. *Eucephalobus*, *Diploscapter*, *Poikilolaimus* sp., *Aphelenchoides* and *Ditylenchus* were found from compost in Russia (Gagarin 2000). Identical observations on species level include *Panagrolaimus labiatus* (China, Andr ssy 1984), *Ditylenchus filimus* (West-Canada, Anderson 1983) and *Halicephalobus gingivalis* (USA, Riverside, Nadler et al. 2003). The presence of a highly similar compost nematode diversity is at first sight difficult to explain given the geographic disparity and different feedstock materials. However, a compost process is a temporally vastly changing environment with food in abundance, selective for opportunistic nematodes that are highly efficient dispersers (Chapter 5). It is well-known that certain nematodes are excellent survivors (Wharton 2004) and very efficient dispersers (Hodda et al. 2009); these characteristics, among others, may cause nearly cosmopolitan distributions (Artois et al. 2011). Mark that the occurrence of nematodes marked in the list as compost nematodes is not restricted to compost. For example the cosmopolitan and free-living *Diploscapter coronatus* was described, next to a terrestrial habitat, as a facultative parasite of humans (e.g. Athari and Mahmoudi 2008) and from necrotic nodules in the skin of snakes (Sabu et al. 2002). Also *Halicephalobus gingivalis* is a free-living terrestrial panagrolaimid that is also capable of infecting and reproducing in horses, humans and zebras (Nadler et al. 2003). Other taxa from compost have a more specific biology, such as Neotylenchidae sp., which has alternating life cycles (parasitic in the insect haemocoel and a free-living, fungal- or plant-feeding generation) or *Ektaphelenchoides* sp., which is known from insects associations in xylem of several woods (Siddiqi 2000 and Hunt 1993 respectively).

#### Literature review and freshwater study

The review of Coomans (1989) and Bert et al. (2003) together listed 290 taxa and another 124 have now been added (Table 3.1). Seven nominal species have been removed from the 1989 list of Coomans because they have been synonymized with other species on the list (i.e. *Cervidellus serratus*, *Basiria minor*, *Filenchus filiformis*, *Meloidogyne deconincki*, *Neopsilenchus minor*, *Rotylenchus fallorobustus* and *Tylenchorinchus judithae*).

Next to the Tylenchomorpha already added in the list of Bert et al. (2003) the study of Coosemans (2002) reported 16 other new records for Belgium. A study on historical pollution (Bert et al. 2009) and one on the effect of exogenous organic matter on the nematode

community in agricultural soil (Leroy et al. 2009) revealed 4 and 6 new genera or taxa respectively. The works of Andrásy 2005 and 2007 together mentioned 2 free-living nematode species (i.e. *Monhystera paludicola* and *Cylindrolaimus melancholicus*) and 3 plant-parasitic species (*Scutylenchus quadrifer*, *Scutylenchus tessellates* and *Criconemoides annulatus*) that had not previously been recorded and according to Tiasi et al. (2010), *Mylonchulus signaturellus* was also found in Belgium. Although *Nanidorus minor* is mentioned from Belgium (Andrásy 2009), this species is not added to the list because its identification is probably not correct and should be *N. renifer* (Braasch and Sturhan 1991). Concerning the plant-parasitic nematodes, Bongers (1994) and an additional 12 studies (Elbadri et al. 1999; Subbotin et al. 2000; Karssen et al. 2000; Rubtsova et al. 2001; Subbotin et al. 2003; Wobalem 2004; Madan et al. 2005; Kovaleva et al. 2005; Viaene et al. 2007; Leroy et al. 2009; Sturhan and Hallmann 2010; Vandenbossche et al. 2011) together yielded 28 new records for Belgium, which now have been added to the list. Six new records of entomopathogenic species were provided by Miduturi et al. (1996), Spiridonov and Moens (1999), Ansari et al. (2003) and Ansari et al. (2007): *Steinernema affine*, *S. carpocapsae*, *S. feltiae*, *S. kraussei* and *Heterorhabditis bacteriophora* and *H. megidis*. A study based on two Belgian brackish water stations in the river Scheldt by De Block (1994) resulted in 23 additional new records for Belgium.

The freshwater nematode species list was updated with 5 new species from farmland ponds (Bert et al. 2007). Additional sampling of several ponds, lakes, and canals in Belgium resulted in 7 new records. *Hirschmanniella behningi* was found from a very small pond, in De Haan (51°16'57.01"N; 3° 3'55.33"E; voucher UGnem79), the pond has been muted in the meantime. *Eutobrilus nothus* and *Semitobrilus pellucidus* were recorded from a small lake in Geel (51°10'23.96"N; 5° 2'34.70"E). *Limnomermis* sp. was found in the river "kleine Nete" in Grobbendonk (51°11'5.71"N; 4°47'1.78"E). *Rhabdolaimus terrestris* and *Chromadorina bioculata* were recovered from lakes that originate from the excavation of white sand in Mol (51°13'48.95"N; 5°10'37.14"E) and Dessel (51°15'47.89"N; 5° 8'15.60"E) respectively. *Panagrolaimus thienemanni* (synonym of *Propanagrolaimus filiformis*) was found in an artificial fish pond in Geel (51°7'37.25"N; 4°59'22.59"E). A series of digital images and the SSU rDNA of each of the above freshwater species is available (Helder et al., unpublished).

### 3.5. Conclusion

In total 124 new records were added to the list of Coomans (1989) combined with Bert et al. (2003): i.e. 21 from the newly explored compost habitat, 7 from freshwater samples and 96 from published data in literature. Although the diversity in the compost samples itself was relatively low (only 2-10 different taxa per sample), more than half of the recorded taxa were new (21 out

of 35) for Belgium. This indicates that the free-living terrestrial taxa, especially from poorly investigated habitats, are still underrepresented and that investigation of other unexplored habitats will easily reveal more new records for Belgium.



**Table 3.1:**

Updated list of the nematode taxa from Belgium. The main characteristic of the site where the taxa were first recorded in Belgium is indicated by T= terrestrial, C= compost, Fw= fresh water, Bw= Brackish water, Bs= Brackish soil or U= unknown. Taxa known to also have a marine distribution in-or outside Belgium are indicated with (M). Numbers refer to studies where the taxa are mentioned; 1: Coomans (1989); 2: Geraert et al. (1988); 3: Bongers (1999); 4: De Block (1994); 5: Miduturi et al. (1996); 6: Spiridonov and Moens (1999); 7: Elbadri et al. (1999); 8: Bert and Geraert (2000); 9: Subbotin et al. (2000); 10: Karssen et al. (2000); 11: Rubtsova et al. (2001); 12: Coosemans (2002); 13: Bert et al. (2003); 14: Subbotin et al. (2003); 15: Ansari et al. (2003); 16: Wobalem (2004); 17: Andrásy (2005); 18: Madan et al. (2005); 19: Kovaleva et al. (2005); 20: Ansari et al. (2007); 21: Bert et al. (2007); 22: Andrásy (2007); 23: Viaene et al. (2007); 24: Bert et al. (2009); 25: Leroy et al. (2009); 26: Tiasi et al. (2010); 27: Sturhan and Hallmann (2010); 28: Vandebossche et al. (2011); 29: Chapter 3 part 2; 30: new data from freshwater samples; 31: present data on compost nematofauna; 32: Fonderie et al., in press.

Class Enoplea	Site	Ref.
Subclass Enoplia		
Order Enoplida		
Suborder Enoplina		
Family Anoplostomatidae		
<i>Anoplostoma campbelli</i> Allgén, 1932	Bs Bw (M)	1
<i>Anoplostoma viviparum</i> (Bastian, 1865) Bütschli, 1874	Bw (M)	4
Suborder Oncholaimina		
Family Oncholaimidae		
<i>Adoncholaimus thalassophygas</i> (de Man, 1876)	Bw Bs (M)	1
<i>Oncholaimus oxyuris</i> Ditlevsen, 1911	Bw Bs (M)	1
<i>Viscosia viscosa</i> (Bastian, 1865) de Man, 1890	Bw (M)	4
Family Enchelidiidae		
<i>Calyptonema</i>	Bw (M)	4
Suborder Ironina		
Family Ironidae		
<i>Syringolaimus striatocaudatus</i> de Man, 1888	Bs (M)	1
Family Oxystominidae		
<i>Halalaimus gracilis</i> de Man, 1888	Bw (M)	4
<i>Nemanema</i>	Bw (M)	4
Suborder Tripyloidina		
Family Tripyloididae		
<i>Tripyloides gracilis</i> (Ditlevsen, 1918)	Bw (M)	4
Suborder Alaimina		
Family Alaimidae		
<i>Alaimus mucronatus</i> Altherr, 1950	T	12
<i>Alaimus proximus</i> Thorne, 1939	T	12
<i>Alaimus primitivus</i> de Man, 1880	T	1
<i>Amphidelus elegans</i> (de Man, 1921) Thorne, 1939	T	1
<i>Paramphidelus dolichurus</i> (de Man, 1876) Andrásy, 1977	T	1
<i>Paramphidelus uniformis</i> (Thorne, 1939) Andrásy, 1977	T	1
Order Triplonchida		
Suborder Diptherophoroidea		

Family Diptherophoridae		
<i>Diphtherophora communis</i> de Man, 1880	T	1
<i>Diphtherophora vanoyei</i> De Coninck, 1931	T Fw	1
<i>Tyolaimophorus typicus</i> de Man, 1880	T	1
Family Trichodoridae		
<i>Nanidorus nanus</i> (Allen, 1957) Siddiqi, 1974	T	1
<i>Paratrachodorus pachydermus</i> (Seinhorst, 1954) Siddiqi, 1974	T	1
<i>Paratrachodorus teres</i> (Hooper, 1972) Siddiqi, 1974	T	1
<i>Trichodorus cylindricus</i> Hooper, 1962	T	1
<i>Trichodorus primitivus</i> (de Man, 1880) Micoletzky, 1922	T	1
<i>Trichodorus similis</i> Seinhorst, 1963	T	1
<i>Trichodorus sparsus</i> Szczygiel, 1968	T	1
<i>Trichodorus variopapillatus</i> Hooper, 1972	T	1
<i>Trichodorus velatus</i> Hooper, 1972	T	1
<i>Trichodorus viruliferus</i> Hooper, 1963	T	1
Suborder Tobrilina		
Family Bastianiidae		
<i>Bastiana gracilis</i> de Man, 1876	T	1
Family Prigmatolaimidae		
<i>Prigmatolaimus dolichurus</i> de Man, 1880	Fw T	1
<i>Prigmatolaimus intermedius</i> (Bütschli, 1873) de Man, 1880	T	1
Family Tobrilidae		
<i>Brevitobrilus stefanskii</i> (Micoletzky, 1925) Tsalolikhin, 2002	Fw	21
<i>Eutobrilus nothus</i> Gagarin, 1989	Fw	30
<i>Neotobrilus diversipapillatus</i> (Daday, 1905) Tsalolikhin, 1981	Fw	21
<i>Semitobrilus pellucidus</i> (Bastian, 1865) Tsalolikhin, 1981	Fw	30
<i>Tobrilus gracilis</i> (Bastian, 1865) Andrásy, 1959	Fw T	1
Suborder Tripylina		
Family Tripylidae		
<i>Tripyla filicaudata</i> de Man, 1880	T	1
<i>Tripyla glomerans</i> Bastian, 1865	Fw T Bw	1
<i>Tripyla setifera</i> Bütschli, 1873	T	1
Subclass Dorylaimia		
Order Dorylaimida		
Suborder Dorylaimina		
Family Belonidiridae		
<i>Axonchium coronatum</i> (de Man, 1906) Thorne & Swanger, 1936	T	3
<i>Dorylaimellus demani</i> Goodey, 1963	T	1
<i>Oxydirus</i> Thorne, 1939	T	25
Family Mydonomidae		
<i>Dorylaimoides limnophilus</i> (de Man, 1880) Loof, 1964	T	1
Family Tylencholaimellidae		
<i>Tylencholaimellus striatus</i> Thorne, 1939	T	1
Family Tylencholaimidae		
<i>Tylencholaimus mirabilis</i> (Bütschli, 1873) de Man, 1876	T	1
<i>Tylencholaimus proximus</i> Thorne, 1939	T	1

<i>Tylencholaimus stecki</i> Steiner, 1914	T	1
Suborder Nygolaimina		
Family Actinolaimidae		
<i>Paractinolaimus macrolaimus</i> (de Man, 1880) Andrásy, 1964	Fw T	1
Family Aporcelaimidae		
<i>Aporcelaimellus obscurus</i> (Thorne & Swanger, 1936) Heyns, 1965	T	1
<i>Aporcelaimellus obtusicaudatus</i> (Bastian, 1865) Heyns, 1965	T Fw Bw	1
<i>Aporcelaimellus tritici</i> (Bastian, 1865) Andrásy, 1986	T Fw	1
<i>Aporcelaimus regius</i> (de Man, 1880) Thorne & Swanger, 1936	T	1
Family Dorylaimidae		
<i>Chrysodorus filiformis</i> (Bastian, 1865) Andrásy, 1988	T	1
<i>Dorylaimus crassus</i> de Man, 1884	T	1
<i>Dorylaimus stagnalis</i> Dujardin, 1845	Fw	21
<i>Mesodorylaimus bastiani</i> (Bütschli, 1873) Andrásy, 1959	T Bw	1
<i>Prodorylaimium brigdammense</i> (de Man, 1876) Andrásy, 1969	T Fw	1
<i>Prodorylaimus rotundiceps</i> Loof, 1985	T	12
Family Longidoridae		
<i>Longidorus attenuates</i> Hooper, 1961	T	1
<i>Longidorus caespiticola</i> Hooper 1961	T	1
<i>Longidorus cylindricaudatus</i> Korlowska & Seinhorst, 1979	T	1
<i>Longidorus elongatus</i> (de Man, 1876) Thorne & Swanger, 1936	T	1
<i>Longidorus goodeyi</i> Hooper, 1961	T	1
<i>Longidorus intermedius</i> Korlowska & Seinhorst, 1979	T	1
<i>Longidorus leptcephalus</i> Hooper, 1961	T	1
<i>Longidorus macrosoma</i> Hooper, 1961	T	1
<i>Longidorus profundorum</i> Hooper, 1966	T	1
<i>Longidorus sturhani</i> Robustova, Subbotin, Brown & Moens, 2001	T	11
<i>Longidorus vineacola</i> Sturhan & Weischer, 1964	T	1
<i>Paralongidorus maximus</i> (Buetschli, 1874) Siddiqi, 1964	T	3
<i>Xiphinema coxi</i> Tarjan, 1964	T	1
<i>Xiphinema diversicaudatum</i> (Micoletzky, 1927) Thorne, 1939	T	1
Family Nordiidae		
<i>Dorydorella pratensis</i> (de Man, 1880) Andrásy, 1986	T Bs	1
<i>Longidorella parva</i> Thorne, 1939	T	1
<i>Pungentus engadinensis</i> (Altherr, 1950) Altherr, 1952	T	1
<i>Pungentus silvestris</i> (de Man, 1912) Coomans & Geraert, 1962	T	1
Family Qudsianematidae		
<i>Crassolabium</i>	T	24
<i>Ecumenicus monohystera</i> (de Man, 1880) Thorne, 1974	T	1
<i>Epidorylaimus consobrinus</i> (de Man, 1918) Andrásy, 1986	T	1
<i>Eudorylaimus acuticauda</i> (de Man, 1880) Andrásy, 1986	T Bs	1
<i>Eudorylaimus carteri</i> (Bastian, 1865) Andrásy, 1959	T Fw Bs Bw	1
<i>Eudorylaimus centrocercus</i> (de Man, 1880) Andrásy, 1959	T	1
<i>Labronema vulvapapillatum</i> (Meyl, 1954) Loof & Grootaert, 1981	T	3
<i>Microdorylaimus modestus</i> (Altherr, 1952) Jairajpuri, 1970	T	12
Family Thornenematidae		

<i>Ophistodorylaimus sylphoides</i> (Williams, 1959) Carbonell & Coomans, 1986	T	12
Family Thorniidae		
<b><i>Nygolaimoides</i></b>	<b>C</b>	<b>31</b>
<i>Thornia</i>	T	24
Family Nygolaimidae		
<i>Nygolaimus</i>	T	24
Order Mononchida		
Suborder Mononchina		
Family Anatonchidae		
<i>Anatonchus tridentatus</i> (de Man, 1876) Cobb, 1916	T	1
Family Mononchidae		
<i>Clarkus papillatus</i> (Bastian, 1865) Jairajpuri, 1970	T	12
<i>Coomansus parvus</i> (de Man, 1880) Jairajpuri & Khan, 1977	T	25
<i>Mononchus aquaticus</i> Coetzee, 1968	Fw	1
<i>Mononchus tunbridgensis</i> Bastian, 1865	Fw	21
<i>Prionchulus muscorum</i> (Dujardin, 1845) Cobb, 1916	T	1
<i>Prionchulus punctatus</i> Cobb, 1917	T	1
Family Mylonchulidae		
<i>Mylonchulus brachyuris</i> (Bütschli, 1873) Cobb, 1917	T	1
<i>Mylonchulus sigmaturellus</i> Mulvey, 1961	T	26
Order Isolaimida		
Family Isolaimiidae		
<i>Isolaimium multistriatum</i> Hogewind & Heyns, 1967	T	1
Order Mermithida		
Family Mermithidae		
<i>Limnomermis</i>	Fw	30
<b>Class Chromadorea</b>		
Subclass Chromadorea		
Order Desmoscolecida		
Suborder Desmoscolecida		
Family Desmoscolecidae		
<i>Desmoscolex vinealis</i> Weischer, 1962	T (M)	3
Order Plectida		
Family Aphanolaimidae		
<i>Aphanolaimus aquaticus</i> Daday, 1894	T Fw	1
<i>Aphanolaimus attentus</i> de Man, 1880	T Fw	1
<i>Aphanolaimus deconincki</i> Coomans & De Waele, 1983	T Fw	1
<i>Aphanolaimus pseudoattentus</i> Coomans & De Waele, 1983	T	1
Family Camacolaimidae		
<i>Deontolaimus papillatus</i> de Man, 1880	Bs (M)	1
<i>Camacolaimus tardus</i> de Man, 1889	Bw (M)	4
Family Chronogasteridae		
<i>Chronogaster typica</i> de Man, 1921	Fw	1
Family Leptolaimidae		
<i>Antomicron elegans</i> (de Man, 1922)	Bw (M)	4

<i>Leptolaimus papilliger</i> de Man, 1876	Bw (M)	4
Family Metateratocephalidae		
<i>Metateratocephalus crassidens</i> (de Man, 1880) Eroshenko, 1973	T	1
Family Plectidae		
<i>Anaplectus granulatus</i> (Bastian, 1865) De Coninck & Schuurmans Stekhoven, 1933	T Bs	1
<i>Plectus acuminatus</i> Bastian, 1865	T	12
<i>Plectus armatus</i> (Bütschli, 1873) Andrásy, 1984	T Bw	1
<i>Plectus cirratus</i> Bastian, 1865	Fw T Bw	1
<i>Plectus geophilus</i> de Man, 1880	T	1
<i>Plectus parvus</i> Bastian, 1865	T	1
<i>Plectus longicaudatus</i> Bütschli, 1873	T	1
<i>Plectus parietinus</i> Bastian, 1865	T	12
<i>Plectus pusillus</i> Cobb, 1893	T	1
<i>Plectus rhizophilus</i> de Man, 1880	T	1
<i>Plectus tenuis</i> Bastian, 1865	T	25
<i>Tylocephalus auriculatus</i> (Bütschli, 1873) Crossman, 1933	T	1
<i>Wilsonema otophorum</i> (de Man, 1880) Cobb, 1913	T	1
<i>Wilsonema schuurmansstekhoveni</i> (De Coninck, 1931) Zell, 1982	T	3
Family Rhabdolaimidae		
<i>Rhabdolaimus terrestris</i> de Man, 1880	Fw	30
Order Araeolaimida		
Family Axonolaimidae		
<i>Axonolaimus paraspinosus</i> Schuurmans Steckhoven & Adam 1931	Bs (M)	4
Family Comesomatidae		
<i>Sabatieria pulchra</i> (Schneider, 1906)	Bs (M)	4
Family Diplopeltidae		
<i>Cylindrolaimus communis</i> de Man, 1880	T	1
<i>Cylindrolaimus melancholicus</i> de Man, 1880	T	17
<i>Southerniella</i>	Bs (M)	4
Order Monhysterida		
Suborder Monhysterina		
Family Monhysteridae		
<i>Diplolaimella allgeni</i> Schneider, 1967	Bw	4
<i>Diplolaimella dievengatensis</i> Jacobs, Van de Velde, Geraert & Vranken, 1990	Bw Bs	1
<i>Diplolaimella ocellata</i> (Bütschli, 1874) Gerlach, 1957	Bw	1
<i>Eumonhystera filiformis</i> (Bastian, 1865) Andrásy, 1981	Fw Bs Bw T	1
<i>Eumonhystera vulgaris</i> (de Man, 1880) Andrásy, 1981	T	1
<i>Geomonhystera villosa</i> (Bütschli, 1873) Andrásy, 1981	T	1
<i>Halomonhystera disjuncta</i> (Bastian, 1865) Andrásy, 2006	Bs Bw (M)	1
<i>Monhystera microphthalma</i> de Man, 1880	Bw (M)	1
<i>Monhystera paludicola</i> de Man, 1981	T	15
<i>Monhystera riemanni</i> Jacobs & Heyns, 1987	Fw	21
<i>Monhystrella macrura</i> (de Man, 1880) Andrásy, 1981	Bs Bw	1
<i>Monhystrella parelegantula</i> (De coninck, 1943) Andrásy, 1981	Bw Bs	1

<i>Thalassomonhystera parva</i> (Bastian, 1865) Jacobs, 1987	Bw Bs (M)	1
Family Spaerolaimidae		
<i>Sphaerolaimus gracilis</i> de Man, 1876	Bs (M)	1
Family Xyalidae		
<i>Daptonema setosum</i> (Bütschli, 1874)	Bw (M)	4
<i>Theristus longisetosus</i> (Schuurmans Stekhoven & De Coninck, 1933)	Bw (M)	1
<i>Theristus velox</i> (Bastian, 1865)	Bs Bw	1
Suborder Linhomoeina		
Family Linhomoeidae		
<i>Desmolaimus zeelandicus</i> de Man 1880	Bw (M)	4
Order Desmodorida		
Suborder Desmodorina		
Family Microlaimidae		
<i>Calomicrolaimus honestus</i> (de Man, 1922)	Bw (M)	4
<i>Microlaimus acuticaudatus</i> Schuurmans Stekhoven & De Coninck, 1933	Bw (M)	1
<i>Microlaimus globiceps</i> de Man, 1880	Bw Bs (M)	1
<i>Microlaimus robustidens</i> Schuurmans Stekhoven & De Coninck, 1933	Bw (M)	1
<i>Prodesmodora</i>	T (M)	24
Order Chromadorida		
Suborder Chromadorina		
Family Achromadoridae		
<i>Achromadora ruricola</i> (de Man, 1880) Micoletzky, 1925	T	1
Family Chromadoridae		
<i>Chromadorina bioculata</i> (Schultze In Carus, 1857) Wieser, 1954	Fw (M)	30
<i>Dichromadora geophila</i> (de Man, 1876) Kreis, 1929	Bw (M)	4
<i>Hypodontolaimus balticus</i> (Schneider, 1906) Filipjev, 1918	Bw (M)	4
<i>Neochormadora complexa</i> Gerlach, 1953	Bw (M)	4
<i>Ptycholaimellus ponticus</i> (Filipjev, 1922) Gerlach, 1955	Bw (M)	4
<i>Spilophorella paradoxa</i> (de Man, 1888) Filipjev, 1917	Bw (M)	4
Family Cyatholaimidae		
<i>Paracanthonchus caecus</i> (Bastian, 1865) Micoletzky, 1924	Bw (M)	4
<i>Paracyatholaimus intermedius</i> (de Man 1880) Filipjev, 1930	Bw T (M)	1
Family Ethmolaimidae		
<i>Ethmolaimus</i>	Bw (M)	4
Order Rhabditida		
Incertae sedis: Family Teratocephalidae		
<i>Teratocephalus terrestris</i> (Bütschli, 1873) de Man, 1876	T	1
<i>Teratocephalus costatus</i> Andrassy, 1958	T	12
Suborder Tylenchina		
Infraorder Panagrolaimomorpha		
Family Panagrolaimidae		
<b><i>Halicephalobus</i> cfr. <i>gingivalis</i> Stefanski, 1954</b>	<b>T C</b>	<b>32</b>
<i>Halicephalobus laticauda</i> Geraert, Sudhaus, Lenaerts & Bosmans, 1988	T	2
<i>Panagrolaimus rigidus</i> (Schneider, 1866) Thorne, 1937	T Fw Bw Bs	1
<b><i>Panagrolaimus labiatus</i> (Kreis, 1929) Andrassy, 1960</b>	<b>C</b>	<b>31</b>
<i>Panagrolaimus subelongatus</i> (Cobb, 1914) Thorne, 1937	T	12

<i>Propanagrolaimus filiformis</i> (de Man, 1880) Andrásy, 2005	Fw	30
<b><i>Procephalobus</i></b>	<b>C</b>	<b>31</b>
<b><i>Panagrellus</i></b>	<b>C</b>	<b>31</b>
Family Steinernematidae		
<i>Heterorhabditis bacteriophora</i> Poinar, 1976	T	15
<i>Heterorhabditis megidis</i> Poinar, Jackson & Klein, 1987	T	15
<i>Steinernema affine</i> (Bovien, 1937) Wouts, Mráček, Gerdin & Bedding, 1982	T	5
<i>Steinernema carpocapsae</i> Weiser, 1955	T	20
<i>Steinernema feltiae</i> (Filipjev, 1934) Wouts, Mráček, Gerdin & Bedding, 1982	T	5
<i>Steinernema kraussei</i> (Steiner, 1923) Travassos, 1927	T	6
Infraorder Cephalobomorpha		
Family Cephalobidae		
<i>Acrobeles ciliatus</i> v. Linstov, 1877	T	1
<i>Acrobelloides nanus</i> (de Man, 1880) Thorne, 1937	T	1
<i>Acrolobus emarginatus</i> (de Man, 1880) Thorne, 1937	T	1
<i>Acrobelophis minimus</i> (Thorne, 1937) Andrásy, 1984	T	1
<i>Acrobelophis deconincki</i> (Coomans, 1962) Vinciguerra & Clausi, 1996	T	1
<i>Cephalobus persegnis</i> Bastian, 1865	T	1
<i>Cervidellus vexilliger</i> (de Man, 1880) Thorne, 1937	T	1
<i>Chiloplacus demani</i> (Thorne, 1925) Schneider, 1939	T	1
<i>Eucephalobus oxyuroides</i> (de Man, 1876) Steiner 1936	T Bw	1
<i>Eucephalobus striatus</i> (Bastian, 1865) Thorne, 1937	T Fw Bw Bs	1
<i>Heterocephalobus elongatus</i> (de Man, 1880) Andrásy, 1967	T Bw	1
<i>Heterocephalobus longicaudatus</i> (Bütschli, 1873)	T	25
<i>Seleborca complexus</i> (Thorne, 1925) Andrásy, 1985	T	1
<i>Seleborca mariannae</i> (Andrásy, 1968) Andrásy, 1985	T	12
Family Osstellidae		
<i>Drilocephalobus goodeyi</i> Suryawanshi & Christy, 1973	T	1
Infraorder Tylenchomorpha		
Family Anguinidae		
<i>Ditylenchus destructor</i> Thorne, 1945	T	13
<i>Ditylenchus dipsaci</i> (Kühn, 1857) Filipjev, 1936	T	1
<b><i>Ditylenchus filimus</i> Anderson, 1983</b>	<b>C</b>	<b>31</b>
<i>Ditylenchus intermedius</i> (de Man, 1880) Filipjev, 1936	T	1
<i>Pseudhalenchus minutus</i> Tarjan, 1958	T	1
<i>Subanguina radicola</i> (Greeff, 1872) Paramonov, 1968	T	1
Family Aphelenchidae		
<i>Aphelenchus avenae</i> Bastian, 1865	T	1
Family Aphelenchoididae		
<i>Aphelenchoides asterocaudatus</i> Das, 1960	T	13
<i>Aphelenchoides bicaudatus</i> (Imamura, 1931) Filipjev & Schuurmans Stekhoven, 1941	T	1
<i>Aphelenchoides blastophorus</i> Franklin, 1952	T	13
<i>Aphelenchoides composticola</i> Franklin, 1957	T	1
<i>Aphelenchoides fragariae</i> (Ritzema Bos, 1890) Christie, 1932	T	1
<i>Aphelenchoides parietinus</i> (Bastian, 1865) Steiner, 1932	T	1

<i>Aphelenchoides ritzemabosi</i> (Schwartz, 1911) Steiner & Buhner, 1932	T	1
<i>Aphelenchoides subtenuis</i> (Cobb, 1926) Steiner & Buhner, 1932	T	1
<i>Aprutides guidettii</i> Scognamiglio, 1974	T	12
<b><i>Ektaphelenchoides</i></b>	<b>C</b>	<b>31</b>
<i>Laimaphelenchus penardi</i> (Steiner, 1914) Filipjev & Schuurmans Stekhoven, 1941	T	13
<i>Seinura diversa</i> (Paesler, 1957) Goodey, 1960	T	1
Family Criconematidae		
<i>Criconema annuliferum</i> (de Man, 1921) Micoletzky, 1925	T	1
<i>Criconema demani</i> Micoletzky, 1925	T	8
<i>Criconema longulum</i> Gunhold, 1953	T	1
<i>Criconema loofi</i> (De Grisse, 1967) Raski & Luc, 1985	T	1
<i>Criconema mutabile</i> (Taylor, 1936) Raski & Luc, 1985	T	12
<i>Criconema princeps</i> (Andrássy, 1962) Raski & Luc, 1985	T	1
<i>Criconema sphagni</i> Micoletzky, 1925	T	1
<i>Criconemoides amorphus</i> De Grisse, 1967	T	1
<i>Criconemoides annulatus</i> Cobb in Taylor, 1936	T	22
<i>Criconemoides informis</i> (Micoletzky, 1922) Taylor, 1936	T	1
<i>Criconemoides morgensis</i> (Hofmänner in Hofmänner & Menzel, 1914) Taylor, 1936	T	1
<i>Criconemoides parvus</i> Raski, 1952	T	1
<i>Crossonema menzeli</i> (Stefanski, 1924) Metha & Raski, 1971	T	1
<i>Hemicriconemoides pseudobrachyurus</i> De Grisse, 1964	T	1
<i>Mesocriconema axeste</i> (Fassuliotis & Williamson, 1959) Loof & De Grisse, 1989	T	1
<i>Mesocriconema crenatum</i> (Loof, 1964) Andrásy, 1965	T	1
<i>Mesocriconema curvatum</i> (Raski, 1952) Loof & De Grisse, 1989	T	1
<i>Mesocriconema dherdei</i> (De Grisse, 1967) Loof & De Grisse, 1989	T	1
<i>Mesocriconema irregulare</i> (De Grisse, 1964) Loof & De Grisse, 1989	T	1
<i>Mesocriconema kirjanovae</i> (Andrássy, 1962) Loof & De Grisse, 1989	T	8
<i>Mesocriconema maritimum</i> (De Grisse, 1964) Loof & De Grisse, 1989	T	1
<i>Mesocriconema ornatum</i> (Raski, 1952) Loof & De Grisse, 1989	T	1
<i>Mesocriconema pseudosolivagum</i> (De Grisse, 1964) Loof & De Grisse, 1989	T	1
<i>Mesocriconema raskiense</i> (De Grisse, 1964) Andrásy, 1965	T	1
<i>Mesocriconema rotundicauda</i> (Loof, 1964) Loof, 1989	T	1
<i>Mesocriconema rusticum</i> (Micoletzky, 1915) Loof & De Grisse, 1989	T	1
<i>Mesocriconema solivagum</i> (Andrássy, 1962) Loof & De Grisse, 1989	T	1
<i>Mesocriconema sphaerocephala</i> (Taylor, 1936) Loof, 1989	T	1
<i>Mesocriconema vadense</i> (Loof, 1964) Loof & De Grisse, 1989	T	1
<i>Mesocriconema xenoplax</i> (Raski, 1952) Loof, 1989	T	1
<i>Ogma cobbi</i> (Micoletzky, 1925) Siddiqi, 1986	T	1
<i>Xenocriconemella macrodora</i> (Taylor, 1936) De Grisse & Loof, 1965	T	1
Family Dolichodoridae		
<i>Amplimerlinius icarus</i> (Wallace & Greet, 1964) Siddiqi, 1976	T	8
<i>Amplimerlinius macrurus</i> (Goodey, 1932) Siddiqi, 1976	T	1



<i>Macrotrophurus arbusticola</i> Loof, 1958	T	1
<i>Merlinius brevidens</i> (Allen, 1955) Brzeski, 1991	T	1
<i>Merlinius joctus</i> (Thorne, 1949) Brzeski, 1991	T	1
<i>Merlinius microdorus</i> (Geraert, 1966) Brzeski, 1991	T	1
<i>Merlinius nanus</i> (Allen, 1955) Brzeski, 1991	T	1
<i>Merlinius nothus</i> (Allen, 1955) Brzeski, 1991	T	1
<i>Nagelus alpinus</i> Doucet & Luc, 1981	Fw	3
<i>Nagelus obscurus</i> (Allen, 1955) Powers, Baldwin & Bell, 1983	Fw	8
<i>Neodolichodorus lamelliferus</i> (de Man, 1880) Filipjev, 1936	T	1
<i>Neodolichodorus microphasmis</i> Loof, 1960	T	1
<i>Quinisulcius capitatus</i> Allen, 1955	T	1
<i>Scutylenchus quadrifer</i> (Andrassy, 1954) Brzeski, 1991	T	1
<i>Scutylenchus tessellatus</i> (Goodey, 1952) Brzeski, 1991	T	1
<i>Telotylenchus ventralis</i> (Loof, 1963) Fortuner & Luc 1987	T	1
<i>Tylenchorhynchus claytoni</i> Steiner, 1937	T	1
<i>Tylenchorhynchus contractus</i> Loof, 1964	T	3
<i>Tylenchorhynchus dubius</i> (Bütschli, 1873) Filipjev, 1936	T	1
<i>Tylenchorhynchus maximus</i> Allen, 1955	T	1
Family Hemicycliophoridae		
<i>Hemicycliophora conida</i> Thorne, 1955	T	1
<i>Hemicycliophora similis</i> Thorne, 1955	T	1
<i>Hemicycliophora thienemanni</i> (Schneider, 1952) Loof, 1984	T	28
<i>Hemicycliophora triangulum</i> Loof, 1968	T	8
Family Hoplolaimidae		
<i>Globodera pallida</i> (Stone, 1973) Behrens, 1975	T	18
<i>Globodera rostochiensis</i> (Wollenweber, 1923) Behrens, 1975	T	1
<i>Helicotylenchus canadensis</i> Waseem, 1961	T	13
<i>Helicotylenchus exallus</i> Sher, 1966	U	8
<i>Helicotylenchus minzi</i> Sher, 1966	T	1
<i>Helicotylenchus multicinctus</i> (Cobb, 1893) Golden, 1956	T	1
<i>Helicotylenchus pseudorobustus</i> (Steiner, 1914) Golden, 1956	T	1
<i>Helicotylenchus varicaudatus</i> Yuen, 1964	T	8
<i>Heterodera aucklandica</i> Wouts & Sturhan, 1995	T	14
<i>Heterodera avenae</i> Wollenweber, 1924	T	1
<i>Heterodera bifenestra</i> Cooper, 1955	T	28
<i>Heterodera cruciferae</i> Franklin, 1945	T	1
<i>Heterodera goettingiana</i> Liebscher, 1892	T	1
<i>Heterodera hordecalis</i> Andersson, 1975	T	28
<i>Heterodera humuli</i> Filipjev, 1934	T	1
<i>Heterodera mani</i> Matthews, 1971	T	28
<i>Heterodera ripae</i> Subbotin, Sturhan, Rumpfenhorst & Moens, 2003	T	19
<i>Heterodera salixophila</i> Kirjanova, 1969	T	9
<i>Heterodera schachtii</i> Schmidt, 1871	T	1
<i>Heterodera trifolii</i> Goffart, 1932	T	1
<i>Heterodera ustynovi</i> Kirjanova, 1969	T	14

<i>Heterodera utricae</i> Cooper, 1955	T	9
<i>Meloidodera alni</i> Turkina & Chizhov, 1986	T	9
<i>Peltamigratus parapachyuris</i> Rashid, 1986	T	3
<i>Punctodera punctata</i> (Thorne, 1928) Mulvey & Stone, 1976	T	1
<i>Rotylenchus goodeyi</i> Loof & Oostenbrink, 1958	T	1
<i>Rotylenchus robustus</i> (de Man, 1880) Filipjev, 1936	T	1
<i>Rotylenchus uniformis</i> (Thorne, 1949) Loof & Oostenbrink, 1958	T	1
<i>Rotylenchulus borealis</i> Loof & Oostenbrink, 1962	T	28
<i>Scutylenchus quadrifer</i> (Andrássy, 1954) Siddiqi, 1979	T	22
<i>Scutylenchus tessellates</i> (Goodey, 1952) Siddiqi 1979	T	22
Family Meloidogynidae		
<i>Meloidogyne arenaria</i> (Neal, 1889) Chitwood, 1949 [greenhouse]	T	16
<i>Meloidogyne ardenensis</i> Santos, 1968	T	1
<i>Meloidogyne chitwoodi</i> (Golden, O' Bannon, Santo and Finley, 1980 ) O' Bannon, Santo & Finley, 1980	T	8
<i>Meloidogyne duytsi</i> Karssen, Van Aelst & Van Der Putten, 1998	T	8
<i>Meloidogyne fallax</i> Karssen, 1996	T	8
<i>Meloidogyne hapla</i> Chitwood, 1949	T	1
<i>Meloidogyne maritima</i> (Jepson, 1987) Karssen, van Aelst & Cook, 1998	T	8
<i>Meloidogyne minor</i> Karssen, Bolk, van Aelst, Van den Beld, Kox, Korthals, Molendijk, Zijlstra, van Hoof & Cook 2004	T	23
<i>Meloidogyne naasi</i> Franklin, 1965	T	1
Family Neotylenchidae		
<b>Unidentified</b>	<b>C</b>	<b>31</b>
Family Pratylenchidae		
<i>Hirschmanniella behningi</i> (Micoletzky, 1923) Luc & Goodey, 1964	Fw	30
<i>Hirschmanniella caudacrena</i> Sher, 1968	Fw	27
<i>Hirschmanniella gracilis</i> (de Man, 1880) Luc & Goodey, 1964	T	8
<i>Hirschmanniella loofi</i> Sher, 1968	T	8
<i>Hoplotylus femina</i> s' Jacob, 1959	T	12
<i>Pratylenchoides crenicauda</i> Winslow, 1958	T	1
<i>Pratylenchoides laticauda</i> Braun & Loof, 1966	T	28
<i>Pratylenchoides magnicauda</i> (Thorne, 1953) Baldwin, Luc & Bell, 1983	T	13
<i>Pratylenchus brzeskii</i> Karssen, Waeyenberge & Moens, 2000	T	10
<i>Pratylenchus crenatus</i> Loof, 1960	T	1
<i>Pratylenchus dellatrei</i> Luc, 1958	T	1
<i>Pratylenchus fallax</i> Seinhorst, 1968	T	1
<i>Pratylenchus flakkensis</i> Seinhorst, 1968	T	8
<i>Pratylenchus neglectus</i> (Rensch, 1924) Filipjev & Schuurmans Stekhoven, 1941	T	1
<i>Pratylenchus penetrans</i> (Cobb, 1917) Filipjev & Schuurmans Stekhoven, 1941	T	1
<i>Pratylenchus pratensis</i> (De Man, 1880) Filipjev, 1936	T	1
<i>Pratylenchus pseudopratensis</i> Seinhorst, 1968	T	1
<i>Pratylenchus thornei</i> Sher & Allen, 1953	T	1
<i>Pratylenchus vulnus</i> Allen & Jensen, 1951	T	1

<i>Radopholus similis</i> (Cobb, 1893) Thorne, 1949	T	7
Family Psilenchidae		
<i>Psilenchus aestuarius</i> Andrassy, 1962	T	13
<i>Psilenchus clavicaudatus</i> (Micoletzky, 1922) Thorne, 1949	T	1
<i>Psilenchus hilarulus</i> de Man, 1921	T	1
<i>Psilenchus terrestremus</i> Hagemeyer & Allen, 1952	T	25
Family Sphaerulariidae		
<i>Prothallonema consobrinum</i> (de Man, 1907) Siddiqi, 1986	T	1
Family Tylenchidae		
<i>Aglenchus agricola</i> (de Man, 1884) Andrassy, 1954	T Fw Bw Bs	1
<i>Basiria aberrans</i> (Thorne, 1949) Siddiqi, 1963	T	1
<i>Basiria duplexa</i> (Hagemeyer & Allen, 1952) Geraert, 1968	T	1
<i>Basiria flandriensis</i> Geraert, 1968	T	1
<i>Basiria gracilis</i> (Thorne, 1949) Siddiqi, 1963	T	1
<i>Basiria graminophila</i> Siddiqi, 1951	T	8
<i>Boleodorus clavicaudatus</i> (Thorne, 1941) Mathur, Khan & Prasad, 1966	T	1
<i>Boleodorus thylactus</i> Thorne, 1941	T	1
<i>Boleodorus volutus</i> Lima & Siddiqi, 1963	T	1
<i>Cephalenchus hexalineatus</i> (Geraert, 1962) Geraert & Goodey, 1964	T	13
<i>Cephalenchus leptus</i> Siddiqi, 1963	T	8
<i>Coslenchus alacinatus</i> Siddiqi, 1981	U	8
<i>Coslenchus andrassyi</i> Brzeski, 1987	T	13
<i>Coslenchus costatus</i> (de Man, 1921) Siddiqi, 1978	T	1
<i>Coslenchus polonicus</i> Brzeski, 1982	T	8
<i>Ecphyadophora tenuissima</i> de Man, 1921	T	1
<i>Filenchus baloghi</i> (Andrassy, 1958) Siddiqi, 1986	T	1
<i>Filenchus discrepans</i> (Andrassy, 1954) Raski & Geraert, 1987	T	12
<i>Filenchus helenae</i> (Szczygiel, 1969) Raski & Geraert, 1987	T	12
<i>Filenchus misellus</i> (Andrassy, 1958) Raski & Geraert, 1987	T	12
<i>Filenchus quartus</i> Szczygiel, 1969	T	1
<i>Filenchus sandneri</i> (Wasilewska, 1965) Raski & Geraert, 1987	T	13
<i>Filenchus terrestris</i> Raski & Geraert, 1987	T	12
<i>Filenchus thornei</i> Andrassy, 1954	T	1
<i>Filenchus vulgaris</i> (Brzeski, 1963) Lownsbery & Lownsbery, 1985	T	8
<i>Irantylenchus vicinus</i> (Szczygiel, 1970) Brzeski & Sauer, 1983	T	1
<i>Lelenchus leptosoma</i> (de Man, 1880) Andrassy, 1954	T	1
<i>Malenchus acarayensis</i> Andrassy, 1968	U	8
<i>Malenchus andrassyi</i> Merny, 1970	T	12
<i>Malenchus bryophilus</i> (Steiner, 1914) Andrassy, 1980	T	1
<i>Miculenchus salvus</i> Andrassy, 1959	T	1
<i>Tylenchus arcuatus</i> Siddiqi, 1963	T Fw	8
<i>Tylenchus davainei</i> Bastian, 1965	T	1
<i>Tylenchus elegans</i> de Man, 1876	T	13
<i>Neopsilenchus magnidens</i> (Thorne, 1949) Thorne & Malek, 1968	T	1
Family Tylenchulidae		

<i>Paratylenchus aculentus</i> Brown, 1959	T	8
<i>Paratylenchus goodeyi</i> Oostenbrink, 1953	T	1
<i>Paratylenchus macrodorus</i> Brzeski, 1963	T	1
<i>Paratylenchus microdorus</i> Andrassy, 1959	T	1
<i>Paratylenchus nanus</i> Cobb, 1923	T	1
<i>Paratylenchus projectus</i> Jenkins, 1956	T	1
<i>Paratylenchus hamatus</i> Thorne & Allen, 1950	T	1
<i>Paratylenchus similis</i> Khan, Prasad & Mathur, 1967	T	8
<i>Paratylenchus straeleni</i> (De Coninck, 1931) Oostenbrink, 1960	T	1
Suborder Rhabditina		
Infraorder Diplogasteromorpha		
Family Diplogasteridae		
<b><i>Achrostichus</i></b>	<b>C</b>	<b>31</b>
<i>Butlerius degrissei</i> (Grootaert & Jaques, 1979) Ebsary, 1986	T	1
<i>Butlerius butleri</i> Goodey, 1929	T	25
<b><i>Diplogaster</i></b>	<b>C</b>	<b>31</b>
<b><i>Diplogasteritus</i></b>	<b>C</b>	<b>31</b>
<b><i>Fictor</i></b>	<b>C</b>	<b>31</b>
<i>Paroigolaimella</i>	T	25
<i>Tylopharynx foetida</i> (Bütschli, 1874) Goodey, 1928	T	1
Family Diplogasteroididae		
<b><i>Diplogasteroides</i></b>	<b>C</b>	<b>31</b>
Family Neodiplogasteridae		
<b><i>Mononchoides composticola</i> Steel, Scholaert, Boshoff, Houthoofd &amp; Bert, 2011</b>	<b>C</b>	<b>29</b>
<i>Pristionchus lheritieri</i> (Maupas, 1919) Paramonov, 1952	T	1
Infraorder Bunonematidomorpha		
Family Bunonematidae		
<i>Bunonema reticulatum</i> Richters, 1905	T	1
<i>Bunonema richtersi</i> Jägerskiöld, 1901	T	12
<i>Craspedonema</i>	T	12
Infraorder Rhabditomorpha		
Family Rhabditidae		
<i>Cephaloboides curvicaudatus</i> (Schneider, 1866) Dougherty, 1953	T	1
<i>Choriorhabditis longicaudata</i> (Bastian, 1865) Sudhaus, 2011	T	12
<b><i>Crusthorhabditis</i></b>	<b>C</b>	<b>31</b>
<b><i>Cruzinema</i></b>	<b>C</b>	<b>31</b>
<b><i>Diploscapter coronatus</i> (Cobb, 1893) Cobb, 1913</b>	<b>Fw T C</b>	<b>31</b>
<i>Mesorhabditis monhystera</i> (Bütschli, 1873) Andrassy, 1976	T	1
<b><i>Parasitorhabditis</i></b>	<b>C</b>	<b>31</b>
<b><i>Pelodera teres</i> Schneider, 1866</b>	<b>C</b>	<b>31</b>
<b><i>Pelodera cylindrica</i> (Cobb, 1898) Dougherty, 1953</b>	<b>C</b>	<b>31</b>
<i>Pelodera cystilarva</i> (Völk, 1950) Dougherty, 1955	T	12
<i>Pellioiditis marina</i> (Bastian, 1865) Andrassy, 1983	Bw (M)	1
<i>Pellioiditis pellioides</i> (Bütschli, 1873) Andrassy, 1983	T	1
<i>Poikilolaimus oxycerca</i> (de Man, 1895) Sudhaus, 1980	T Fw	1

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<i>Protorhabditis filiformis</i> (Bütschli, 1873) Sudhaus, 1976	T Fw	1
<i>Protorhabditis oxyuroides</i> Sudhaus, 1974	T	1
<b><i>Rhabditella axei</i> (Cobbold, 1884) Chitwood, 1933</b>	<b>T C</b>	<b>1</b>
<i>Rhabditis terricola</i> Dujardin, 1845	T	1
<b><i>Rhabditophanes cobbi</i> (Hnatewytch, 1929) Andrassy, 1983</b>	<b>C</b>	<b>31</b>
<i>Rhabditophanes schneideri</i> (Bütschli, 1873) Goodey, 1953	T	12
<b><i>Teratorhabditis</i></b>	<b>C</b>	<b>31</b>

**PART 2: *MONONCHOIDES COMPOSTICOLA* N. SP. (NEMATODA: DIPLOGASTERIDAE)****ASSOCIATED WITH COMPOSTING PROCESSES: MORPHOLOGICAL, MOLECULAR AND AUTOECOLOGICAL CHARACTERIZATION.****3.6 Abstract**

*Mononchoides composticola* n. sp. was isolated from compost and is described based on light and scanning electron microscopy, supplemented with SSU rDNA sequence data. It is characterised by the following features: a denticulate ridge in addition to the dorsal claw-like tooth, a small tooth-like swelling at the stegostom base, ca 26 longitudinal ridges on the female body, a uterine sac associated with two dumb-bell-shaped pouches, relatively small spicules (30-38 µm long), a simple gubernaculum shorter than half the spicule length, the genital subventral papillae (v6) consisting of three very small papillae, and a long filiform tail (female: 391-550 µm, 18-26 anal body diam.; male: 304-548 µm, 19-30 anal body diam.). Phylogenetic analyses placed the new species together with *M. striatus*, sister to *Tylopharynx foetida*. Since the use of nematodes as functional indicators often relies on the allocation of nematodes to feeding groups, experiments were performed to elucidate the feeding strategy of the new species. Both its ability to move actively to bacterial food sources and to prey on other compost nematodes were tested. *Mononchoides composticola* n. sp. actively moved towards the compost bacterium *Achromobacter*, a taxis that was temperature dependent, and also preyed on other nematodes. Predation was selective, with a higher predation rate on the relatively small and slow-moving *Rhabditella* sp. than on the considerably larger and more motile *Rhabditis (Poikilolaimus)* sp. Adults of *M. composticola* n. sp. have a dual feeding behaviour and can apparently alternate between bacterial and nematode prey.

**3.7. Introduction**

Until recently, knowledge of the nematode assemblages and population dynamics associated with composting processes was completely lacking. The nematode community in a Controlled Microbial Composting (CMC) process was analysed in Chapter 2. Compared to many soil ecosystems, nematode succession in compost differs mainly by the absence of K-strategists and by the prominence of diplogastrids. At the beginning of the composting process (thermophilic phase), immediately after the heat peak, the nematode population is primarily composed of bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogasteridae) followed by bacterial-feeding (cp-2) (Cephalobidae) and fungal-feeding general opportunists (Aphelenchoididae). At the end of the process, at the most mature stage, the

fungal-feeding Anguinidae (mainly *Ditylenchus filimus* Anderson, 1983) were dominant. However, before this final stage, during the cooling and maturation stage, an unknown *Mononchoides* n. sp. became dominant ( $\geq 30\%$  of nematodes). In view of the high abundance of this undescribed *Mononchoides* n. sp., it is reasonable to suggest that it may have a significant role in the compost-associated foodweb. *Mononchoides* Rahm, 1928 is a cosmopolitan, quite common, genus and by far the most diverse genus of the family Diplogasteridae *sensu lato* (Sudhaus and Fürst von Lieven 2003) (= taxon Diplogastromorpha in De Ley and Blaxter 2002). *Mononchoides* inhabits various terrestrial habitats and is often associated with compost, dung, mud, other decaying materials and with different kinds of beetles. Some *Mononchoides* species have been described from freshwater (e.g., sediment of rivers and lakes) and even marine habitats (e.g., sewage) (Sudhaus and Fürst von Lieven 2003). Within *Mononchoides*, Calaway and Tarjan (1973) listed 18, Andrassy (1984) 17 and Gagarin (1998) 24 species. Sudhaus and Fürst von Lieven (2003), following Gagarin (1998), considered *Glauximena* Allgén, 1947 synonymous with *Mononchoides*, an approach that is also followed in the current paper. In a comprehensive review on diplogastrid nematodes, also taking into account the detailed stoma morphology (see Fürst von Lieven and Sudhaus 2000), 43 species were listed within the genus *Mononchoides*. Andrassy (2005b) did not accept the synonymisation of *Mononchoides* and *Glauximena* based on the presence of a left ventro-sublateral plate in the buccal cavity of *Mononchoides* species. Andrassy (2005b) accepted only 29 valid *Mononchoides* species and nine valid *Glauxinema* species.

Since the review of Sudhaus and Fürst von Lieven (2003), *M. gaugleri* Siddiqi, Bilgrami & Tabassum, 2004 and *M. megaonchus* Mahamood, Ahmed & Shah, 2007 have been described while *M. tokobaevi* Lemzina, 1990 was not listed in Sudhaus and Fürst von Lieven (2003). Within *Glauxinema* (= synonym of *Mononchoides* according to Sudhaus and Fürst von Lieven, 2003), *G. aquaticum* Gagarin & Thanh, 2006 was recently described (Gagarin and Thanh 2006). Despite their high diversity and numerical importance, the exact feeding habits of *Mononchoides* species, and indeed of most diplogastrids, are barely known. In general they are considered bacterial-feeders and/or predators (Yeates et al., 1993). However, Fürst von Lieven and Sudhaus (2000) observed *Mononchoides* sp. feeding on fungal spores and ciliates. It is also very unclear which stages act as predators and which stages can switch to a bacterivorous mode when prey is absent. Knowledge of feeding type is important for our understanding of nematode ecology and for our use and interpretation of nematode-based indices used in community analyses and environmental monitoring (e.g., Index of Trophic Diversity; Heip et al. 1985).

In this paper we describe the new *Mononchoides* species isolated from compost based on morphology (studied by light microscopy (LM) and scanning electron microscopy (SEM)) and on molecular data (SSU rDNA sequences). Aspects of the feeding ecology of this new species are experimentally tested and the ecological implications of the observed feeding habits are considered.

### **3.8. Materials and methods**

#### 3.8.1. Collection and culture

*Mononchoides composticola* n. sp. was extracted from a compost heap at the Institute for Agricultural and Fisheries Research in Merelbeke near Ghent, Belgium (Plant Science Unit, Growth and Development research area), using a modified Baermann funnel method. The heap was composed of three different feedstock materials: 43% fine wood chips, 43% dry hay and 14% fresh grass. The compost was prepared according to the CMC method, but no microbial starter was added. A composting process is typically subdivided into three different phases based on the temperature profile: the thermophilic phase (45-75 °C), the cooling phase (45 °C - ambient temperature) and the maturation phase ( $\approx$  ambient temperature) (approximately 3, 3 and >10 weeks, respectively, in the composting process studied in Chapter 2). *Mononchoides composticola* n. sp. could be detected during the cooling and maturation phase from day 10 until day 165 of the process. A culture with bacteria (i.e., *Achromobacter* sp.) and nematodes (*Rhabditis (Poikilolaimus)* sp. and *Rhabditella* sp.) as food sources was established from one female and one male *M. composticola* n. sp.

Cultures were maintained on agar (bacterial agar 2.7 g 400 ml<sup>-1</sup> (Oxoid, Basingstoke, UK)) and nutrient agar (1.3 g 400 ml<sup>-1</sup> (Oxoid) plates containing cholesterol (final concentration of 1 µg ml<sup>-1</sup> (Sigma-Aldrich, St Louis, MO, USA)). The cultures were kept in an incubator at 25 °C and generally handled as described by Brenner (1974).

The nutrient portion of the agar also stimulated the development of the natural bacteria present in the compost. An unknown compost bacterial strain was isolated and cultured in LB-medium (2 g yeast extract (Sigma Cell Culture), 4 g tryptone (Oxoid), 2 g NaCl (Acros Organics, Geel, Belgium), 0.4 g (1 M) NaOH and 400 ml distilled water, autoclaved and stored at 4 °C). Subsequently, the compost bacteria used for the feeding experiments were identified to genus level at the Laboratory of Microbiology, Faculty of Sciences, Ghent University. The bacteria used for the feeding experiments belonged to *Achromobacter*, a genus known from aquatic habitats and soil and which can also be found in clinical samples (Coenye et al. 2003).



### 3.8.2. Morphological characterisation

Type material was collected directly from modified Baermann funnel method extractions in a small drop of water in an embryo dish. Formalin (4% with 1% glycerin) was heated to 70 °C and an excess (4-5 ml) was quickly added to the specimens to fix and kill the nematodes instantly (Seinhorst 1966). The fixed nematodes were processed to anhydrous glycerin following the glycerin-ethanol method (Seinhorst 1959 as modified by De Grisse 1969). Measurements and drawings were prepared manually with a camera lucida on an Olympus BX51 DIC Microscope (Olympus Optical, Tokyo, Japan) equipped with an Olympus C5060Wz camera for photographs.

The holotype was also recorded as a video clip mimicking a multifocal observation through a LM microscope following the Video Capture and Editing procedures developed by De Ley and Bert (2002). The resulting virtual specimens are available at [www.nematology.ugent.be/vce.html](http://www.nematology.ugent.be/vce.html).

For SEM, specimens preserved in anhydrous glycerin were transferred to a drop of glycerin in an embryo dish. Two drops of water were added every 10 min for 2 h. A subsequent ultrasonic treatment (8 min) of the specimens in a single drop of water removed particles adhering to the body surface. The specimens were dehydrated by passing them through a graded ethanol concentration series of 20, 50, 75, 95, 100% (1 h each), 100% (overnight) and 100% (20 min, next morning). Afterwards, the specimens were critical point- dried with liquid CO<sub>2</sub>, mounted on stubs with carbon discs and coated with gold (25 nm) before observation with a JSM-840 EM (JEOL, Tokyo, Japan) at 15 kV.

The terminology describing the parts of the stoma follows De Ley et al. (1995) and that of other structural details of the buccal cavity is in accordance with Fürst von Lieven and Sudhaus (2000), which is an essential paper for the correct interpretation of the morphological structures of the diplogastrid stoma region. The male genital papillae formula used was as proposed by Sudhaus and Fürst von Lieven (2003).

### 3.8.3. Molecular characterisation

For the molecular characterisation one specimen from each of two different cultures was used. One culture was started from *M. composticola* n. sp. specimens isolated on day 31 of the composting process using agar plates (isolate 'culture, day 31') and the other culture was started from *M. composticola* n. sp. specimens isolated on day 84 of the composting process using the modified Baermann funnel method (isolate 'direct extraction, day 84').

DNA extraction, PCR reaction and sequencing the SSU rDNA were done as in Bert et al. (2008). The sequences were deposited in GenBank under the accession numbers GU943511 and GU943512. Additional sequences of diplogastrids for phylogenetic analyses were obtained from GenBank. The SSU rDNA sequences were aligned with Clustal W (Thompson et al. 1994) and manually checked. This resulted in an alignment of 1679 characters of which 445 were

parsimony-informative. Differences between sequences were counted using the BioEdit sequence alignment options (Hall 1999). Bayesian phylogenetic inference (BI) was performed with MrBayes v3.1.2 (Ronquist and Huelsenbeck 2003). A general time-reversible model with rate variation across sites and a proportion of invariable sites (GTR + I + G) was used, as estimated by PAUP\*/MrModeltest 2.0b (Nylander 2004). Two independent, simultaneous analyses were run for  $3 \times 10^6$  generations and the trees were generated using the last  $10^6$  generations, well beyond the burn-in value and the point of convergence between the two runs, the latter confirmed by the average standard deviations of split frequencies which approached zero ( $<0.0012$ ). Other analyses (maximum parsimony, maximum likelihood and LogDet-transformed distance) were done but did not alter the tree topology (except for the support values) and are not further discussed.

#### 3.8.4. Feeding experiments

Preliminary tests were done to identify the best medium and temperature for successful culturing of *M. composticola* n. sp. Two kinds of feeding/foraging experiments were performed, assessing, respectively, the ability of *M. composticola* n. sp. to detect and actively move to a bacterial food source and its potential to feed as a predator on other compost nematodes. These experiments were born out of expectations based on literature information documenting, or at least suggesting, predatory feeding and bacterivory in other diplogastrid nematodes (Yeates et al. 1993; Moens et al. 2004).

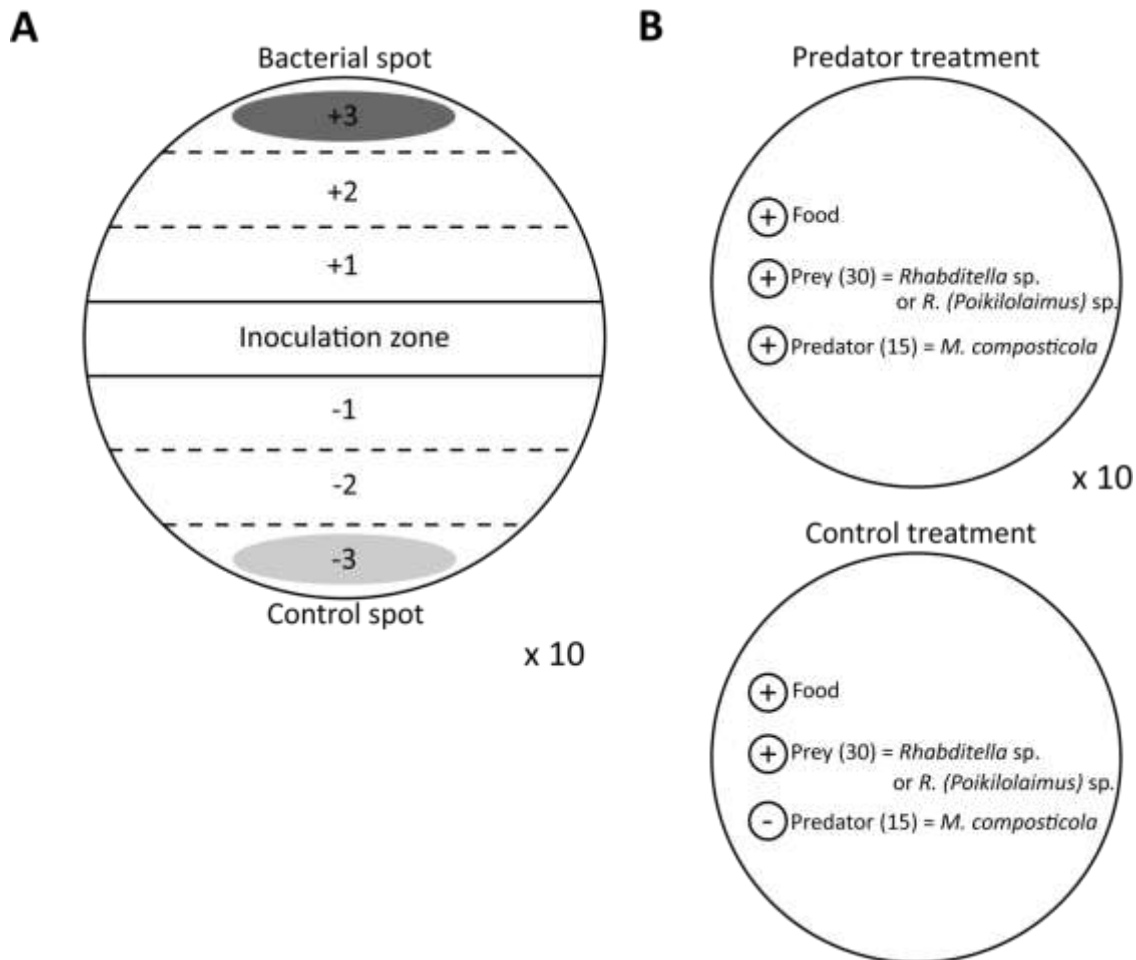
To test directional active movement to bacterial food, a Petri dish (8.7 cm diam.) with a 1% agar layer (bacterial agar 4 g 400 ml<sup>-1</sup> (Oxoid)) was subdivided into seven parallel regions, i.e., an inoculation zone with three positive regions to one side and three negative regions to the other. At the two most extreme, opposite sides (+3 and -3 region, respectively) of the Petri dish, either a 80 µl drop of the bacteria *Achromobacter* in LB medium (=bacterial spot) or a 80 µl drop of distilled water (= control spot) was placed (Figure 3.1A) Ten nematode specimens were washed in distilled water and added to the inoculation zone in the centre of the plate ca 1 h after spotting the candidate attractants. To emphasise the distance moved towards or away from the bacterial food source each nematode was scored: nematodes that had moved towards the bacterial attractant were awarded a positive score; the ones moving in the opposite direction were given a negative score, corresponding to the region in which they were recorded (so individual scores ranging from 0 to +3 and from 0 to -3 for migration towards or away from the bacterial spot, respectively). A Leica Mz95 binocular was used for observations. The movement towards or away from a bacterial food source was scored at 1, 2, 4 and 24 h after incubation. Once inside a bacterial spot, most nematodes tended to stay inside it. This experiment was repeated at six different temperatures (15, 20, 30, 40, 45 and 60 °C) with ten replicates of each,

always with ten *M. composticola* n. sp. per replicate. For the statistical analyses, only the data at 15, 20 and 30 °C were used because the nematodes did not survive the entire 24 h incubation at the higher three temperatures. Replicated G-tests for goodness of fit (Sokal and Rohlf 1995) were used to test the null hypothesis of random movement and hence no preferential migration of *M. composticola* n. sp. towards bacteria. This should result in a 1 : 1 ratio of nematode numbers inside bacterial and control spots. Differences in rate and degree of migration among different temperature treatments were analysed using repeated measures ANOVA followed by post hoc Tukey HSD tests for unequal number of replicates. These analyses were performed on an Attraction Index (Troemel et al. 1997) calculated for each replicate. In brief, this index sums the scores of each nematode on a plate and divides this sum by the number of nematodes recovered. It thus takes into account the position of all nematodes on a plate. The more positive the index, the closer, on average, nematodes on a plate were to the bacterial spot; the more negative the index, the closer, on average, nematodes were to the control spot.

Secondly, the ability of *M. composticola* n. sp. to feed on other compost nematodes was tested. The experiments were executed with two different candidate prey species, *Rhabditis (Poikilolaimus)* sp. and *Rhabditella* sp., with ten replicates of each. Petri dishes were filled with a nutrient agar layer covered with a layer of compost bacteria (70 µl bacteria in LB medium spread evenly). The predator treatments consisted of 15 adult *M. composticola* n. sp., 30 adult *R. (Poikilolaimus)* sp. or *Rhabditella* sp. and *Achromobacter* compost bacteria, while controls were similarly incubated but contained no *M. composticola* n. sp. (Figure 3.1B). Before inoculation on to the agar plates, nematodes were washed in distilled water to remove adhering debris. Prey and predator nematode numbers were counted after 24 and 48 h. Prey consumption was calculated as the difference between prey numbers remaining in the control and in the predator treatment (Moens et al. 2000). Any small juvenile prey nematodes produced during the experimental incubation were not taken into account for our calculations. The edges, walls and lids of the Petri dishes were checked to ensure that no prey had escaped from the agar layers. Natural mortality of both prey and predator was easily detectable since decay times of dead nematodes were longer than the incubation time of the experiments. The occurrence of empty prey cuticles was treated as removed prey. Statistical analysis of differences in the number of prey remaining after 24 and 48 h between the predator and control treatment used Student t - tests in Statistica 6.0. Differences in prey removal between the two different prey species after 24 h were also examined using a Student t -test.

**Figure 3.1:**

Schematic overview of the experimental setup of the feeding experiments performed with *Mononchoides composticola* n. sp. A: To test directional active movement to bacterial food, a Petri dish was subdivided into seven parallel regions (i.e. one inoculation zone, three positive regions and three negative regions). The movement of the nematodes was scored 1, 2, 4 and 24 h after incubation and the experiment was repeated at 15, 20, 30, 40, 45 and 60°C in ten replicates. B: The ability of *M. composticola* to feed on other compost nematodes was tested by comparing the number of prey (*Rhabditella* sp. or *R. (Poikilolaimus)* sp.) in the predator treatment (including food, predators and prey) and the control treatment (including only food and prey).



### 3.9. Results

*Mononchoides composticola*\* n. sp. (Figures 3.2-3.4)

#### 3.9.1. Measurements

See Table 3.2.

#### 3.9.2. Description

##### Female

Body long, straight to slightly arcuate ventrally after fixation. Cuticle clearly annulated, ca 1 µm at midbody, with conspicuous longitudinal ridges (ca 26 at head level). Lip region continuous with body contour, consisting of six fused lips, each with a small papilla. Stoma s.l. longer than

\* The specific epithet refers to the type habitat of the new species.

wide. First stoma part or cheilostom (= stoma s.s.) wide, walls heavily cuticularised. Cheilostom subdivided into several (14-18) narrow, rod-like plates (= cheilorhabdions). Bifurcated apex of cheilorhabdions mostly extending beyond labial contour. Second part of stoma consisting of gymnostom and stegostom, both anisotropic with ventro-sublateral walls longer than dorsal. Relatively small elliptical aperture of amphid located at gymnostom level. According to Fürst von Lieven and Sudhaus (2000), inner wall of gymnostom bearing two dorsolateral denticles, although these could not be explicitly distinguished in this study. Antermost part of stegostom bearing a large, claw-like dorsal tooth, a right ventro-sublateral pyramidal hooked tooth and a left ventro-sublateral denticulate ridge. Claw-like dorsal tooth with tip pointing dorsally and with prominent duct of dorsal gland. Posterior part of stegostom (= meta- and telostegostom) forming a broad cylindrical tube (on average 4 µm diam. and 12 µm long). Stegostom cylinder on average three times longer than broad. Tooth-like swelling at base of stegostom. Neck region comprising ca 11-17% of body. Pharynx divided into muscular procorpus slightly expanding posteriorly into oval muscular metacarpus with valves and a short, non-muscular, glandular isthmus with non-muscular elongated oval basal bulb without valves. Corpus, isthmus and basal bulb in ratio 3 : 1 : 1. Nerve ring encircling isthmus in anterior half. Secretory-excretory pore more posterior (7-13 µm posterior to nerve ring) at transition of isthmus to basal bulb. Reproductive system amphidelphic with both branches equally developed, anterior branch on right, posterior branch on left side of intestine. Ovary long with oocytes arranged in one to two indistinct rows in germinal zone. Uterine sac ca 20 µm long, connecting both uteri. Vulval opening anterior to mid-body, barely visible as a small circular pore. Vulva lips weakly cuticularised, not protruding. Vagina muscular, with narrow lumen. Pair of dumb-bell-shaped pouches present at level of uterine sac. Phasmids prominent, located laterally posterior to anus. Tail long, filiform.

#### Male

General morphology similar to female but body slightly smaller, typically J-shaped after fixation. Anterior part with four additional cephalic setae situated on edge of lip region and elliptical amphidial aperture at gymnostom level. Denticulate ridge of different shape to that of female, but precise structure not unequivocal as seen by LM. Testis single, anteriorly ventrally reflexed. Spicules separate slightly arcuate. Gubernaculum with small distal sleeve and inconspicuously formed proximal apophysis. Nine pairs of genital papillae present: three pairs precloacal, six pairs postcloacal. Genital papillae formula: v1, v2, v3d/v4, ad, ph, (v5, v6(3), v7), pd. Papillae with subventral origin marked as 'v1 to v7', numbered from anterior to posterior. Papilla marked as 'v3d' originating laterally next to spicules, 'v6(3)' consisting of three very small papillae

grouped close together. Papillae marked as 'ad' (anterior dorsal papilla) and 'pd' (posterior dorsal papilla) originating subdorsally, ad located close to prominent phasmids (ph) and pd situated laterally at attenuating point of tail. Tail mostly shorter than female, filiform.

### 3.9.3. Type habitat and locality

Compost heap at the Institute for Agricultural and Fisheries Research in Merelbeke, Belgium (Plant Science Unit, Growth and Development research area); 50°59'16.62" N, 3°46'30.66" E; altitude: 18.6 m. During the composting process *M. composticola* n. sp. was present from day 10 until at least day 163. The heap was composed of three different feedstock materials: 43% (vol/vol) fine wood chips, 43% (vol/vol) dry hay and 14% (vol/vol) fresh grass.

### 3.9.4. Type material

Holotype female, four female paratypes and two male paratypes at the Museum voor Dierkunde (collection number UGMD 104180), Ghent University, Ghent, Belgium. Two female paratypes and two male paratypes at the Wageningen Nematode Collection (WT 3475), University and Research Centre, Landbouwhogeschool, Wageningen, The Netherlands.

### 3.9.5. Diagnosis and relationships

The most important traits to discriminate species within the genus *Mononchoides* are: (i) the shape and number of teeth or tooth-like structures in the stegostom, (ii) the length of the filiform tail, (iii) the position of the vulva, (iv) the length and shape of the spicules and gubernaculum and (v) the genital papillae formula. *Mononchoides composticola* n. sp. is characterised by a combination of the following morphological features: a denticulate ridge in addition to the dorsal claw-like tooth, a small tooth-like swelling at the stegostom base, ca 26 longitudinal ridges on the female body, a uterine sac associated with two dumb-bell-shaped pouches, spicules that are relatively small (30-38 µm), a simple gubernaculum less than half the spicule length long, the genital subventral papillae (v6) consisting of three very small papillae and an especially long filiform tail (female: 391-550 µm, 18-26 anal body diam.; male: 304-548 µm, 19-30 anal body diam.).

*Mononchoides composticola* n. sp. is most similar to the *Mononchoides* sp. described by Mahmood et al. (2007) but differs by having a longer tail (female: 391-550 vs 330-475 µm; male: 304-548 vs 204-369 µm), a longer female basal bulb (19-32 vs 16-20 µm), a shorter neck in the male (97-113 vs 118-143 µm), shorter and smaller spicules and gubernaculum (respectively 30-38 vs 37-43 µm and 10-14 vs 14-22 µm), the position of the female phasmids (1.4-1.9 vs 0.8-1.3 anal body diam. posterior to anus) and the 6th subventral genital papilla comprising three very small subpapillae vs a single papilla.

*Mononchoides composticola* n. sp. is also similar to the following species in having similar morphology and measurements: *M. andrassyi* (Timm, 1961) Gagarin, 1998; *M. flagellicaudatus*

Andrássy, 1962; *M. longicaudatus* Khera, 1965; *M. ruffoi* Zullini, 1981 and *M. parastriatus* Paesler, 1946. It differs from *M. andrassyi* by having a denticulate ridge in addition to the dorsal claw-like tooth and the smaller subventral tooth, a shorter female body length (810-1150 vs 1008-1420  $\mu\text{m}$ ), shorter spicules and gubernaculum (30-38 vs 36-42  $\mu\text{m}$  and 10-14 vs 17-19  $\mu\text{m}$ , respectively), a longer male tail (18-30 vs 12-16 anal body diam.) and by the different shape of the spicules (not cephalated) and shape of the gubernaculum; from *M. flagellicaudatus* by having a denticulate ridge, a larger stoma in the female (14-27 vs 13-14  $\mu\text{m}$ ), a shorter rectum (0.8-1.5 vs 1.8 anal body diam.), a shorter vulva-anus distance (less than two-thirds of tail length), a shorter gubernaculum (10-14 vs 15-16  $\mu\text{m}$ ), a higher tail/anal body diam. ratio in the male (19-30 vs 13-16) and by the lack of the hooked proximal end of the gubernaculum; from *M. longicaudatus* by having a shorter female body (810-1150 vs 1100-1400  $\mu\text{m}$ ), a shorter female isthmus (13-28 vs 48  $\mu\text{m}$ ), a shorter male procorpus (34-45 vs 62  $\mu\text{m}$ ), longer spicules (30-38 vs 23-25) without cephalated heads and most obviously by the shape of the dorsal tooth which is not tripartite; from *M. ruffoi* by the lack of an additional serrate cuticularised ring lining the base of the cheilostom and by having a shorter gubernaculum (10-14 vs 14-18  $\mu\text{m}$ ), more genital papillae (9 vs 7 pairs) and a longer male tail (304-548 vs 270-310  $\mu\text{m}$ ); and from *M. parastriatus* by having shorter and less heavily cuticularised cheilorhabdions, a lower c and b ratio in the male (1.9-2.8 vs 2-4 and 4.9-6.7 vs 6-8, respectively) and the lack of a pointed distal end to the gubernaculum. *Mononchoides composticola* n. sp. is relatively similar to *M. andersoni* Ebsary, 1986 but differs by having a longer metacarpus (101-115 vs 17-34  $\mu\text{m}$ ), a shorter stegostom cylinder (10-12 vs 18-25  $\mu\text{m}$ ), two subventral teeth at the stegostom base and by the presence of males. It also resembles *M. paramonovi* Gagarin, 1998; *M. pulcher* Zullini, 1981 and *M. vulgaris* Gagarin, 2000 morphometrically but lacks the small onchium at the base of the stegostom cylinder. *Mononchoides composticola* n. sp. has a sister relation to *M. striatus* (Bütschli, 1876) Goodey, 1963 based on the limited molecular data but differs by having a lower c ratio in females (1.9-2.8 vs 5.2-6.5), shorter spicules and gubernaculum (30-38 vs 40-48  $\mu\text{m}$  and 10-14 vs 24-26  $\mu\text{m}$ , respectively) and the 6th subventral genital papilla comprising three very small subpapillae vs a single papilla.

#### 3.9.6. Phylogenetic analyses

The phylogenetic analysis (Figure 3.5) places the two compost isolates of *Mononchoides composticola* n. sp. together with maximal support, sister to *Mononchoides striatus*. The monophyletic *Mononchoides* clade has a maximally supported sister relation with *Tylopharynx foetida* (Bütschli, 1874) Goodey, 1928. The two isolates of *M. composticola* n. sp. only differ in two nucleotides (0.1%) from each other, while they differ in 15 nucleotides (0.9%) from the *M. striatus* sequence obtained from GenBank. The *M. composticola* n. sp. clade and *M. striatus*

(however, only represented by one sequence) were both supported by five autapomorphies (Figure 3.5).

### 3.9.7. Feeding experiments

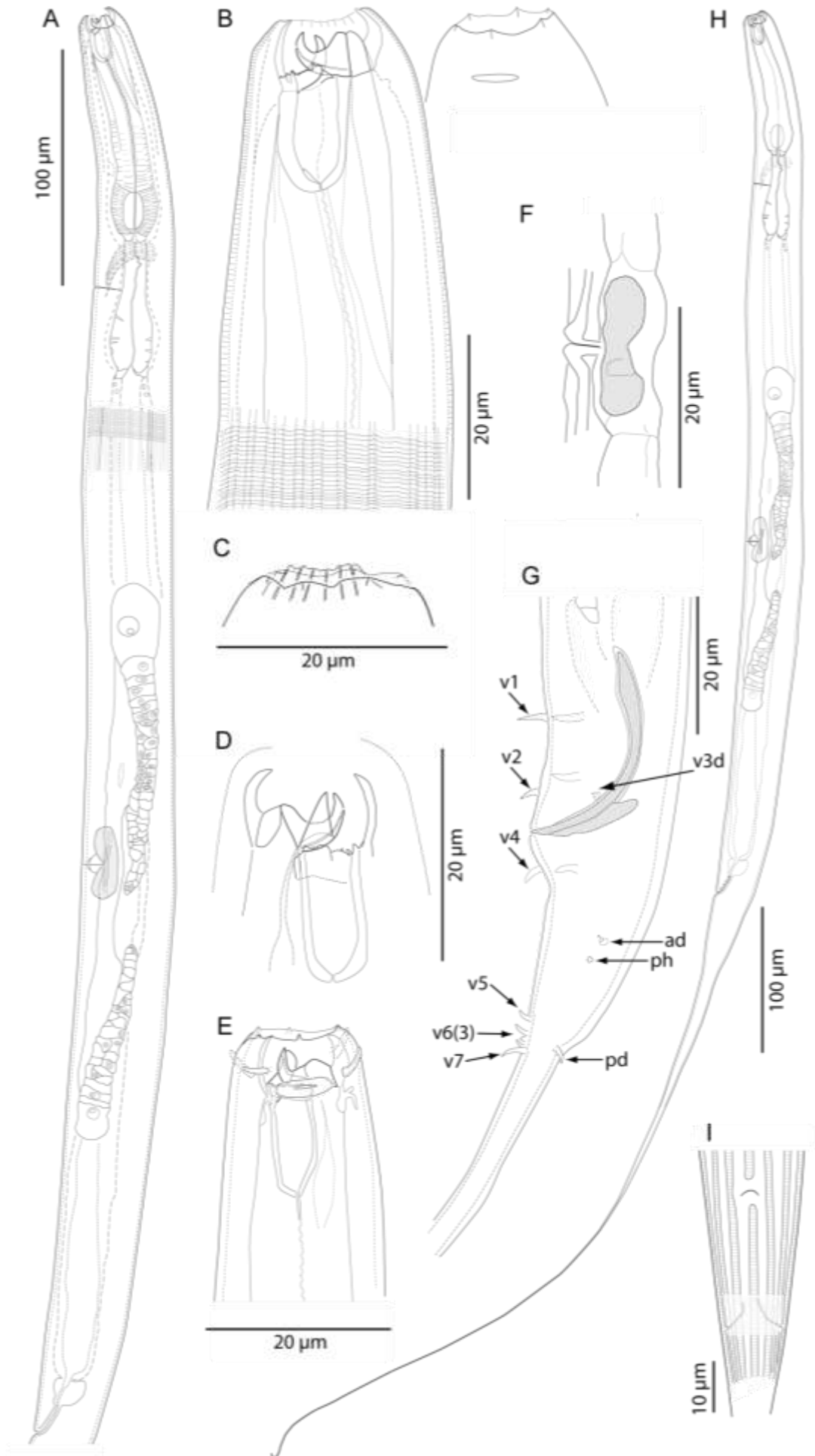
The ratio of *M. composticola* n. sp. reaching the bacterial and control spots after 24 h differed significantly from 1 : 1 at 15, 20 and 30 °C ( $P < 0.05$ ), proving the attractiveness of this bacterial strain to the nematode. The positive response to bacteria, when taking into account all nematodes in the plate (Attraction Index), was most pronounced at 20 °C and the response showed a significant difference between the temperature treatments of 15 and 30 °C ( $P = 0.02$ ). On average  $3.86 \pm 1.35$ ,  $4.8 \pm 1.81$  and  $6.25 \pm 2.3$  out of ten *M. composticola* n. sp. moved into the bacterial spot after 24 h at 15 °C, 20 °C and 30 °C, respectively, compared to an average  $2.71 \pm 2.30$ ,  $0.4 \pm 0.84$  and  $2.17 \pm 1.9$  *M. composticola* n. sp. in the control spot.

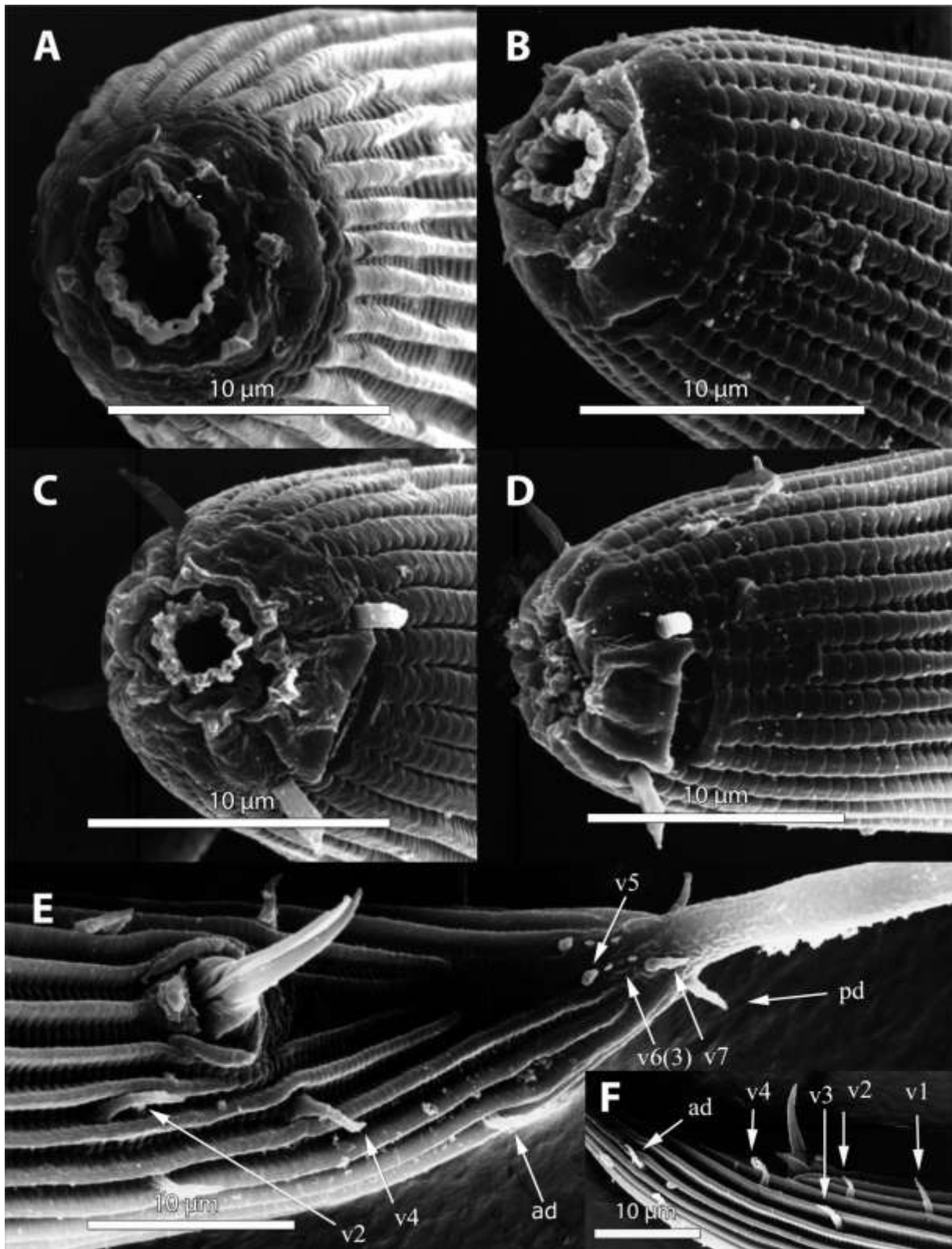
Figure 3.6 shows the change in prey numbers over a 2-day period in the presence (predator treatment) and absence (control treatment) of predators. On average, 50 and 80% of prey specimens (i.e., *R. (Poikilolaimus)* sp. and *Rhabditella* sp., respectively) were caught in the first 24 h and on average 70 and 92% prey (i.e., *R. (Poikilolaimus)* sp. and *Rhabditella* sp., respectively) had been removed after the full 48 h incubation, compared to 18 and 23% of *R. (Poikilolaimus)* sp. and of *Rhabditella* sp., respectively, that disappeared in the controls without predators after 48 h. Control and predator treatments showed significant differences ( $P < 0.005$ ) in prey numbers remaining after 24 and after 48 h with both prey species. Over the first 24 h, each *M. composticola* n. sp. consumed on average  $1.2 \pm 0.3$  *R. (Poikilolaimus)* sp. and  $2 \pm 0.7$  *Rhabditella* sp. During the next 24 h, *M. composticola* consumed on average  $0.9 \pm 0.5$  *R. (Poikilolaimus)* sp. and  $1.1 \pm 0.3$  *Rhabditella* sp. After 24 h, the predation rate of *M. composticola* n. sp. on *Rhabditella* sp. was significantly higher compared to *R. (Poikilolaimus)* sp. ( $P = 0.02$ ).

### Figure 3.2:

*Mononchoides composticola* n. sp. from compost. A: Female (holotype) with neck region and reproductive system (without tail); B: Female head region: stoma *s.l.* and first part of procorpus with transverse striations and longitudinal ridges on cuticle plus superficial view of amphidial aperture; C: Rod-like plates (= cheilorhabdions) in cheilostom; D: Detail of female stegostom (lateral view) with dorsal claw-like tooth with prominent duct of dorsal gland, ventro-sublateral right pyramidal hooked tooth and left ventro-sublateral denticulate ridge; E: Male head region: stoma *s.l.* and cephalic setae and amphidial aperture; F: Detail of vulva and dumb-bell-shaped pouches at level of uterine sac; G: Detail of male posterior end with separate spicules, gubernaculum and nine pairs of genital papillae (v1, v2, v4, v5 and v7: subventral papillae. v3d: lateral papilla. v6(3): 6th subventral papilla consists of three very small papillae grouped close together. ad: anterior dorsal papilla. pd: posterior dorsal papilla. ph: phasmid); H: Habitus female (holotype); I: Female anus and phasmids (ventral view).

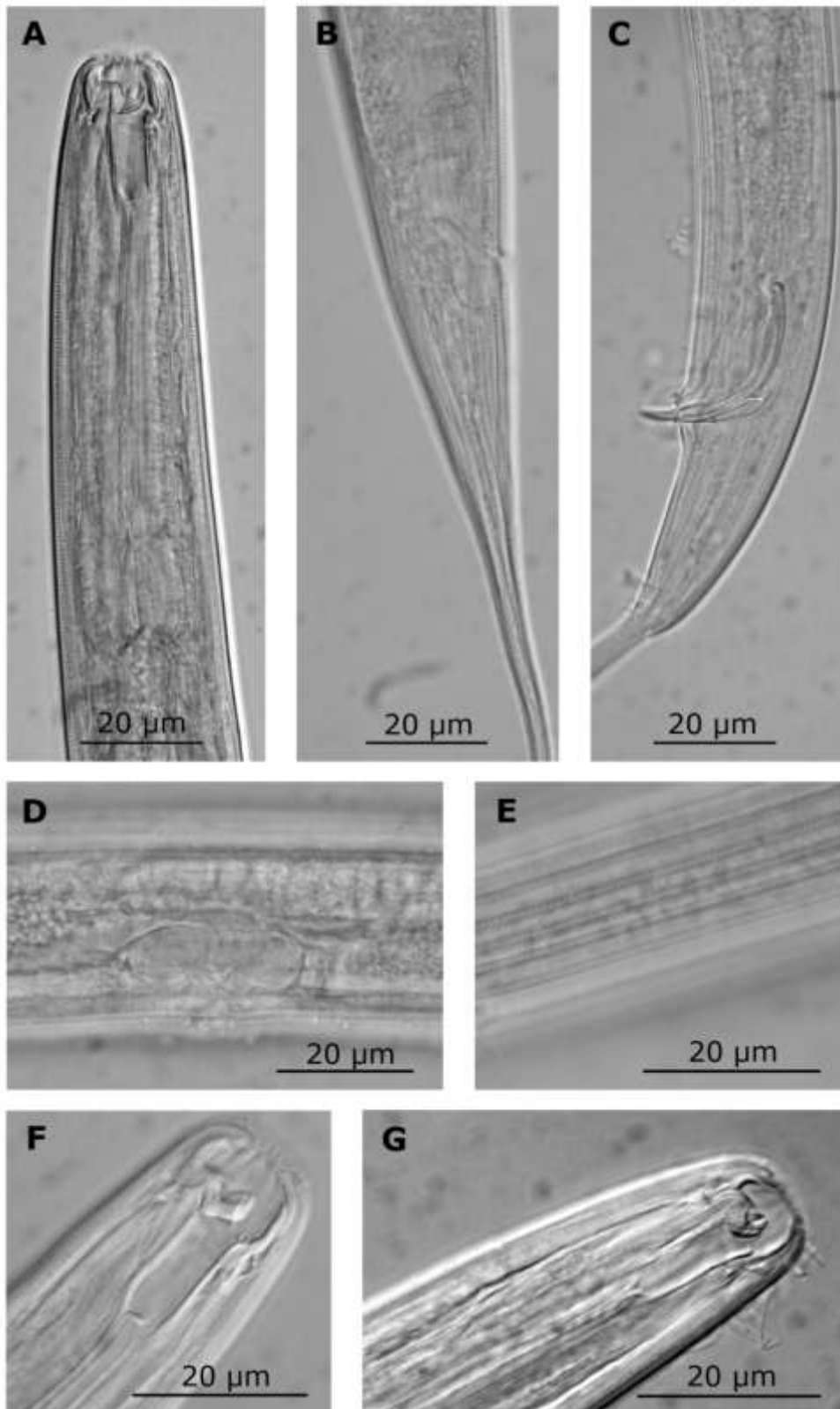






**Figure 3.3:**

SEM photographs of *Mononchoides composticola* n. sp. from compost. A: Female head region showing six fused lips, each with small papilla; B: Elliptical aperture of female amphid; C: Male lip region with four cephalic setae; D: Elliptical aperture of male amphid; E, F: Caudal genital papillae. Abbreviations as in Figure 3.2.



**Figure 3.4:**

LM Photographs of *Monochoides composticola* n. sp. from compost. A: Female buccal cavity and first part of pharynx; B: Posterior end of female with anus; C: Posterior end of male with spicules and gubernaculum; D: Dumb-bell-shaped pouches at level of uterine sac; E: Annulated cuticle with longitudinal ridges; F: Detail of female stoma with denticulate ridge; G: Detail of female stoma with right pyramidal ventro-sublateral tooth and claw-like dorsal tooth with prominent duct of dorsal gland.

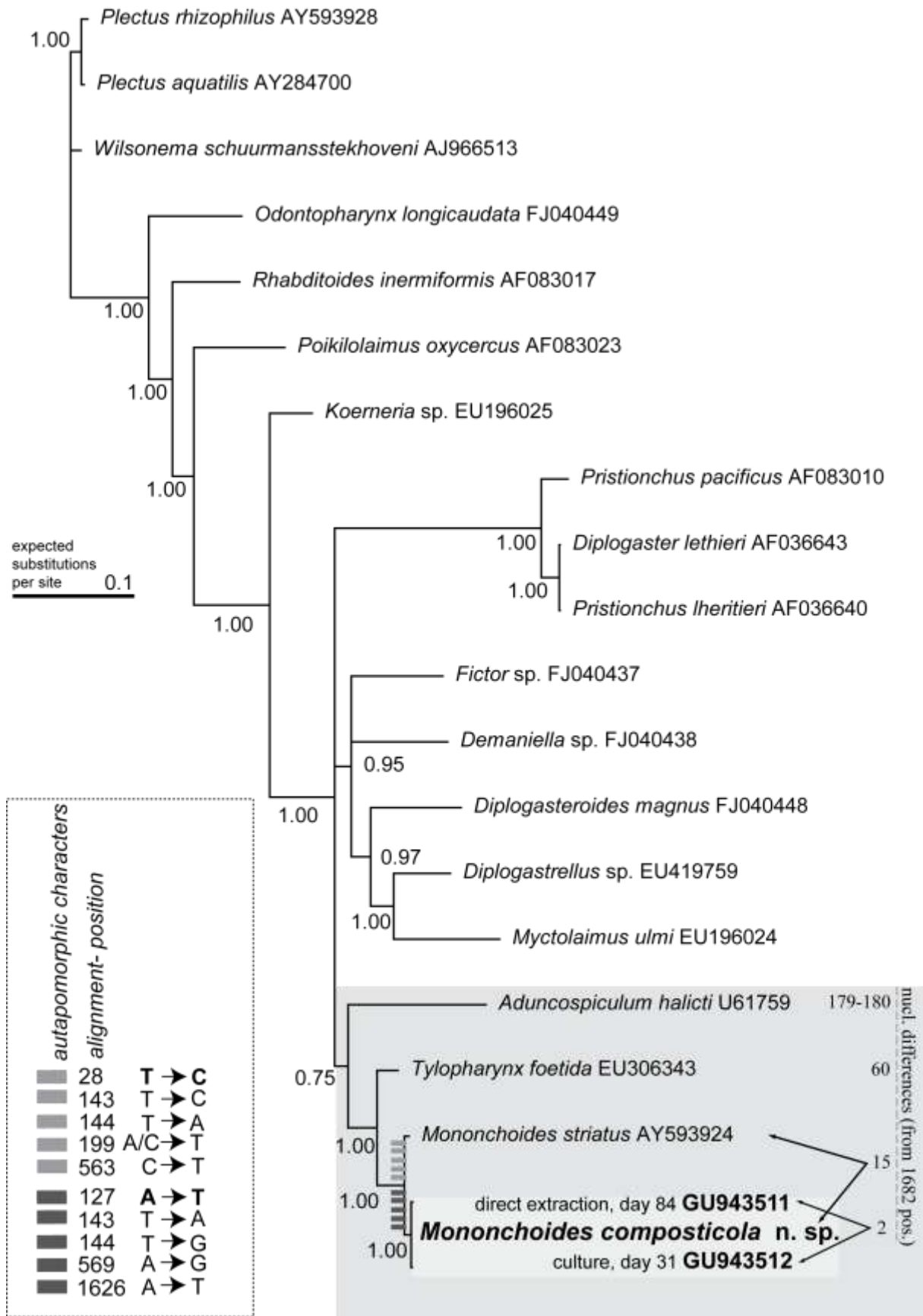
**Table 3.2:**

Morphometrics of *Mononchoides composticola* n. sp. from compost. All measurements are in  $\mu\text{m}$  and in the form: mean  $\pm$  s.d. (range) CV.

Character	Female		Male
	Holotype	Paratypes	Paratypes
<i>n</i>	-	30	16
L	1148	1028 $\pm$ 105 (810-1150) 10.2	830 $\pm$ 88 (761-1029) 10.6
L'	602	555 $\pm$ 100 (377-696) 17.9	441 $\pm$ 55 (382-572) 12.5
a	31.9	29.8 $\pm$ 3.6 (24-36) 12	31.2 $\pm$ 4.6 (26.3-40.4) 14.9
b	7.3	7.9 $\pm$ 0.9 (5.8-9.4) 12.5	5.6 $\pm$ 0.7 (4.9-6.7) 12.7
c	2.1	2.2 $\pm$ 0.3 (1.9-2.8) 11.7	2.2 $\pm$ 0.3 (1.9-2.8) 13.7
c'	25.4	23.5 $\pm$ 2.5 (18.5-26.3) 10.4	21.3 $\pm$ 3.8 (18.7-30.5) 17.8
V	33	33.1 $\pm$ 3.9 (26.7-40.1) 12	-
V'	63	62 $\pm$ 13 (44-86) 20.5	-
Max. body diam.	35.9	34.6 $\pm$ 3.6 (30-44) 10.4	25.9 $\pm$ 3.2 (16-30) 12.5
Stoma length	22	20 $\pm$ 2.4 (14.5-27.3) 12	16.8 $\pm$ 2 (13.3-20.9) 12.2
Head diam. (at amphid)	17.4	19 $\pm$ 1.5 (16.2-22.6) 8	15 $\pm$ 1.6 (13-17.4) 10.8
Stoma length/head diam.	1.3	1 $\pm$ 0.1 (0.8-1.3) 9.7	1.1 $\pm$ 0.1 (0.9-1.3) 8.8
Amphid width	5.8	6.1 $\pm$ 0.9 (5.2-7.5) 14.4	5.3 $\pm$ 1.4 (3-8.7) 25.8
Stegostom length	12.2	11.6 $\pm$ 1.6 (9.3-16.2) 14.3	10.3 $\pm$ 1.3 (8.7-13.9) 13
Stegostom width	5.2	4.0 $\pm$ 0.7 (2.9-5.8) 20	3.3 $\pm$ 0.6 (3-4.6) 16.8
Cheilostom width	8.7	7.5 $\pm$ 1.4 (6-11) 18.2	5.8 $\pm$ 1 (5-7) 17.2
Neck length	154	134 $\pm$ 9 (117-157) 6.7	116 $\pm$ 8.4 (94-128) 7.3
Corpus length	100	90 $\pm$ 6 (79-103) 6.2	73 $\pm$ 6.8 (52-84) 9.4
Procorpus length	75	67 $\pm$ 6 (55-80) 8.4	41 $\pm$ 3 (34-45) 7.5
Metacorpus length	25	23 $\pm$ 4 (17-34) 17.6	16 $\pm$ 3 (14-21) 16.8
Isthmus length	27	20 $\pm$ 3 (13-28) 15.7	25 $\pm$ 5 (14-32) 17.5
Bulb length	27	24 $\pm$ 4 (19-32) 16.3	17 $\pm$ 3 (13-23) 16.2
Corpus/isthmus+bulb	1.8	2.2 $\pm$ 0.2 (1.7-2.7) 10.4	1.7 $\pm$ 0.3 (1.2-2.3) 14.5
Secretory -excretory pore position (EP)	122	109 $\pm$ 12* (89-121) 11	94 $\pm$ 6 (85-103) 6.2
Nerve ring position (NR)	107	98 $\pm$ 11* (83-113) 11.5	77 $\pm$ 6 (60-86) 8.3

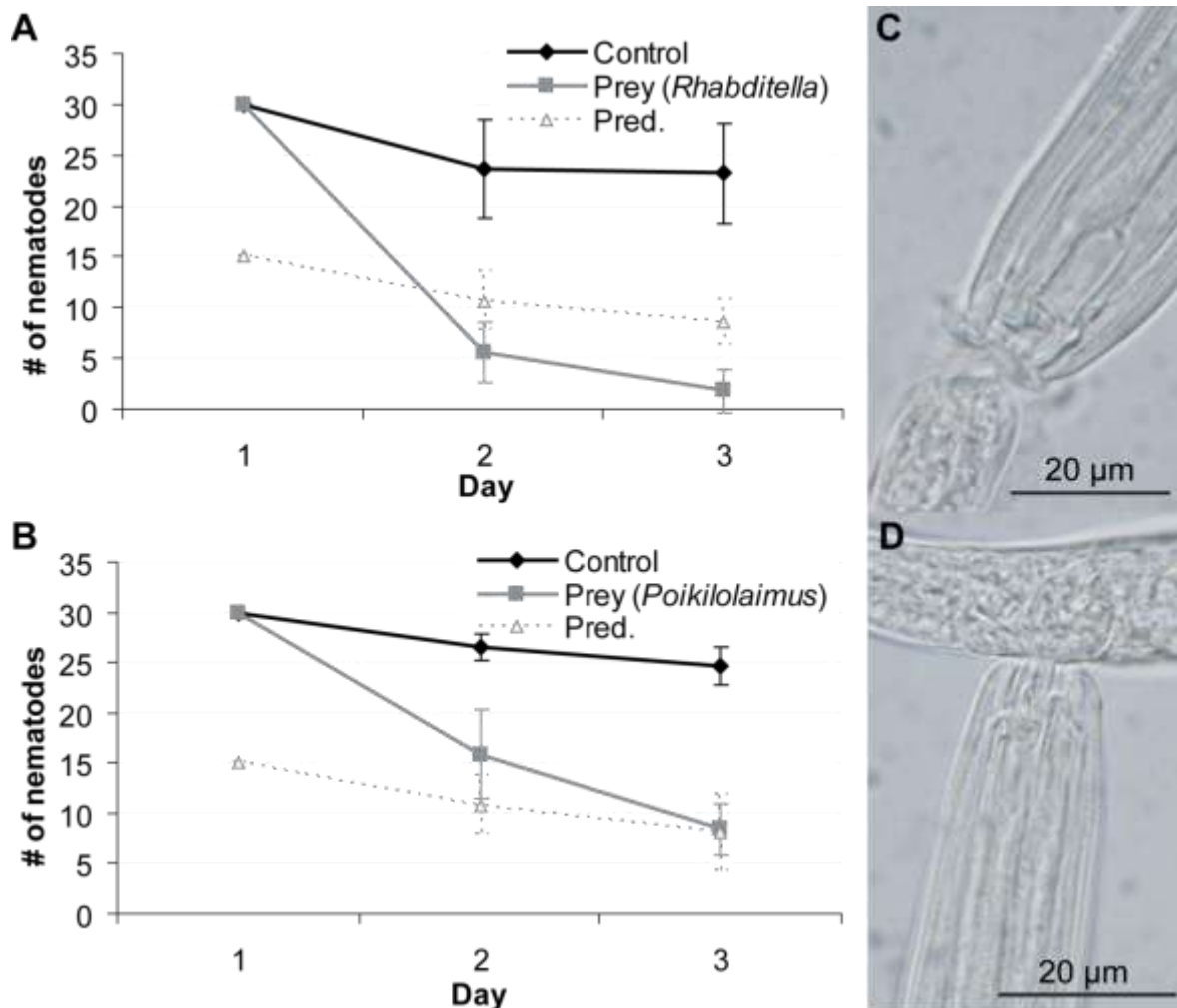
**Table 3.2** (Continued)

Character	Female		Male
	Holotype	Paratypes	Paratypes
EP (as % Neck length)	77	77 ± 4* (71-81) 5.7	64 ± 4 (60-73) 6
NR (as % Neck length)	68	69 ± 2* (66-72) 3.2	52 ± 3 (48-61) 5.8
Tail length	545	473 ± 40 (391-550) 8.5	389 ± 71 (304-548) 18.3
Anal body diam. (ABD)	21.5	20.3 ± 2.2 (17.4-24.9) 10.8	17.3 ± 1.5 (13.9-19.7) 9
Tail/ABD	25.4	23.7 ± 2.4 (18.5-26.4) 10.1	22.5 ± 4.4 (18.7-30.5) 19.3
Anus to phasmid distance	32.5	26.6 ± 5.6* (20-33) 21.2	20.7 ± 3 (17-26) 14.4
Anus to phasmid/ABD diam.	1.5	1.5 ± 0.2* (1.4-1.9) 11.4	1.2 ± 0.2 (0.9-1.5) 17.4
Rectum length	23	22 ± 3 (16-28) 13.2	-
Rectum/ABD	1.1	1.1 ± 0.2 (0.8-1.5) 15.7	-
Tail/Rectum	23.5	20.9 ± 7.6 (17.3-30.2) 17.3	-
Branch length	249	205 ± 46 (132-316) 22.3	-
Posterior gonad	126	103 ± 28 (60-178) 26.9	-
Anterior gonad	123	102 ± 22 (66-145) 21.2	-
Vulva position	382	333 ± 32 (288-392) 9.5	-
Vulva body diam.	37.1	33 ± 4 (25-39) 10.8	-
Vulva to anus distance	262	227 ± 30 (168-307) 13.3	-
Seta length	-	-	4.1 ± 0.7 (2.9-5.8) 18.3
Testis length	-	-	222 ± 30 (175-274) 13.6
Spicule length	-	-	34 ± 1.9 (30-38) 5.6
Spicule/ABD	-	-	2 ± 0.2 (1.6-2.4) 10.2
Gubernaculum length	-	-	12 ± 1 (10.4-13.9) 8.2
Gubernaculum/spicule	-	-	0.4 ± 0.02 (0.3-0.4) 6.4



**Figure 3.5:**

Bayesian inference 50% majority rule consensus phylogeny of *Mononchoides composticola* n. sp. and other Diplogastromorpha sequences from GenBank based on SSU rDNA data. *Plectus rhizophilus*, *Plectus aquatilis* and *Wilsonema schuurmansstekhoveni* were designated as outgroup. Branch support values are indicated with Posterior Probability.

**Figure 3.6:**

Changes in prey and predator numbers over a 2-day incubation with two different prey species. Values are means  $\pm$  s.d. of ten replicates per treatment. A: Prey = *Rhabditella* sp.; B: Prey = *Rhabditis (Poikilolaimus)* sp.; C, D: LM pictures of *Mononchoides composticola* n. sp. feeding on other compost nematodes.

### 3.10. Discussion

#### 3.10.1. Phylogenetic position of *Mononchoides composticola* n. sp. and species characterisation

Our phylogenetic analysis indicates a sister relationship between *Mononchoides* and *Tylopharynx*, confirming the morphologically-based hypothesis that both genera are closely related (Figure 3.5). According to Fürst von Lieven and Sudhaus (2000), the right ventro-sublateral tooth was acquired in the ancestral line leading to both genera, whereas the stegostom cylinder and the firmly attached lateral tooth are an apomorphy for *Mononchoides* and *Tylopharynx*. The genus *Tylopharynx* figured prominently in the long lasting controversy over the origins and relationships of Tylenchomorpha (Maggenti 1963, 1983; Siddiqi 1980; Poinar 1983; Andrassy 1984 in Wu et al. 2001), especially because of the apparent similarity of its stoma armature to the tylenchid stylet. Based on the stoma structure of *T. foetida*, De Ley et al. (1993) suggested a different origin of the stoma of *Tylopharynx* and the stylet of *Tylenchida*. The common origin of *Tylopharynx* and *Mononchoides* stoma structures is now well supported, both by morphological and molecular data. The genus *Koerneria* Meyl, 1961 also has a stegostom cylinder, but according to Fürst von Lieven and Sudhaus (2000) it is unclear whether it is homologous with the stegostom cylinder of *Mononchoides* and *Tylopharynx*. Our results indicate that the two structures have evolved independently from each other since *Koerneria* is well separated from *Mononchoides* and *Tylopharynx* in our phylogenetic analysis (Figure 3.5).

Within *Mononchoides*, five autapomorphies for *M. composticola* n. sp. as well as *M. striatus* provide evidence of lineage exclusivity for both species. Thus, the species status of *M. composticola* n. sp. is consistent with an amalgamation of evolutionary and phylogenetic species concepts according to Adams (1998). A set of discovery operations to minimize the risk of making systematic errors (Adams 1998; Nadler 2002) make this approach both theoretically sound and practically feasible, especially in nematode taxonomy. However, we have to bear in mind that there are currently too few *Mononchoides* sequences available to depict a complete phylogenetic framework for the genus.

*Mononchoides* is an excellent example of a genus where molecular data are welcome to complete the current morphology-based species descriptions. The morphometric variation in this genus is striking and is clearly influenced by the environment and habitat (e.g., Gagarin 1998), and in our analyses it turned out that most measurements and ratios have remarkably high coefficients of variation (CV) (mostly between 10 and 20). Evidently, morphometric data alone are insufficient to argue lineage exclusivity in *Mononchoides*. Besides the inherent problem with intraspecific variability, the genus suffers from inadequate descriptions of some species and suggested synonymisations by several authors. Therefore, it is possible that several of the valid names according to Sudhaus and Fürst von Lieven (2003) are actually synonyms of other taxa: for an update of this list with morphometric data, see <http://www.nematology.ugent.be/vce.html>. Description based on detailed morphological observations (LM as well as SEM), morphometric data from multiple



specimens, molecular data and easily accessible digital vouchers would render many dubious species identities more solid.

### 3.10.2. Feeding behaviour of *M. composticola* n. sp.

Under natural conditions, many diplogastrids are known to feed on bacteria in addition to preying on nematodes (Pillai and Taylor 1968; Yeates 1969; Bilgrami and Jairajpuri 1989; Yeates et al. 1993; Fürst von Lieven and Sudhaus 2000). Our results are in agreement with this, since *M. composticola* n. sp. detected and migrated to bacterial colonies and preyed upon bacterial-feeding nematodes. Several *Mononchoides* species have been reported as predators on other nematodes: *M. potohikus* (Yeates, 1969), *M. longicaudatus* (Bilgrami and Jairajpuri, 1988), *M. fortidens* (Bilgrami and Jairajpuri, 1988), *M. gaugleri* (Bilgrami et al., 2005), *M. bollingeri* (Goodrich et al., 1968) and *M. changi* (Goodrich et al., 1968). As demonstrated in Figure 3.6C and D, and as described by Bilgrami and Jairajpuri (1989) and Fürst von Lieven and Sudhaus (2000), *Mononchoides* species pierce the cuticle of their prey by using their movable dorsal tooth, in addition to pharyngeal suction. They subsequently feed by ingesting some of the body contents of their prey. Our observations suggest that *Mononchoides* species do not always act as an ingester (as described by Yeates et al. 1993) but can also act as a piercer, as described in Bilgrami and Jairajpuri (1989) and Fürst von Lieven and Sudhaus (2000). *Mononchoides* sp. has also been reported feeding on large fungal spores (Fürst von Lieven and Sudhaus 2000), ciliates (Fürst von Lieven and Sudhaus 2000), oligochaetes (Small 1987), tardigrades (Small 1987), insect larvae (Small 1987) and amoebae (Small 1987). Both our experiments illustrate the dual feeding behaviour of adult *M. composticola* n. sp., which can apparently alternate between bacterial and nematode prey. The dual feeding behaviour hampers an unequivocal assignment of *M. composticola* n. sp. to a particular feeding type. Yeates et al. (1993) list the genus as bacterial-feeder (type 3) and predator (type 5a). In foodweb terminology, an organism feeding at more than one trophic level is an omnivore (Moens et al. 2004), yet the term omnivore also represents a feeding type (type 8) in the classification of Yeates et al. (1993), where it is not clearly defined. Its use appears to be restricted to certain dorylaimid nematodes. However, assigning a nematode to more than one feeding type (i.e., types 3 and 5a) hinders its inclusion in nematode-based environmental indices such as the enrichment and structure index or the index of trophic diversity.

Difficulties in maintaining *M. composticola* n. sp. in laboratory culture indicate that their high abundance during the composting process (Chapter 2) is intimately linked to aspects of their natural microhabitat in compost, involving a diversity of bacteria and nematodes and a particular temperature regime with temperatures up to 30 °C or more for several days. The better we mimicked such a compost environment, the higher the reproduction of *M. composticola* n. sp. (data not shown). Nevertheless, the results of the taxis experiments at different temperatures illustrate that the foraging efficiency of *M. composticola* n. sp. is maintained at temperatures down to 20 °C.

At still lower temperature (15 °C), food (bacteria) finding was significantly reduced. When food (bacteria and prey nematodes) availability was low, *M. composticola* n. sp. often exhibited cannibalism or died while searching for food, as already observed by Pillai and Taylor (1968).

The number of nematode prey decreased significantly after 24 and 48 h for both *R. (Poikilolaimus)* and *Rhabditella*. The per capita predation rates of *M. composticola* n. sp. on *R. (Poikilolaimus)* and *Rhabditella* after 24 h were  $1.2 \pm 0.3$  and  $2 \pm 0.7$ , respectively. These rates are low compared to previous studies. Yeates (1969) reported a per capita predation rate of approximately 20 prey per 24 h for *M. colobocercus* (Andrássy, 1964) Sudhaus & Fürst von Lieven, 2003 feeding on *Bursilla littoralis* (Yeates, 1969) Andrásy, 1983, *Panagrolaimus australis* Yeates, 1969 and *Acrobelloides syrtisus* Yeates, 1967. *Mononchoides longicaudatus* and *M. fortidens* both consumed on average approximately 10 *Rhabditis* sp. in 24 h (Bilgrami et al. 2005). Predation rates can be influenced by prey density and by interference between different predators in the same habitat (Hamels et al. 2001). Yeates (1969), Bilgrami and Jairajpuri (1989) and Bilgrami et al. (2005) demonstrated that *Mononchoides* species show prey density-dependent predation rates.

Predation rates on *Rhabditella* sp. were significantly higher (at least during the first 24 h) than on *R. (Poikilolaimus)* sp. This may be related to prey size (on average 650 µm and 800 µm long, respectively) and/or motility. More motile prey have a higher encounter probability with predators (Moens et al., 2000), but may also have a better chance of escape upon a predator-prey encounter (Bilgrami and Jairajpuri 1989). In our experiment, *Rhabditella* sp. were considerably smaller and less motile than *R. (Poikilolaimus)* sp., the latter in fact exceeding *M. composticola* n. sp. in size, suggesting that it was less vulnerable to attack by *M. composticola* n. sp. Prey preference was also reported for *M. longicaudatus*, *M. fortidens* (Bilgrami and Jairajpuri 1988) and *M. gaugleri* (Bilgrami et al. 2005) and has been attributed to a variety of factors such as prey density, prey secretions, predator ability to wound prey, prey ability to avoid predation, and temperature.

The high abundance of *M. composticola* n. sp. during the composting process, its capacity to prey on other nematodes and its high foraging activity at temperatures below those typical of the compost microenvironment all suggest that the abundance of *M. composticola* n. sp. in maturing compost may be an important factor in determining the biocontrol potential of compost when applied to soils. The microclimate and abundant food sources in compost apparently render compost an ideal 'carrier medium' of *M. composticola* n. sp.

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## 4. The nematode community as a proxy of the microbial community in a rapidly changing compost environment

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Modified from:

Steel H, Buchan D, De Neve S, Couvreur M, Moens T and Bert W. Nematode and microbial communities in a rapidly changing compost environment: how nematode assemblages reflect composting phases. Submitted to European Journal of Soil Biology.

## 4.1 ABSTRACT

The microbial community (fungi and bacteria) is the main decomposer of organic matter during composting. Its composition is sometimes used as a proxy to assess compost maturity. Although nematodes are probably its most important grazers, only one previous study has highlighted clear shifts in nematode species composition during composting, and the assumption that nematodes reflect changes in the microbial community in compost has not yet been formally tested. Here, the microbial and nematode communities of a single composting process are analyzed together for the first time. Although both displayed broadly similar patterns, the abundance of fungal-feeding nematodes showed a distinct delay as compared to the increase in fungal PLFA. We argue that the nematode community may be a more promising tool to use in assessing compost maturity because it allows to discriminate between the three composting phases. First, during the thermophilic phase, bacterial-feeding nematodes dominate; during cooling, the bacterial feeders/predators bloom; and during maturation, the abundance of fungal feeders increases. Based solely on the microbial community, it was only possible to discriminate between the thermophilic phase and the rest of the process. Bacteria dominated during the thermophilic phase, while bacterial and fungal PLFA had more-or-less equal shares during cooling and maturation.

## 4.2 INTRODUCTION

Aerobic composting is the controlled biological oxidative decomposition of organic (waste) materials by successive communities of microorganisms under various temperature regimes, leading to the production of carbon dioxide (CO<sub>2</sub>), water, minerals, and a humified end product (Butler et al. 2001). In nature, the mineralization of organic material is a slow process that does not produce a recognizable heat peak (Kutzner 2000). Composting mimics this natural process, but it does so under optimized environmental conditions (moisture levels, temperature, substrate composition, and oxygenation), resulting in a much faster process that yields a stable, high-quality end product (Zucconi and de Bertoldi 1987). The benefits of compost addition to the soil's physical and chemical characteristics include increased soil organic matter content (Termorshuizen et al. 2004) and the subsequent improvement of soil aeration, soil porosity, drainage, and water holding capacity (Cogger 2005). Furthermore, composts may have disease-suppressive properties that operate via a combination of physiochemical and biological mechanisms (Bailey and Lazarovits 2003; Oka 2010). Microbial and faunal communities in

compost shift continuously during composting. Eventually, at compost maturity, a more-or-less stable community of organisms becomes established (Ryckeboer et al. 2003; Chapter 2). An important question in compost research is how to identify reliable indicators of compost stability and maturity, which may be used to establish an optimal composting time. Such indicators may be chemical, physical, and/or biological in nature (Butler et al. 2001). Previously, numerous tests, based on both physical and chemical parameters, have been proposed (for a review, see Wichuk and McCartney (2010). However, none of these have been proven to be rigorous, reliable, or consistent enough to be used as a stand-alone maturity and stability measure, or they require such a substantial investment in laboratory equipment and staff training that their routine use is hampered (Wichuk and McCartney 2010).

Microorganisms play key roles in the composting process, and their succession may reflect the status of maturing compost (Herrmann and Shann 1997; Ryckeboer et al. 2003). Phospholipid fatty acid (PLFA) analysis is widely used to quantitatively assess the microbial community composition of soils. One of the advantages of this approach is that it covers a wide range of microbial groups, including both bacteria and fungi, in one analysis (Frostegård et al. 2011). However, it has been suggested that nematodes have advantages over soil microbes in terms of their role as biological indicators (Neher 2001). First, by being at a higher trophic level, their assemblages integrate the physical, chemical, and biological properties related to their food resources. Second, their generation times (days to months) are longer than those of metabolically active microbes (hours to days), rendering their assemblages less responsive to short-term fluctuations, such as those resulting from ephemeral nutrient flushes (Nannipieri et al. 1990).

These nematode-specific advantages prompted us to explore the potential of nematodes in assessing the maturity and quality of compost (Chapter 2 and 7). A shift in species composition was observed during the composting process (Chapter 2). Mature composts appear to harbor a typical assemblage of bacterivorous, fungivorous, and bacterivorous/predatory nematodes. The changing trophic structure, expressed as the relative contributions of bacterivorous versus fungivorous nematodes (f/b ratio), proved to be an especially promising proxy for compost maturity (Chapter 2). However, the underlying assumption that nematodes reflect changes in the microbial community has not yet been tested. So far, this has limited our ability to relate nematode community patterns to microbial patterns. The available evidence that changes in the occurrence and abundance of various trophic groups of nematodes are associated with changes in the food web, is mostly limited to soils or aquatic systems. For example, increasing microbial activity associated with the decomposition of barley roots was rapidly followed by an increase in

the proportion of gravid female bacterial-feeding nematodes and then by an increase in total populations (Griffiths and Caul 1993). Another example of bottom-up effects resulted from experiments showing that poultry, but not farmyard manure, increased the relative abundance of bacterial-feeding species (Griffiths et al. 1994). In contrast, De Mesel et al. (2004) demonstrated the significant top-down effect of bacterial-feeding nematodes on the composition of a bacterial community, even at low grazer densities. This effect of the nematodes on the diversity of the microbial community was, however, only observed under high grazing pressure from *Panagrolaimus paetzoldi*. In the early stages of organic matter decomposition, at C/N ratios  $\geq 30$ , fungal abundance, as derived from PLFAs, was lower in the presence of the fungivorous nematode *Aphelenchoides composticola* than in its absence (Chen et al. 2001).

In terrestrial stand-alone decomposition processes, such as composting, the link between the microbial community and metazoan organisms remains especially poorly understood. The objectives of this study were to: (1) analyze the generality of nematode community succession patterns during the composting process and the clear shifts that occur between the composting phases as described in chapter 2, (2) assess whether the profiles and dynamics of the microbial and nematode communities follow similar patterns and whether shifts in one community can be related to shifts in the other, and (3) compare the potential of the nematode community vs. that of the microbial community as potential indicators of compost maturity.

## **4.3. MATERIALS AND METHODS**

### **4.3.1 Study site and sampling**

The compost was prepared according to the Controlled Microbial Composting (CMC) method ("Leubke compost") (Diver 2004). The composting is carried out in windrows and during the composting process, parameters like CO<sub>2</sub> and temperature are intensively monitored. The compost is aerated by turning the compost heap and can be covered to prevent nutrient leaching and/or reduce gaseous emissions and heat loss. Often, a microbial starter is added to inoculate the compost (Diver 2004), but this was not the case in the examined compost. The examined compost heap was located at the Institute for Agricultural and Fisheries Research in Merelbeke, Belgium. The heap was 15 m long, 3 m wide and 1.5 m high, comprised 3 m<sup>3</sup> feedstock materials per lineal meter and consisted of 43% (% vol/vol) fine poplar bark wood chips, 43% grass seed hay and 14% fresh grass with C/N ratios of 90/1, 30/1 and 15/1, respectively. The composting process examined here actually is a repetition of one that was

incubated exactly one year earlier, and is composed of the same feedstock materials, in the same proportions and at the same composting site (Chapter 2).

On each of 20 consecutive sampling events, covering the entire 6 months of the composting process (September 2008 to March 2009), 3 composite samples were taken. In addition to a time 0 sample, samples were taken twice a week (12 sampling events) during the first six weeks; once a week in the next two weeks (2 sampling events); and once every two weeks for the next 4 weeks (2 sampling events). Subsequently, during the second 3-month period of the process, the heap was sampled once a month (3 sampling events). Hence, samples were taken at days 0, 3, 7, 10, 14, 17, 21, 24, 28, 31, 35, 38, 42, 49, 56, 70, 84, 112, 140 and 162 after the start of the composting process.

Each composite sample consisted of 20, randomly picked and thoroughly mixed compost samples of 50 ml. Of this total volume of 1l, a subsample of 400 ml was taken for nematode extraction. For a mathematical justification of taking a subsample from a bulk sample to estimate nematode population densities, see (Been and Schomaker 2006). The remainders of the composite samples ( $\pm$  600 ml) were freeze-dried (Christ, Gamma 1-20, Osterode am Harz, Germany), ground, and stored at -20 °C for carbon, nitrogen and PLFA analyses.

#### **4.3.2 Abiotic data**

Temperature was monitored every hour during the composting process at a depth of at least 30 cm using 5 data-loggers (Testo 175-T2, Ternat, Belgium). Ambient temperature data were obtained from the Royal Meteorological Institute (RMI) weather station, located within 3 km from the sampling site. At every sampling time, moisture content, pH and C/N ratio were measured using material from the composite samples. 20 g compost was shaken by hand in 100 ml distilled water, 3 times with 2-h intervals, and the pH was measured with standard electrodes (Consort P400, Turnhout, Belgium). Moisture content was calculated by determining the dry weight (DW) of 50 ml compost after drying for 48 h at 102 °C. Total C- and N-content was measured with a Variomax CNS element analyzer on 1 g of freeze-dried (Elementar GmbH, Hanau, Germany) compost applying the Dumas method.

#### **4.3.3 Nematode community**

Nematodes of each sample (400 ml) were extracted using the modified Baermann funnel method (tray 49 x 37.5 cm, basket 38.5 x 19.5 cm) (Hooper 1986), counted, and 100 individuals were randomly picked using a stereomicroscope (Leica Mz95). For light microscopy observations the specimens were collected in a very small drop of water in an embryo dish. Formaldehyde (4% with 1% glycerol) was heated to 70 °C and an excess (4-5 ml) was quickly added to kill and

preserve the nematodes (Seinhorst 1966). The preserved nematodes were processed to anhydrous glycerol following the glycerol-ethanol method (Seinhorst 1959; as modified by De Grisse 1969) and mounted on aluminium slides with double cover slips (Cobb 1917), or on mass slides (slide 40 x 76 mm; cover glass 34 x 60 mm). Nematodes were identified to genus or, if possible, to species level. The abundance of every genus or species in each sample was expressed as individuals/100 gram dry weight (DW) compost using relative abundance and total count. The nematode genera were assigned to the “coloniser-persister” cp-scale according to their r and K life history characteristics (Bongers 1990) and also classified according to their feeding type (Yeates et al. 1993, see also 1.4.4). These allocations were used to calculate the Maturity Index (MI) (Bongers 1990) and the fungivores/bacterivores ratio (F/F+B ratio) (Yeates et al. 1993), respectively. In the F/F+B ratio, only the fungal and bacterial feeders *sensu stricto* were included, i.e. bacterial-feeding/predators such as some diplogasterid nematodes were not included because their feeding habit can be either bacterivorous, predatory (see Chapter 3) or even fungivorous; furthermore their behavior most likely changes during the compost process. Nematode diversity during the process was expressed using the Shannon-Wiener index, which is mainly determined by evenness among taxa and the Margalef index, which measures taxon richness (Magurran 2004).

#### **4.3.4 Microbial community**

Phospholipid fatty acids (PLFAs) of samples of all sampling days except for days 24, 31, 38, 49, 70 and 112 were extracted using a modified Bligh and Dyer (Bligh and Dyer 1959) technique (Moeskops et al. 2010). For the unsaturated fatty acids, the shorthands refer to the number of carbon atoms, the number of double bond(s), and their position as counted from the methyl group end ( $\omega$ ). The suffix c (cis) refers to isomers. The shorthand notation for saturated fatty acids is the same, except for the location of the cyclopropyl (cy) ring and the presence of a methyl group (Me), either on iso (i) or anteiso (a) carbon. Briefly, lipids were extracted from 1.00 g freeze-dried compost with a one-phase mix of phosphate buffer (pH 7.0), chloroform and methanol in a 0.9:1:2 ratio (vol:vol). Lipids were then fractionated into neutral lipids, glyco- and phospholipids using SiOH SPE cartridges (Chromabond, Macherey-Nagel GmbH, Düren, Germany). Neutral lipids and glycolipids were discarded and the phospholipid fraction was subjected to mild alkaline methanolysis to give fatty acid methyl esters (FAMES). These were dried under N<sub>2</sub> atmosphere and re-dissolved in 300  $\mu$ l hexane containing 8 ppm 19:0 nonadecanoic acid methyl ester (Sigma-Aldrich Inc., St. Louis, USA) as an internal standard. Samples were analyzed by capillary gas chromatography–mass spectrometry (Thermo Focus GC coupled to Thermo DSQ MS; Thermo Fischer Scientific Inc., Waltham, USA), using splitless

injection, helium as a carrier gas and a Restek Rt-2560 capillary column (100 m length x 0.25 mm internal diameter, 0.2  $\mu\text{m}$  film thickness; Restek, Bellefonte, USA). FAMES were identified by comparison with the chromatographic retention times of a standard quantitative FAME mixture (Restek Food Industry FAME mix 35077) and a qualitative FAME mixture (Supelco Bacterial Acid Methyl Ester mix 28039U, to which individual standards of  $\alpha 16:0$ ,  $\alpha 17:0$ ,  $16:1\omega 5$ ,  $10Me16:0$  and  $10Me18:0$  were added). FAMES were quantified using serial dilutions of the quantitative FAME mix. For FAMES for which only qualitative standards were available, the calibration curve of the nearest analogous component was used, so that the concentration of all FAMES could be expressed in  $\text{nmol g}^{-1}$  dry soil. Only FAMES which could be accurately identified based on the retention time of known standards were measured and included in further analysis; no major peaks remained unidentified in any of the sample chromatograms. Out of a total of 37 identified FAMES, only those that were present in proportions of more than 1% of the total, were retained for further analysis and summed to give 'total PLFA' ( $n= 24$ ). Taxon-specific markers were as in (Moeskops et al. 2010), except that  $i14:0$  was used as an additional marker for Gram-positive bacteria (Zelles 1999),  $cy19:0$  as an additional marker for Gram-negative bacteria (Zelles 1999) and  $18:1\omega 9c$  as an additional fungal biomarker (Joergensen and Wichern 2008). The concentration of each marker fatty acid was scaled with the organic C present in each sample. The total fungal community was represented by the sum of  $18:1\omega 9c$  and  $18:2\omega 6,9$  while the sum of  $10Me16:0$  and  $10Me18:0$  was regarded as an indicator for Actinomycetes. The total bacterial community was assumed to be represented by the sum of the marker PLFAs for Gram-negative ( $16:1\omega 7c$ ,  $18:1\omega 7c$ ,  $cy17:0$  and  $cy19:0$ ), and Gram-positive ( $i14:0$ ,  $i15:0$ ,  $\alpha 15:0$ ,  $i16:0$ ,  $\alpha 16:0$ ,  $i17:0$  and  $\alpha 17:0$ ), and the PLFAs  $15:0 + 17:0$ . The fungi/bacteria ratios were calculated by dividing the respective sums of marker fatty acids. The PLFA  $16:1\omega 5$  was found in our study in every sample with the highest concentrations during maturation and has been reported as biomarker of arbuscular mycorrhizal fungi (AMF) (Olsson et al. 1995). However, this marker also occurs in Gram-negative bacteria (Zelles 1999), is a poor indicator of AMF if bacterial biomass is high (Frostegård et al. 2011), and AMF were never reported from compost before. Therefore, this PLFA marker was provided for completeness (Table 4.4) but not included in further data analyses.

#### 4.3.5 Statistical analysis

First, a correlation matrix was calculated (Pearson product moment correlation coefficients ( $r$ ) in Statistica 6.0 (Statsoft Inc.)) to unravel possible colinearity among abiotic variables (temperature, pH, moisture, C/N ratio, ambient temperature). Subsequently, changes in the abiotic factors during the composting process were analyzed using Principal Component Analysis

(PCA) in Primer 6 (Clarke and Warwick 2001). Total nematode numbers, and the diversity indices across sampling times were compared using one-way ANOVA and subsequent post hoc Tukey HSD tests in Statistica 6.0. For the MI, F/F+B ratio (nematode data), and the total and functional group (Gram-positive, Gram-negative, Actinomycetes, total bacteria, fungi and AMF) PLFA amounts of the different composting phases, assumptions of normality and homogeneity of variances were not fulfilled. Therefore, these data were analysed using non-parametric Kruskal-Wallis and Mann-Whitney U pairwise tests with Bonferroni corrections ( $\alpha = 0.016$ ), in Statistica 6.0. Nematode community compositions (species abundance data) of the different moments during the composting process were compared using non-metric MultiDimensional Scaling (nMDS) and significant differences between composting phases were evaluated using Analysis of Similarities (ANOSIM) in Primer 6. Composting phases were predefined based mainly on the temperature profile of the composting process (see 4.4.1 and Chapter 2). For both nMDS and ANOSIM, Bray-Curtis similarity matrices on square-root transformed abundance data (individuals/100 g DW compost) were used. The relative PLFA concentrations (mol%) of the fatty acid markers were subjected to a PCA, and significant differences between composting phases were investigated using Analysis of Similarities (ANOSIM) in Primer 6. Finally, correlations of the nematode community with the microbial community and vice versa were analyzed. To provide a measure for statistical significance in terms of the canonical relationships among the two sets of variables, a canonical correlation analysis (CANCORR) was done in SAS 9.3 (SAS Institute Inc., Cary, NC, USA). Only the best explaining variables of each of the two sets of variables (nematode and PLFA data) were used, which were selected using the BEST (BIOENV) procedure in Primer 6.

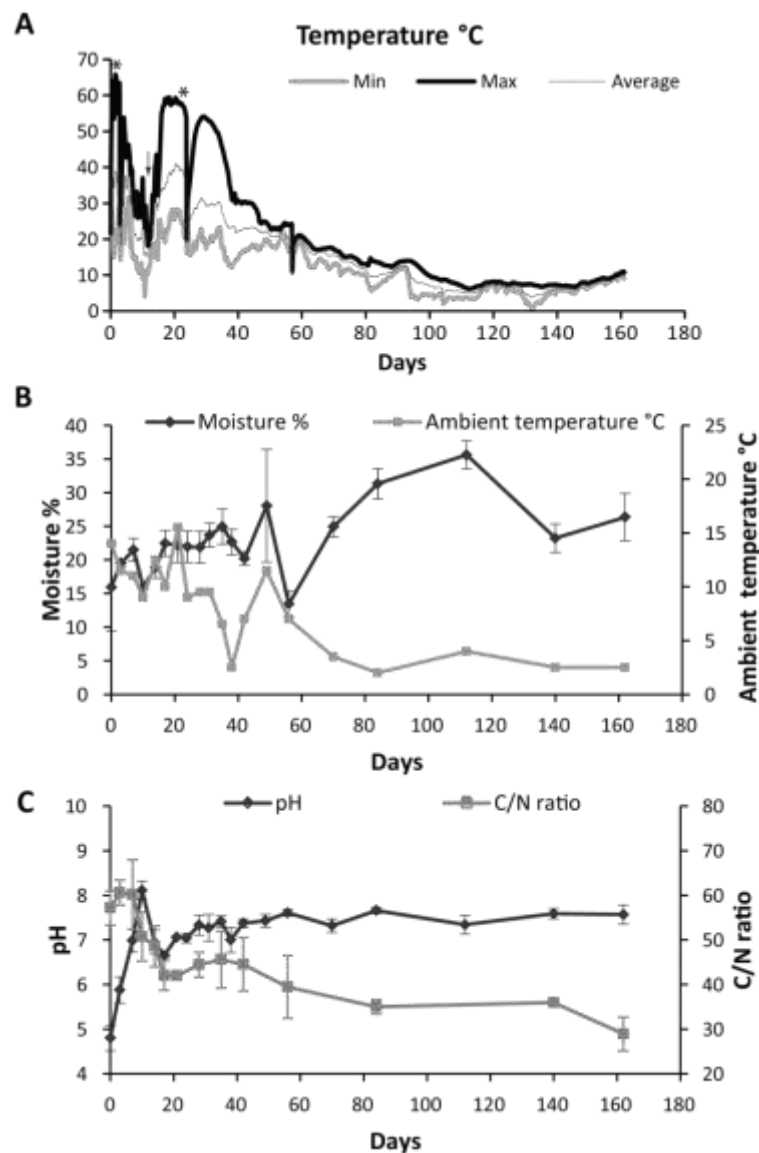
## **4.4. RESULTS**

### **4.4.1 Abiotic variables**

Based on temperature, the composting process is typically divided into three phases: the thermophilic phase from day 1 until day 28, the cooling phase from day 28 until day 84, and the maturation phase from day 84 until day 162. Here, the thermophilic phase showed two distinct heat peaks: The first was from day 3 to day 7 (37 °C on average, with maxima up to 65 °C), and the second was from day 17 to day 23 (38 °C on average, with maxima up to 60 °C). After day 28, the temperature gradually decreased (cooling phase) until it reached 8 to 10 °C (Figure 4.1A), which approximates the ambient temperature (Figure 4.1B). The moisture content fluctuated during the process, with a maximum of  $36 \pm 2.1\%$  on day 112 (Figure 4.1B). The C/N ratio gradually decreased from  $57 \pm 3.8$  on day 0, to  $29 \pm 3.8$  on day 162 (Figure 4.1C). The pH



increased sharply from  $4.8 \pm 0.3$  on day 0, to  $8.1 \pm 0.2$  on day 10. On day 17, it decreased to  $6.7 \pm 0.04$ , and afterwards, it remained more-or-less constant (between  $6.9 \pm 0.3$  and  $7.6 \pm 0.2$ ) (Fig 4.1C). As expected, the C/N ratio significantly correlated with decreasing compost temperature and increasing pH (Table 4.1). The PCA grouped samples according to composting phase (Figure 4.2). The first two axes of the PCA (Figure 4.2, vector loadings of eigenvectors in Table 4.1) explained 73% of the variation in the abiotic variables. The first axis accounts for 51% of the variation and separates the samples of the various composting phases based on C/N ratio and pH. Along the second axis, which explains an additional 22% of the variation, temperature was the most determining variable.



**Figure 4.1**

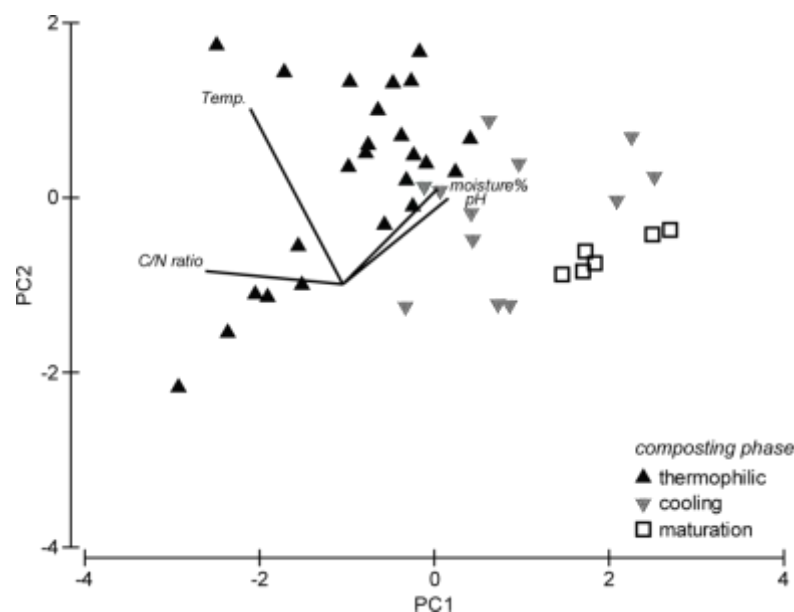
Abiotic variables measured during the composting process including (A) Temperature of the compost (°C). Data of 5 dataloggers, programmed to measure temperature every hour, were averaged (Average) and minimum (Min) and maximum (Max) temperatures are displayed. The asterisks indicate the addition of water followed by turning of the heap on day 3 and 24, while the arrow indicates turning of the heap on day 17. (B) Moisture content (%) and mean ambient temperature per day (24 h)(°C). (C) pH values and C/N ratio. Error bars indicate SD (based on 3 replicates).

**Table 4.1**

Pearson correlation coefficients and product moment correlation coefficients among continuous environmental variables (Temperature, Moisture content, pH, Env. Temperature and C/N ratio) measured during the composting process and vector loadings of the Principal Component Analyses (PCA).

	Temperature	pH	Moisture	C/N	Env. Temp	Vector loadings	
						PCA 1	PCA 2
Temperature	1					-0.42	0.8
pH	-0.26	1				0.48	0.39
Moisture	-0.2	0.28	1			0.43	0.43
C/N	0.71**	-0.53	-0.47	1		-0.63	0.06
Env. Temp	0.78***	-0.61*	-0.53*	0.69**	1	-	-

\* $p \leq 0.05$ ; \*\* $p < 0.01$ ; \*\*\* $p \leq 0.001$

**Figure 4.2**

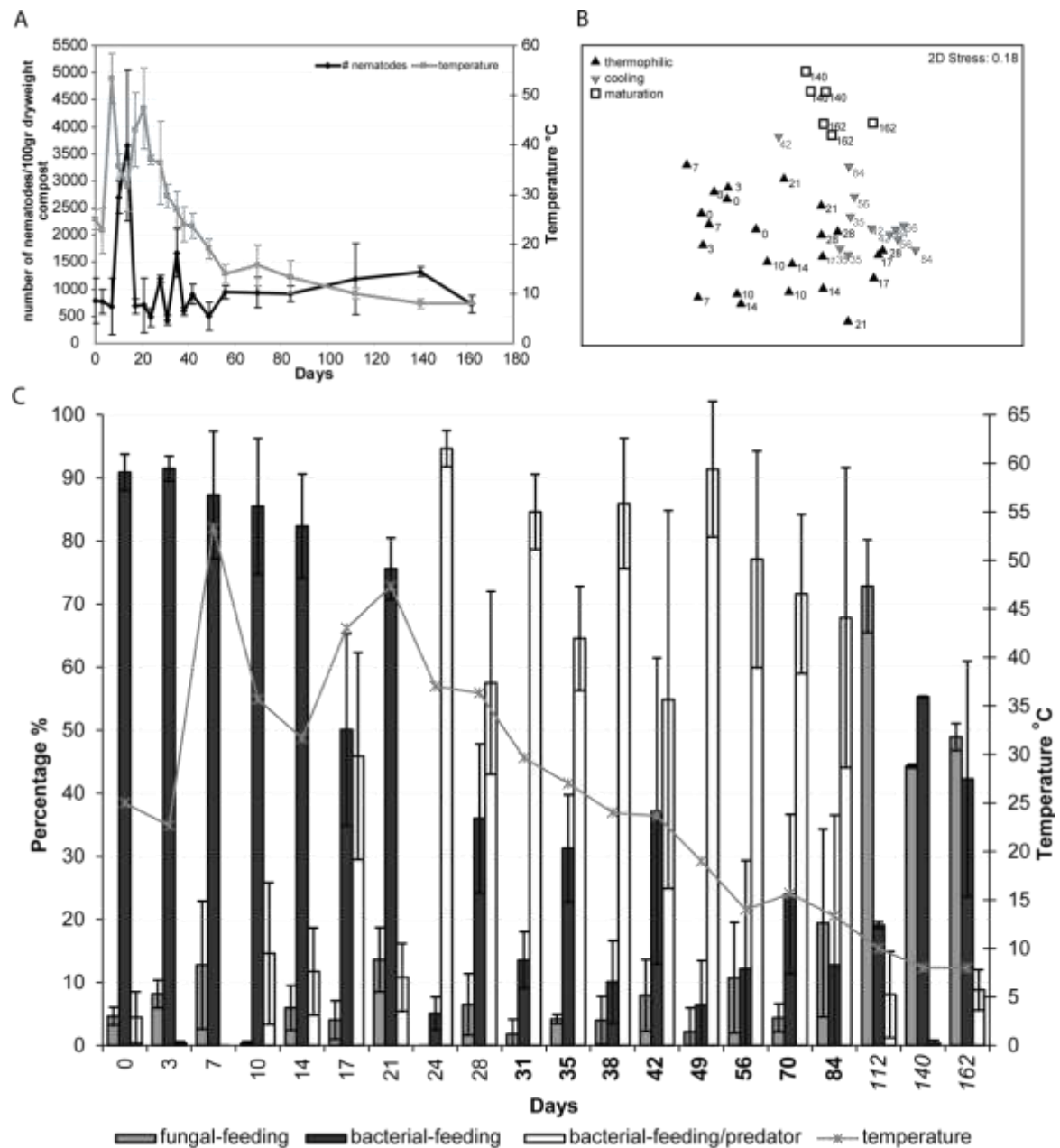
Two-dimensional PCA ordination of the abiotic variables of the composting process. The variables used in the analyses are displayed (i.e. temperature,  $CO_2$ , pH, moisture content (%), C/N ratio). PC1 (y-axis) and PC2 (x-axis) together account for 67% of the total variation.

#### 4.4.2 Nematode population dynamics

All samples contained high densities of nematodes (on average  $1097 \pm 309/100$  g DW compost). During the thermophilic phase, nematode numbers were relatively low during the two heat peaks (on average  $683 \pm 113/100$  g DW compost). In between these peaks, however, nematode numbers spectacularly increased up to  $3657 \pm 1400$  nematodes/100 g DW compost. This was concomitant with a temporary temperature drop to  $32 \pm 5$  °C from day 10 to day 14 (Figure 4.3A). The total nematode numbers fluctuated during the cooling phase and remained more-or-less constant (i.e., on average  $1046 \pm 436$  nematodes/100 g DW compost) during maturation. In total, 30 genera that belonged to 14 families were identified (Table 4.2). Irrespective of the index used, nematode diversity remained rather stable (Table 4.3); between four (day 42) and eight

(day 21) genera were recorded at each individual sampling moment. The most common taxa that occurred throughout the composting process were *Aphelenchoides* sp., *Diploscapter coronatus*, *Ditylenchus* sp., *Mononchoides composticola*, and *Pelodera* sp. Other species, such as *Glauxinemella* sp., *Myolaimus* sp., *Panagrolaimus* sp., *Poikilolaimus* sp. 2, and *Teratrorhabditis* sp. 2, were restricted to specific moments in the composting process (Table 4.2). The nMDS visualizes (Figure 4.3B) groupings of nematode communities that broadly correspond with the composting phases; the average nematode species composition was significantly different ( $P \leq 0.002$ ) in each of these predefined phases (ANOSIM). The species composition in the compost was best explained by a combination of the temperature and C/N ratio of the compost heap ( $r = 0.49$ , stepwise BIOENV). Bacterial-feeding nematodes were present in all compost samples, though most samples contained fungal feeders and predators (days 0, 10, 14 up to 162) as well. From the start of the process up to day 112, the bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogasteridae) were the most abundant, followed by the bacterial-feeding general opportunists (cp-2) (Cephalobidae), and the fungal-feeding general opportunists (cp-2) (Aphelenchoididae). However, clear successional shifts can be distinguished in every composting phase. First, during the thermophilic phase, *Panagrolaimus labiatus* and/or *Halicephalobus* cfr. *gingivalis* (both Panagrolaimidae) were abundantly present (days 0, 3, 7, 10, 14, and 17, and days 14 and 21, respectively). Second, from day 10 onwards, the relative abundances of the bacterial-feeding/predator diplogasterids (mainly *Mononchoides composticola*) gradually increased to > 30% during the cooling phase (from day 28 to 84). Third, during maturation (from day 84 onwards), the relative abundances of the fungal-feeding nematodes increased, specifically the fungal-feeding Anguinidae (mainly *Ditylenchus filimus*) (Table 4.2). The MI and the F/F+B ratio showed a significant increase during the maturation phase as compared to both cooling and thermophilic phases (Table 4.3).





**Figure 4.3**

(A) Total nematode numbers per 100 g dry weight compost and the temperature of the compost during the process. (B) MDS ordination of square root transformed nematode species abundances of every sampling moment. Time of composting is indicated as a number next to the mark of the sample. (C) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator) at every sampling moment. Omnivores are not represented in the graph because they only occurred in one sample. Samples of the thermophilic, cooling and maturation phases are represented by labels in regular, **bold** and *italics*, respectively.

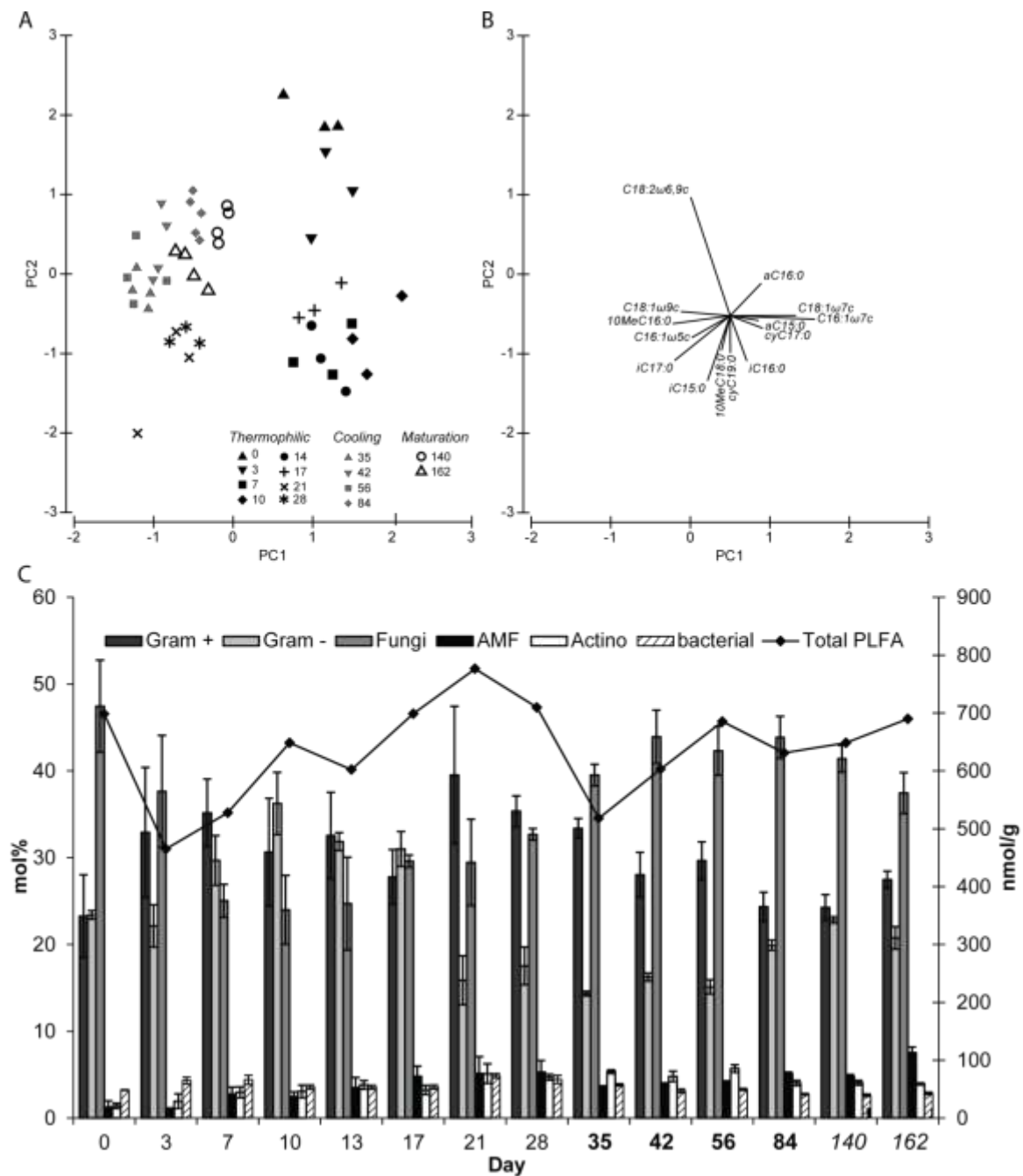
**Table 4.3**

Overview of the means  $\pm$  SD of the abundance of nematodes (per 100g dry weight compost), number of genera, Shannon-Wiener index (H'), Margalef's diversity index (d), percent contribution to the functional groups (trophic groups: type 2 (fungal-feeding nematodes), type 3 (bacterial-feeding nematodes), type 3-5a (bacterial-feeding/predator nematodes), type 8 (omnivorous nematodes) and cp-groups: cp-1 (enrichment opportunists), cp-2 (general opportunists), cp-4 (persisters) and the values of the indices: F/F+B (fungivorous/bacterivorous ratio) and MI (Maturity Index) at every sampling moment based on 3 replicates.

	Day																			
	0	3	7	10	14	17	21	24	28	31	35	38	42	49	56	70	84	112	140	162
<b>Abundance</b>	791 $\pm$ 416	772 $\pm$ 222	672 $\pm$ 522	2700 $\pm$ 295	3657 $\pm$ 1401	683 $\pm$ 141	703 $\pm$ 506	473 $\pm$ 164	1183 $\pm$ 61	425 $\pm$ 84	1667 $\pm$ 449	586 $\pm$ 69	905 $\pm$ 187	498 $\pm$ 251	881 $\pm$ 102	938 $\pm$ 286	912 $\pm$ 143	1185 $\pm$ 663	1323 $\pm$ 82	722 $\pm$ 158
<b># Genera</b>	7 $\pm$ 1	6 $\pm$ 2	5 $\pm$ 4	7 $\pm$ 3	7 $\pm$ 5	6 $\pm$ 2	8 $\pm$ 1	4 $\pm$ 2	7 $\pm$ 3	5 $\pm$ 2	7 $\pm$ 2	5 $\pm$ 3	5 $\pm$ 1	7 $\pm$ 5	5 $\pm$ 4	6 $\pm$ 1	4 $\pm$ 4	5 $\pm$ 1	7 $\pm$ 1	7 $\pm$ 1
<b>H'</b>	0.9 $\pm$ 0.18	1.2 $\pm$ 0.35	1 $\pm$ 0.34	1.5 $\pm$ 0.37	1.3 $\pm$ 0.43	1.1 $\pm$ 0.62	1.4 $\pm$ 0.36	0.3 $\pm$ 0.23	1.2 $\pm$ 0.61	0.7 $\pm$ 0.4	1.1 $\pm$ 0.06	0.5 $\pm$ 0.65	0.7 $\pm$ 0.42	0.6 $\pm$ 0.7	0.8 $\pm$ 0.6	0.8 $\pm$ 0.44	0.7 $\pm$ 0.84	1.2 $\pm$ 0.1	1.5 $\pm$ 0.24	1.6 $\pm$ 0.18
<b>d</b>	1 $\pm$ 0.02	0.8 $\pm$ 0.27	0.8 $\pm$ 0.96	0.9 $\pm$ 0.44	0.8 $\pm$ 0.54	0.7 $\pm$ 0.3	1.2 $\pm$ 0.06	0.6 $\pm$ 0.36	0.9 $\pm$ 0.45	0.7 $\pm$ 0.15	0.9 $\pm$ 0.21	0.7 $\pm$ 0.59	0.5 $\pm$ 0.07	1 $\pm$ 0.89	0.6 $\pm$ 0.42	0.8 $\pm$ 0.11	0.5 $\pm$ 0.59	0.6 $\pm$ 0.18	0.9 $\pm$ 0.08	1 $\pm$ 0.1
	Functional groups %																			
Trophic groups %																				
<b>type 2</b>	4.7 $\pm$ 2.5	8.15 $\pm$ 3.8	12.75 $\pm$ 17.6	0.29 $\pm$ 0.6	5.94 $\pm$ 6.1	4.05 $\pm$ 5.3	13761 $\pm$ 8.8	0	6.51 $\pm$ 8.5	1.8 $\pm$ 4	4.2 $\pm$ 1.3	3.99 $\pm$ 6.6	7.94 $\pm$ 9.9	2.16 $\pm$ 6.6	10.7 $\pm$ 15.2	4.39 $\pm$ 3.9	19.41 $\pm$ 25.8	72.82 $\pm$ 12.8	44.3 $\pm$ 0.5	48.93 $\pm$ 37
<b>type 3</b>	90.9 $\pm$ 5	91.49 $\pm$ 3.4	87.25 $\pm$ 17.6	85.48 $\pm$ 8.6	82.34 $\pm$ 14.3	50.07 $\pm$ 26.3	75.58 $\pm$ 8.5	5.07 $\pm$ 4.5	35.99 $\pm$ 20.5	13.56 $\pm$ 7.7	31.25 $\pm$ 14.7	10.07 $\pm$ 11.3	37.2 $\pm$ 42	6.45 $\pm$ 12.1	12.1 $\pm$ 14.5	24.02 $\pm$ 18.6	12.75 $\pm$ 15.4	19.1 $\pm$ 1	55.27 $\pm$ 0.2	42.26 $\pm$ 32.3
<b>type 3-5a</b>	4.5 $\pm$ 7	0.36 $\pm$ 0.5	0	14.6 $\pm$ 19.5	11.72 $\pm$ 12	45.88 $\pm$ 28.4	10.8 $\pm$ 9.3	94.64 $\pm$ 4.9	57.5 $\pm$ 25.1	84.62 $\pm$ 10.3	64.55 $\pm$ 14.3	85.94 $\pm$ 17.9	54.86 $\pm$ 51.9	91.38 $\pm$ 18.6	77.1 $\pm$ 29.7	71.59 $\pm$ 21.9	67.84 $\pm$ 41.2	8.08 $\pm$ 11.8	0.42 $\pm$ 0.7	8.81 $\pm$ 5.8
<b>type 8</b>	0	0	0	0	0	0	0	0.29 $\pm$ 0.6	0	0	0	0	0	0	0	0	0	0	0	0
Cp-groups %																				
<b>cp-1</b>	93.75 $\pm$ 6.1	88.97 $\pm$ 8.6	87.19 $\pm$ 17.4	99.71 $\pm$ 0.6	94.06 $\pm$ 6.1	95.58 $\pm$ 5	84.79 $\pm$ 10.6	99.2 $\pm$ 1	93.15 $\pm$ 8.3	98.19 $\pm$ 4	93.81 $\pm$ 3.7	95.3 $\pm$ 7.1	92.06 $\pm$ 9.9	97.69 $\pm$ 7.2	58.92 $\pm$ 15.2	95.61 $\pm$ 3.9	80.59 $\pm$ 25.8	27.18 $\pm$ 12.18	55.69 $\pm$ 0.5	51.07 $\pm$ 37
<b>cp-2</b>	6.25 $\pm$ 6.1	11.03 $\pm$ 8.6	12.81 $\pm$ 17.4	0.29 $\pm$ 0.6	5.94 $\pm$ 6.1	4.42 $\pm$ 5	15.21 $\pm$ 10.6	0.51 $\pm$ 1.1	6.85 $\pm$ 8.3	1.81 $\pm$ 4.04	6.18 $\pm$ 3.7	4.69 $\pm$ 7.1	7.94 $\pm$ 9.9	2.3 $\pm$ 7.2	0 $\pm$ 15.2	41 $\pm$ 3.9	19.41 $\pm$ 25.8	72.82 $\pm$ 12.8	44.31 $\pm$ 0.5	48.93 $\pm$ 37
<b>cp-4</b>	0	0	0	0	0	0	0	0.29 $\pm$ 0.6	0	0	0	0	0	0	0	0	0	0	0	0
	Indices																			
<b>F/F+B</b>	0.05 $\pm$ 0.02	0.08 $\pm$ 0.04	0.13 $\pm$ 0.18	0.003 $\pm$ 0.01	0.07 $\pm$ 0.06	0.07 $\pm$ 0.07	0.11 $\pm$ 0.1	0	0.11 $\pm$ 0.15	0.09 $\pm$ 0.16	0.13 $\pm$ 0.07	0.11 $\pm$ 0.19	0.12 $\pm$ 0.11	0.28 $\pm$ 0.25	0.24 $\pm$ 0.24	0.16 $\pm$ 0.17	0.35 $\pm$ 0.32	0.78 $\pm$ 0.04	0.45 $\pm$ 0.001	0.56 $\pm$ 0.26
<b>MI</b>	1.08 $\pm$ 0.06	1.13 $\pm$ 0.09	1.14 $\pm$ 0.17	1.0 $\pm$ 0.0	1.06 $\pm$ 0.06	1.04 $\pm$ 0.05	1.12 $\pm$ 0.11	1.0 $\pm$ 0.02	1.07 $\pm$ 0.08	1.02 $\pm$ 0.04	1.06 $\pm$ 0.04	1.05 $\pm$ 0.07	1.1 $\pm$ 0.1	1.05 $\pm$ 0.07	1.11 $\pm$ 0.15	1.04 $\pm$ 0.04	1.17 $\pm$ 0.26	1.71 $\pm$ 0.12	1.44 $\pm$ 0	1.45 $\pm$ 0.37

#### 4.4.3. Microbial community dynamics

The total PLFA concentration (Table 4.4) showed no significant differences between the compost phases. It was lowest during the first heat peak, on day 3 ( $465 \pm 60$  nmol/g), and after the second heat peak, on day 35 ( $518 \pm 103$  nmol/g). During the cooling and maturation phases, however, total PLFA fluctuated between  $528 \pm 110$  and  $776 \pm 93$  nmol/g (Table 4.4). On average, 67% of the total PLFA (min = 35%, max = 74%) could be used as biomarkers for a functional microbial group. The PCA of the relative PLFA concentrations of the biomarkers resulted in a clear discrimination, mainly along the first axis, between compost of the early thermophilic phase (days 0, 3, 7, 10, 14, and 17) and compost of the cooling and maturation phases (days 35, 42, 56, 84, 140, and 162) (Figure 4.4A). The first axis explained 39% of the variation, and the second explained an additional 31%. The marker fatty acids of bacteria (increasing 16:1 $\omega$ 7c and 18:1 $\omega$ 7c and decreasing *i*17:0 and 10*Me*16:0) contributed the most to the first axis, while the fungal marker 18:2 $\omega$ 6,9c contributed the most to the second axis (Figure 4.4B). The average marker fatty acids compositions (mol%) were significantly different in the the thermophilic phase than they were in the cooling phase (ANOSIM). In the first sample, before the temperature began to increase, fungi and bacteria contributed equally to the microbial community. With increasing temperature during the first heat peak (days 3-7), the amount of Gram-negative and Gram-positive bacteria and Actinomycetes PLFAs began to increase, while the fungal biomass decreased (Figure 4.4C). During the intermediate temperature drop (days 10-17), the Gram-negative bacteria reached their maximum and the fungi began increase again, while the Gram-positive bacteria continued to increase and reached their maximum levels during the second heat peak (days 17-28). During the early cooling phase, both the fungi and the Actinomycetes reached their maximum concentrations; the fungi concentration was relatively stable during the remainder of the compost process, being significantly higher than during the thermophilic phase (Table 4.4). The Actinomycetes' concentration, however, slightly decreased again. During maturation, the Gram-negative bacteria were significantly more abundant than during cooling (Table 4.4). The fungi/bacteria ratio (based on PLFA) (Figure 4.5) was low (< 1) during the thermophilic phase, but it increased significantly ( $P < 0.001$ ) and remained relatively constant ( $\pm 1$ ) during the subsequent cooling and maturation phases. This increase in the fungi/bacteria ratio did not coincide with an increase in the nematode-based equivalent (F/F+B), which only began to increase at the onset of the maturation phase.



**Figure 4.4**

(A) Two-dimensional PCA ordination of biomarker fatty acids (mol%). (B) Vector loading plot with all individual marker fatty acids. (C) Percent contributions of functional groups (mol%) (bars) and total PLFA concentration (nmol/g) (line) during the composting process.

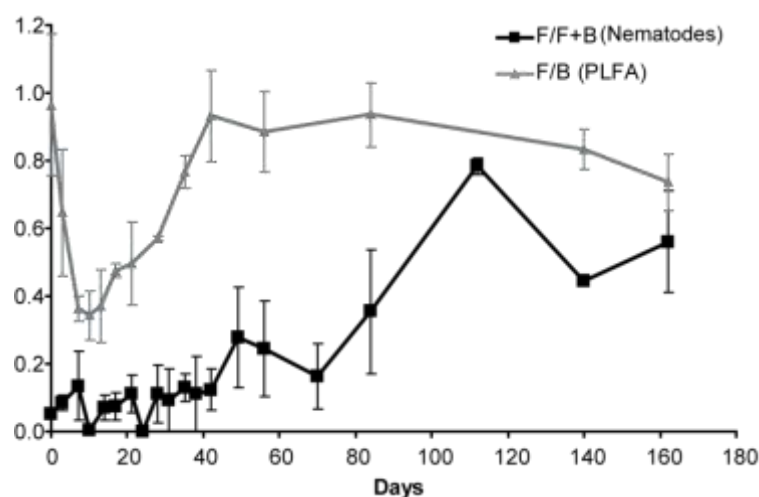


**Table 4.4**

Total PLFA and main biomarker concentrations (nmol g<sup>-1</sup> dry soil) ± standard deviation, during the composting process. Different letters after means indicate significant differences between composting phases using pairwise Mann-Whitney U tests with Bonferroni corrections ( $\alpha = 0.016$ ). If no letters no significant differences were found.

Day & Phase	total PLFA	Gram +	Gram -	Actino- mycetes	Total Bacteria	Fungi	AMF*	
Thermophilic	0	698±307	57.4±7.18	60.6±20.46	3.8±2.08	126.4±30.31	126.1±57.46	2.8±0.96
	3	465±60	70.3±17.36	47.1±3.89	4.1±1.56	126.7±14.26	80.4±14.71	2.3±0.33
	7	528±110	108.2±17.9	93.2±26.76	9.1±2.27	214.9±42.42	78.8±22.36	8.7±4
	10	648±240	119.2±18.57	149.8±61.36	12±2.6	283.3±80.89	101±46.18	10.5±4.9
	13	602±259	125.5±40.57	126.5±49.57	14.8±4.55	266.2±95.95	103.6±53.91	15.2±9.05
	17	699±29	131±18.57	145.9±8.31	15.3±3.02	293.7±16.79	139.4±4.86	22.6±5.58
	21	776±94	196±21.69	80.4±20.24	25.5±3.5	300.8±8.43	149±35.27	26.3±11.4
	28	710±118	165.1±20.15	81.6±11.02	21.9±1.75	267.5±27.43	152.5±15.31	25.2±8.63
Cooling	35	518±103	122.9±26.12	52.6±10.2	19.6±3.41	189.5±33.56	145.1±26.41	13.2±2.52
	42	603±51	126.5±20.98	73.1±7.51	21.7±4.14	213.7±25.9	196.4±7.10	17.3±2.07
	56	685±152	152±37.52	77.1±17.26	29.3±7.73	245.9±49.94	215.4±43.43	22.4±3.04
	84	631±82	116.6±16.02	95.6±13.86	19.3±181	225.3±30.91	210.1±29.35	24.5±3.52
Matura tion	140	648±50	121±13.65	113.7±7.72	20.3±2.49	247.9±18.73	206±12.58	23.8±2.48
	162	690±40	141.4±10.17	107±11.47	20.3±0.85	263±18.78	192.5±13.77	38.9±4.88

\* The used biomarker for AMF is questionable in a compost environment (see materials and method section). For completeness the concentrations of this group are provided but not used in further community analyses.

**Figure 4.5**

F/B ratio based on fungal and bacterial PLFA data and F/F+B ratio based on the fungal-and bacterial-feeding nematode densities during the composting process. Data are means ± SD of 3 replicates indicated as error bars.

#### 4.4.4. Relationships between microbial and nematode communities

The BEST procedure indicated the fatty acids 10Me16:0, 10Me18:0 (both indicators of Actinomycetes), and 18:2 $\omega$ 6,9 (an indicator of fungi) as the variables best explaining the microbial community pattern during the composting process ( $r = 0.43$ ) and the nematode taxa *Glauxinemella* sp., *Mononchoides composticola*, *Myolaimus* sp., *Rhabditella* sp., and *Teratorhabditis* sp1 as best explaining shifts in the nematode community structure during the composting process ( $r = 0.39$ ). The canonical correlation analyses between these two sets of selected variables revealed a significant ( $P = 0.036$ ) first axis canonical correlation ( $r = 0.64$ ). *Mononchoides composticola* and *Rhabditella* sp. contributed most to the nematode-based first canonical variable, while 10Me18:0 and 18:2 $\omega$ 6,9 contributed most to the PLFA-based canonical variable.

#### 4.5. DISCUSSION

The nematode assemblage and succession observed here are remarkably similar to those of an earlier study in 2006-2007 (Chapter 2). To the best of our knowledge, this was the first study on nematode community dynamics during a composting process. Although, in this former study, nematodes were absent during the thermophilic phase, the nematode abundances of the final composting stages were similar. The presence of nematodes during the heat peak in the present study may be explained by the strong environmental temperature drop during the thermophilic phase. This may have resulted in the patchiness of high-temperature spots and thus the presence of refuges where nematodes could escape the most extreme temperatures. Most importantly, the shifts between the functional groups showed the same pattern: from a thermophilic phase dominated by bacterial-feeding nematodes – at first exclusively enrichment opportunists and later supplemented with general opportunists – to a community with increasing numbers and the eventual dominance of bacterial-feeding/predator enrichment opportunists (mainly *Mononchoides*) in the cooling phase to the maturation phase, in which the fungal-feeding general opportunists became more important. These functional groups are also largely represented by the same taxa as in the 2006-2007 study (Chapter 2), i.e., *Aphelenchoides* sp., *Diploscapter coronatus*, and *Mononchoides* sp., together with *Pelodera* sp. and *Ditylenchus filiformis*, were the most common species. The current study confirms that the nematode functional group shifts correspond to the three composting phases and that the F/F+B ratio and MI significantly increase during maturation. Except for temperature, the BIOENV procedure selected the C/N ratio as variable best explaining nematode community structure. Apparently,

the considerably lower moisture content (< 30%) at most of the sampling points, as compared to the study of 2006-2007 (Chapter 2), did not significantly affect the nematode community. However, it should be noted that these differences in moisture content might also be related to the potentially different organic matter contents of the composts because high levels of organic matter content increase the water holding capacity.

The microbial community during composting has been better studied than the nematode community. In accordance with Steger et al. (2003) and Bolta et al. (2003), the total PLFA, as a measure of total microbial biomass, remained more-or-less stable during the composting process. In contrast, Klamer and Bååth (1998) and Hellmann et al. (1997) described an increase during the thermophilic phase and a subsequent decrease of total PLFA during the remainder of the composting process. The overall succession of the microbial community, as described in this study, has already been reported (Herrmann and Shann 1997; Klamer and Bååth 1998; Steger et al. 2003; Ryckeboer et al. 2003). Fungal biomass is high at the onset of the composting process, after which it sharply declines when temperatures peak. It increases again when temperatures drop below 45°C during cooling and maturation. Gram-positive bacteria dominate during the thermophilic phase, while Gram-negative bacteria increase after the thermophilic phase. This pattern can be explained by the higher sensitivity of fungi to high temperatures and their slower recovery after heating than bacterial communities (Bárcenas-Moreno and Bååth 2009). However, this does not agree with Carpenter-Boggs et al. (1998), who observed no significant changes in fungal biomarkers during composting, and Bolta et al. (2003) found a decrease in fungal biomass with compost time. Most authors (Hellmann et al. 1997; Klamer and Bååth 1998; Steger et al. 2003; Bolta et al. 2003; and in this study) found higher levels of Actinomycetes in the later composting stages, although Herrmann and Shann (1997) reported high levels during the thermophilic phase. Steger et al. (2007) already suggested that Actinomycetes may be a good indicator of compost maturity based on the changes in species composition and their increased share in the microbial communities during the later compost stages. Our BEST analyses also selected the biomarkers of Actinomycetes (i.e., 10Me16:0 and 10Me18:0) as being among the variables best explaining the composition of the nematode community. The explanations of several more-detailed aspects of microbial community structure in our study also correspond with those of previous studies. For example, the increase of Gram-positive bacteria with increasing temperature during the thermophilic phase corresponds to an increase in iso-fatty acids, while the level of anteiso-fatty acids remained more-or-less constant during the process (Klamer and Bååth 1998). High levels of monounsaturated PLFAs, such as the iso-fatty acids and 16:1 $\omega$ 7 and 18:1 $\omega$ 7, indicate high substrate availability (Moore-Kucera and Dick

2008). This may be especially true during the thermophilic phase, when readily available substances of the feedstock materials are decomposed mainly by thermophilic Gram-positive bacteria when temperatures are high (> 50 °C) and mainly by Gram-negative bacteria when temperatures are low (< 50 °C). The decomposition of complex structural compounds, such as lignin and lignocellulose, is generally assumed to take place during the cooling and the maturation phase because it is mostly performed by fungi (Vargas-García et al. 2012). Indeed, the fungal biomass was low during the first heat peak of the thermophilic phase (on day 7), and from this point onwards, it began to increase from cooling until the beginning of the maturation phase, when it remained more-or-less constant. However, fungal-feeding nematodes did not increase until the beginning of the maturation phase (day 112). This delayed increase of fungal-feeding nematodes is also illustrated by the different timings of the maximum values of the F/B (based on the microbial community) and those of the F/F+B (based on nematodes). There are several possible explanations for the delayed increase of fungal-feeding nematodes. First, the relatively long generation time of cp-2 fungal-feeding nematodes (Ferris et al. 2001) and the high maximum temperatures in the beginning of the cooling phase might have hampered the development of the fungal-feeding nematodes. The inhibition of the reproduction of the fungal-feeding taxa *Aphelenchoides rutgersi* at 33 °C and *Ditylenchus* sp. at 39 °C has been reported based on *in vitro* cultures (Pillai and Taylor 1967; Moens et al. 1996). Secondly, nematode predators also may have contributed to the delayed increase in the number of fungal-feeding nematodes. During the cooling phase, when the microbial community was shifting from bacterial dominance to more-or-less equal shares of fungi and bacteria, the nematode population was dominated by the bacterial-feeding/predator *Mononchoides composticola*, which exploited its nutritional advantage in this changing environment, i.e. being able to feed on both bacteria and on other compost nematodes (Chapter 3, part 2). Furthermore it is possible that they are capable of feeding on fungi as well, as has been demonstrated for some other diplogasterid taxa, including *Pristionchus pacificus* (von Lieven and Sudhaus 2000), making them excellent generalists. Despite this delay, the microbial and nematode communities largely followed the same pattern, as was confirmed by the canonical correlation analysis.

In conclusion, although the microbial and the nematode communities showed largely similar patterns, based on the microbial community, it is only possible to discriminate between the thermophilic phase and the rest of the process. There is bacterial dominance during the thermophilic phase, and there are more-or-less equal shares of bacteria and fungi during cooling and maturation. However, based on the nematode community, it is possible to discriminate between the three composting phases: dominance of bacterial-feeding nematodes during the

thermophilic phase, dominance of bacterial-feeding/predators (diplogasterids) during cooling, and an increased abundance of fungal-feeding nematodes during maturation. Furthermore, the PLFA method has the drawback of being much more expensive, time-consuming, and labor-intensive than the extraction and identification (up to family level or feeding type) of the nematode community. Therefore, this study demonstrates that the nematode community holds promise as a tool for use in assessing compost maturity. However, further research on more compost processes is warranted in order to transform the characteristics of the nematode community into threshold values for mature compost.

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# 5. Survival and colonization of nematodes in a compost process

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Modified from:

Steel H, Verdoodt F, Čerevková A, Couvreur M, Fonderie P, Moens T and Bert W. Survival and colonization of nematodes in a compost process. Submitted to *Invertebrate Biology*.

## 5.1 ABSTRACT

Nematodes are omnipresent in composts and are active in virtually all stages of the composting process. Major shifts in species composition, life strategies and feeding behavior occur during the composting process. Due to the heat peak, nematodes can be virtually absent, but several taxa appear immediately when the temperatures drop. These comprise both taxa present before the heat peak and new taxa. However, it is completely unknown how nematodes are able to populate the compost. In this paper we aimed to assess the survival and colonization capacity of nematodes in compost. Our results showed that composting processes inaccessible to insects and/or not in contact with soil did not significantly influence the nematode succession during composting. However, for some specific taxa differences between treatments were found (i.e. for *Achrostichus* sp., Neodiplogasteridae sp., *Nygolaimoides* sp. and Rhabditidae sp.1) illustrating the importance of insects for the dispersal of nematodes to compost. Experiments in the lab with the blue bottle fly as a possible carrier demonstrated actual transport of nematodes isolated from compost by the fly (i.e. *Halicephalobus* cfr. *gingivalis*, *Diploscapter coronatus*, *Diplogasteritus* sp., *Acrostichus* sp., *Mesorhabditis* sp.). *Aphelenchoides* sp., *Panagrolaimus* sp. and rhabditid juveniles and dauer stages survived an experimentally induced temperature peak while Tylenchidae did not. In conclusion, our results indicate that the rapidly changing nematode community in a compost process is the result of both differential survival and colonization capacities.

## 5.2 INTRODUCTION

Nematodes are omnipresent in composts (on average 26 ind./g dry weight compost in Chapter 7) and are active in all stages of the composting process, except during the heat peak where they can be virtually absent (Chapter 2). Major shifts in species composition, life strategies and feeding behavior occur during the composting process. At the beginning of the process (thermophilic phase), immediately after the heat peak, the nematode population is primarily composed of bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogasteridae), followed by the bacterial-feeding general opportunists (cp-2) (Cephalobidae) and the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, during the cooling and maturation stages, the bacterial-feeding/predator enrichment opportunistic nematodes (e.g., *Mononchoides composticola*; Chapter 3, part 2) become dominant. Finally, at the most mature stages, the fungal-feeding Anguinidae (mainly *Ditylenchus filimus*), Tylenchidae en

Neotylenchidae are most prominent. This remarkable succession and the distinct advantages of nematodes as bio-indicators (Chapter 1) prompted us to explore the potential of nematodes to assess the maturity and quality of compost (Chapter 2).

However, it is completely unknown how nematodes are able to populate the compost. Although nematodes can be virtually absent during the heat peak, several taxa appear immediately when the temperatures drop. These comprise both taxa present before the heat peak and new taxa. Nematode populations present from the early stages of composting may survive the heat peak as dauer stages or eggs, and/or find refuge in the cooler outer edge of the compost heap. However, other factors must also be important since the nematode community continuously changes during the composting process. New taxa appear after the heat peak, and given that the active mobility of nematodes is in most cases limited to small-scale migrations (Hunt et al. 2001), the question arises as to the origin of these compost colonizers. In general, dispersal by water and wind are thought to be important in generating and maintaining nematode diversity (Hodda et al. 2009). However, many terrestrial nematodes are transported by insects and other mobile invertebrates that share habitat or food resources (Timper and Davies 2004). In this paper we aimed to assess the survival and colonization capacity of nematodes in compost and focused on the following research questions: (1) Does nematode succession differ between a normal, open (control) process and processes that are inaccessible to insects and/or not in contact with soil?, (2) Can vectoring insects effectively be responsible for the transport of nematodes to the composting environment? And (3) are compost nematodes able to survive the temperature increase during the thermophilic phase?

## **5.3 MATERIALS AND METHODS**

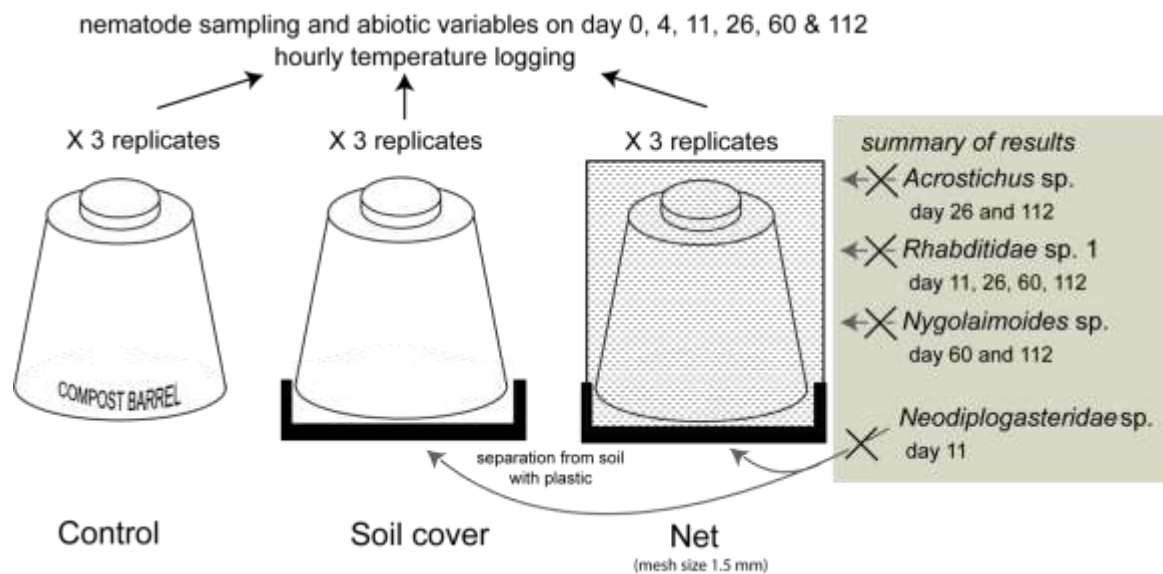
### **5.3.1 Closed vs. non-closed compost processes and its influence on nematode succession**

A randomized design with three treatments and three replicates, i.e. nine compost barrels, was set up in a garden in Heusden, Belgium (51° 0'44.5"N; 3° 48' 24.4"E). The barrels had a total volume of 290 l each (height=96 cm, upper diameter=52 cm and lower diameter=80 cm) (Figure 5.1). A first group of three barrels was covered from the soil with plastic canvas, precluding soil organisms from entering the barrels. The second group was covered from soil with plastic canvas and protected with a mosquito net, preventing both soil organisms and insects from reaching the compost. The third group was the control group without any special manipulations affecting insect access and the barrels were placed directly on the soil. These groups will be referred to as

soil cover, net and control treatment, respectively. All barrels were filled with the same amount of feedstock materials on a volume to volume base (v/v): 38 % (v/v) of pure wood chips and 62 % (v/v) of a homogenous mixture. This mixture consisted of 55% fresh grass and 45% mixed wood chips (mainly boxwood and young willow twigs). The compost in the barrels was mixed once, on day 7, during the heat peak. Samples for nematode extraction were taken on the day of the setup (day 0), directly after the heat peak during the thermophilic phase (day 4) and additionally on days 11, 26, 60 and 112. Each sample was a composite sample that consisted of 5 subsamples of 100ml each, taken randomly from different levels in the compost heap. Relevant abiotic variables were measured at every sampling event. For the pH measurements, extractions of 20 g compost in 100 ml distilled water were made, shaken by hand a few times during a 6 hour period, and pH was measured with standard electrodes (Consort P400). Moisture content was determined by weighing 50ml of compost before and after drying for 48h at 104 °C. Total C- and N-content were measured with a Variomax CNS element analyzer, using 1 g of freeze-dried compost (Elementar GmbH, Hanau, Germany), applying the Dumas method (EN<sup>5</sup> 13654-2). Temperature was monitored hourly in the center of the barrels using data-loggers (Testo 175-T2, Ternat, Belgium). To collect insects, traps (pitfalls) were placed in the compost barrel and sticky strips were hung up in and around the barrels. Caught insects were identified up to family level. For an overview of the collected insects see Table 5.S1. These insects were placed on Petri dishes bottom-covered with an agar layer to allow any insect-associated nematodes to colonize the agar (agar medium: 2% bacteriological agar in distilled water (Oxoid, Basinstoke, Uk) and cholesterol (1 µg/ml; Sigma-Aldrich, Belgium), to which *Escherichia coli* OP50 was added as a food source).

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<sup>5</sup> EN: European Standard. European Standards are developed by CEN, the European Commission for Standardization. Numbers refer to the specific protocols.



**Figure 5.1:**

Overview of the experimental setup. Each setup (control, soil cover, net) was replicated 3 times. The 9 barrels were positioned randomly relative to each other and all received the same kinds and amounts of feedstock. In the control group no special manipulations were made to the compost barrel. In the second group (soil cover) the barrels were covered from the soil with plastic canvas, precluding soil organisms from entering the barrel, while in the third group (net) barrels were protected with a mosquito net and covered from soil with plastic canvas, preventing both soil organisms and flying insects from reaching the compost. Compost samples were taken on days 0, 4, 11, 26, 60 and 112 and temperature was measured hourly using data loggers. Nematode species which were absent in the net and/or the soil cover treatments compared to the control are displayed with indication of the days on which they were absent compared to the other treatments.

Nematodes of all 54 400-ml compost samples (3 replicates X 3 treatments X 6 time points) were extracted using the modified Baermann funnel method (tray 49x37.5 cm, basket 38.5x19.5 cm) (Hooper, 1986), counted and 50 individuals (2700 individuals in total) were randomly picked using a stereomicroscope (Leica Mz95). For light microscopy observations the specimens were collected in a very small drop of water in an embryo dish. Formaldehyde (4 % with 1 % glycerol) was heated to 70 °C and an excess (4-5 ml) was quickly added to the specimens to kill and preserve them (Seinhorst 1966). The preserved nematodes were processed to anhydrous glycerol following the glycerol-ethanol method (Seinhorst 1966 as modified by De Grisse 1969) and mounted on mass slides (slide 40x76 mm; cover glass 34x60 mm). Nematodes were identified to genus level. The abundance of each genus or species in each sample was calculated as individuals/gram dry weight compost. Nematode genera were assigned to the 1-5 “coloniser-persister” cp-scale according to their r and K life strategy characteristics (Bongers 1990, 1999), and also classified according to their feeding type (Yeates et al. 1993). These allocations were used to calculate the Maturity Index (MI) (Bongers 1990) and the fungivores/bacterivores ratio (F/F+B ratio) (Yeates et al. 1993). In the F/F+B ratio, only the fungal and bacterial-feeders *sensu*

*stricto* were included, i.e. bacterial-feeding/predators such as some diplogasterid nematodes were not included. A hierarchical cluster analysis based on Bray-Curtis similarities of square root transformed species abundance data was performed in Primer 6 to assess differences in community composition (Clarke and Warwick 2001). Significant differences in the nematode community between treatments were investigated using Analyses of Similarities (ANOSIM) in Primer 6. Differences in nematode abundances and nematode-based indices (F/F+B and MI) between treatments were tested using non-parametric Kruskal-Wallis and Mann-Whitney U pairwise tests in Statistica 6.0 (Statsoft Inc.) with Bonferroni corrections.

### 5.3.2 Nematode survival

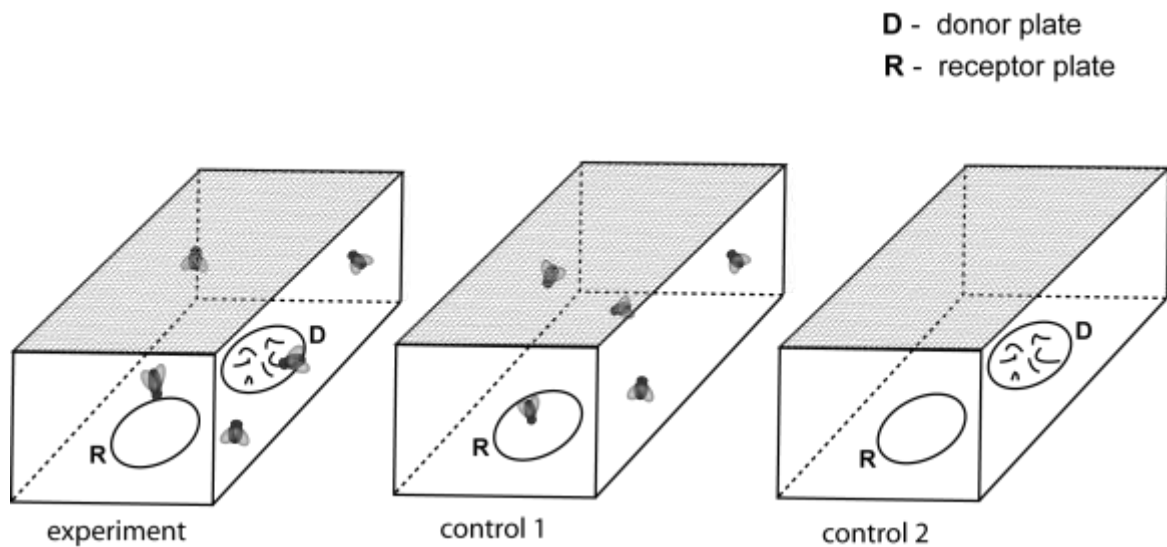
In a first experiment the temperature tolerance of compost nematodes was tested with monoxenic cultures of nematodes isolated from different composting processes. The used species were: *Diploscapter coronatus*, Rhabditidae sp.1, *Poikilolaimus* sp., *Mesorhabditis* sp., *Acrostichus* sp.1, *Diplogasteritus* sp., *Halicephalobus* cfr. *gingivalis* and *Procephalobus* sp. Three replicates of each culture at or near carrying capacity (with all life cycle stadia present) were placed at 65, 50 and 40 °C for 24h. Afterwards the agar pads of the heat exposed plates were divided in 4 and each piece was transferred to a new plate consisting of solid culture medium (2% bacteriological agar in distilled water; Oxoid, Basinstoke, Uk) with cholesterol (1 µg/ml; Sigma-Aldrich, Belgium), to which *Escherichia coli* OP50 was added as a food source. Nematode recovery (survival and reproduction) was checked once a week for four consecutive weeks.

In the second experiment, 6 subsamples of the samples of day 0 (from the experiment described in 5.2.1) were split in two. One half of the samples was used to extract nematodes using the modified Baermann-funnel method (control) and the other half was first exposed (in an oven) to a temperature peak before nematodes were extracted. This temperature peak imitated the ones that took place in the compost barrels as closely as possible: in the first 12 hours the temperature was raised from 25 to 53° C, then remained constant for 12 hours, and in the following 12 hours was increased to 60 °C, then remaining at that temperature for 24h. Afterwards, during the next three days the temperature was gradually decreased by 10 °C every day. Nematode communities between the control and heat exposed samples were compared based on presence and absence of taxa. However, it should be noted that the used compost samples were stored for over 6 months at 4 °C before the experiment with the induced temperature peak started; of the species present in the original compost material, *Pelodera* sp., Cephalobidae sp. and Neotylenchidae sp. could not be recovered 6 month later at the start of the temperature peak experiment.

### 5.3.3 Insect phoresy

To further study insect phoresy of compost nematodes, the phoresy of several species by *Calliphora vomitoria* (blue bottle fly) was tested under controlled laboratory conditions. Experiments were carried out in plastic containers, covered with an insect net. They were placed in a closed culture room at a constant temperature (22 °C) and humidity (60%). Each container held 20 adult flies, a donor plate maintaining a monoxenic culture of compost nematodes, and a nematode-free receptor plate. Both donor and receptor plate contained solid culture medium (2% bacteriological agar in distilled water; Oxoid, Basinstoke, Uk) with cholesterol (1 µg/ml; Sigma-Aldrich, Belgium), to which *Escherichia coli* OP50 was added as a food source (Figure 5.2). The densities of nematodes on the donor plates were determined before and after the six-day period. Every 48 hours (T1: 0-48h; T2: 48-96h; T3: 96-144h), receptor plates were checked and replaced by new ones, in order to prevent the reproduction of already transferred nematodes from significantly altering our estimates of the numbers of nematodes transferred by insects. To determine the mean nematode density of the donor plate during the course of the experiment, the average of the pre- and post-experimental density was calculated by quantifying specimens in three defined regions of 0.25 cm<sup>2</sup>, distributed evenly on the radius of the circular plate.

This experiment was performed in 2 replicates (R 1 and R 2) with several nematode species isolated from compost. They belonged to three families (Panagrolaimidae: *Halicephalobus* cfr. *gingivalis*; Rhabditidae: *Poikilolaimus* sp., *Diploscapter coronatus*, *Mesorhabditis* sp.; and Diplogasteridae: *Achrostichus* sp., *Diplogasteritus* sp.) and were cultured on solid agar medium. To assess whether flies could have already carried associated nematodes prior to their introduction into our experimental containers, a control treatment was designed without donor plate (control 1). Additionally, a control treatment (control 2) was performed to test for non-fly-dependent transfer of nematodes (e.g. through any circulation of air inside the containers).



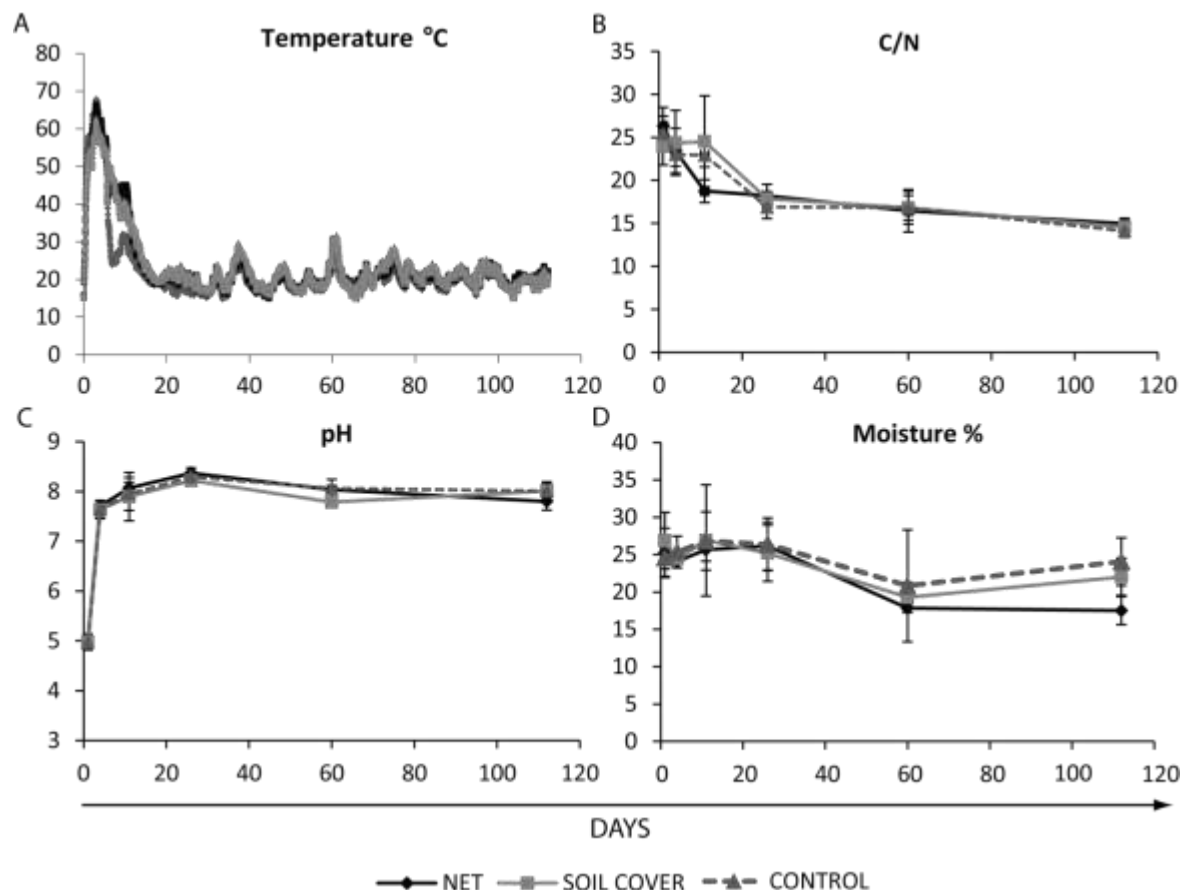
**Figure 5.2:**  
Experimental set-up to test insect phoresy of compost nematodes by *Calliphora vomitoria* (blue bottle fly).

## 5.4 RESULTS

### 5.4.1 Closed vs. non-closed compost processes and its influence on nematode succession

Temperature increased quickly after mixing of the feedstock materials in all barrels (Figure 5.3A), exceeding 40 °C within 12 hours and reaching peaks >60 °C within 72 hours. Thereafter, temperature fluctuated probably due to day and night alternation but with an overall gradual decline towards ambient temperatures. The C/N ratio declined from ca. 25 to 15 over 112 days of composting (Figure 5.3B). The pH rose from ca. 5 to 8 during the first 4 days, whereafter it remained fairly constant (Figure 5.3C). Moisture levels remained stable between 20 and 30% (Figure 5.3D).





**Figure 5.3:**

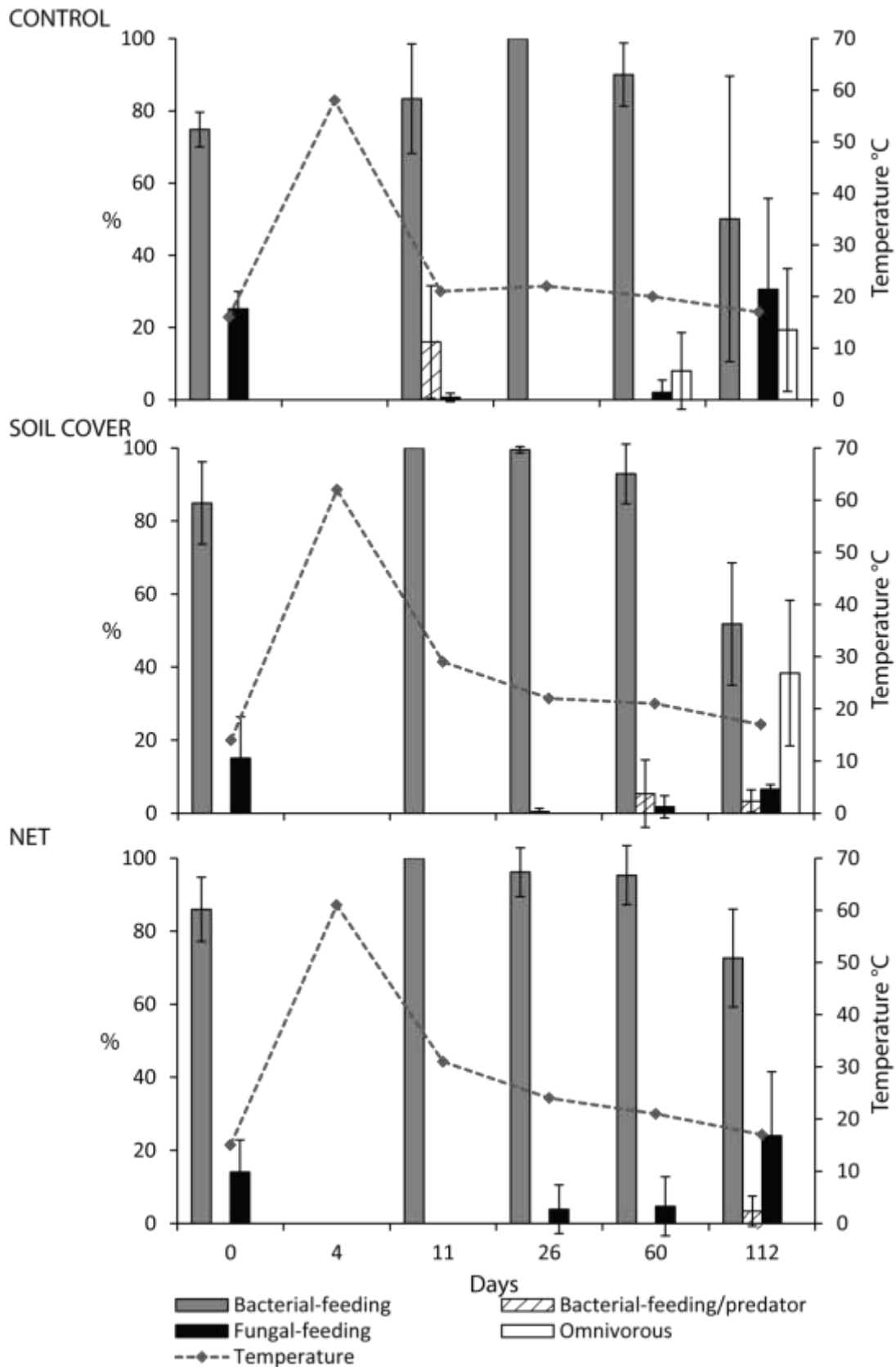
Abiotic variables during the composting process for each of three experimental setups: control, exclusion of soil fauna ('soil cover') and exclusion of both soil fauna and vectoring insects ('net'). (A) Temperature (°C) was measured hourly using data loggers, (B) C/N ratio, (C) pH values, (D) moisture content (%). Data are means of three replicates  $\pm$  SD.

Irrespective of the experimental setup (control, soil cover or net), very similar patterns in the nematode community were found during the composting process (Figure 5.4 and Table 5.1). For an overview of all nematode taxa found in compost and their feeding type see Table 5.S2. In the feedstock mixture bacterial-feeding and fungal-feeding nematodes were found, making up ca. 80 and 20%, respectively, of the community. During the heat-peak nematodes were absent from all barrels, while on days 11, 26 and 60 there was again a clear dominance of bacterial-feeding nematodes (>80%). On day 112 the proportion of the fungal-feeding nematodes had increased in all setups, though only significantly in the control ( $p=0.026$ ) and soil cover ( $p=0.018$ ) treatment. *Aphelenchoides* sp., *Pelodera* sp., and *Panagrolaimus* sp. were present both before and after the temperature peak, while *Acrostichus* sp.1, *Rhabditidae* sp.1, *Nyggolaimoides* sp. and *Neodiplogasteridae* sp. were only recorded after the heat peak (Table 5.1). The timing of occurrence and/or presence or absence of the species from the latter group differed between experimental setups (see further). However, overall, differences in nematode community structure were more related to the composting phase than to the treatments including or

excluding nematode migration or transfer. The cluster analysis based on community composition clearly indicated a higher similarity between times of composting than between 'exclusion' treatments (Figure 5.5). Apart from a small cluster (cluster C) which included samples of days 11 and 26 of the control and soil cover treatments, two large clusters could be distinguished: cluster A consisted of all samples from day 0, 11 and 26 and cluster B comprised all samples from day 60 and 112. Furthermore, no significant treatment differences in species composition were found (ANOSIM,  $p \geq 0.08$  for all pairwise tests), nor for the nematode abundances or the nematode-based indices (F/F+B and MI) (Figure 5.6).

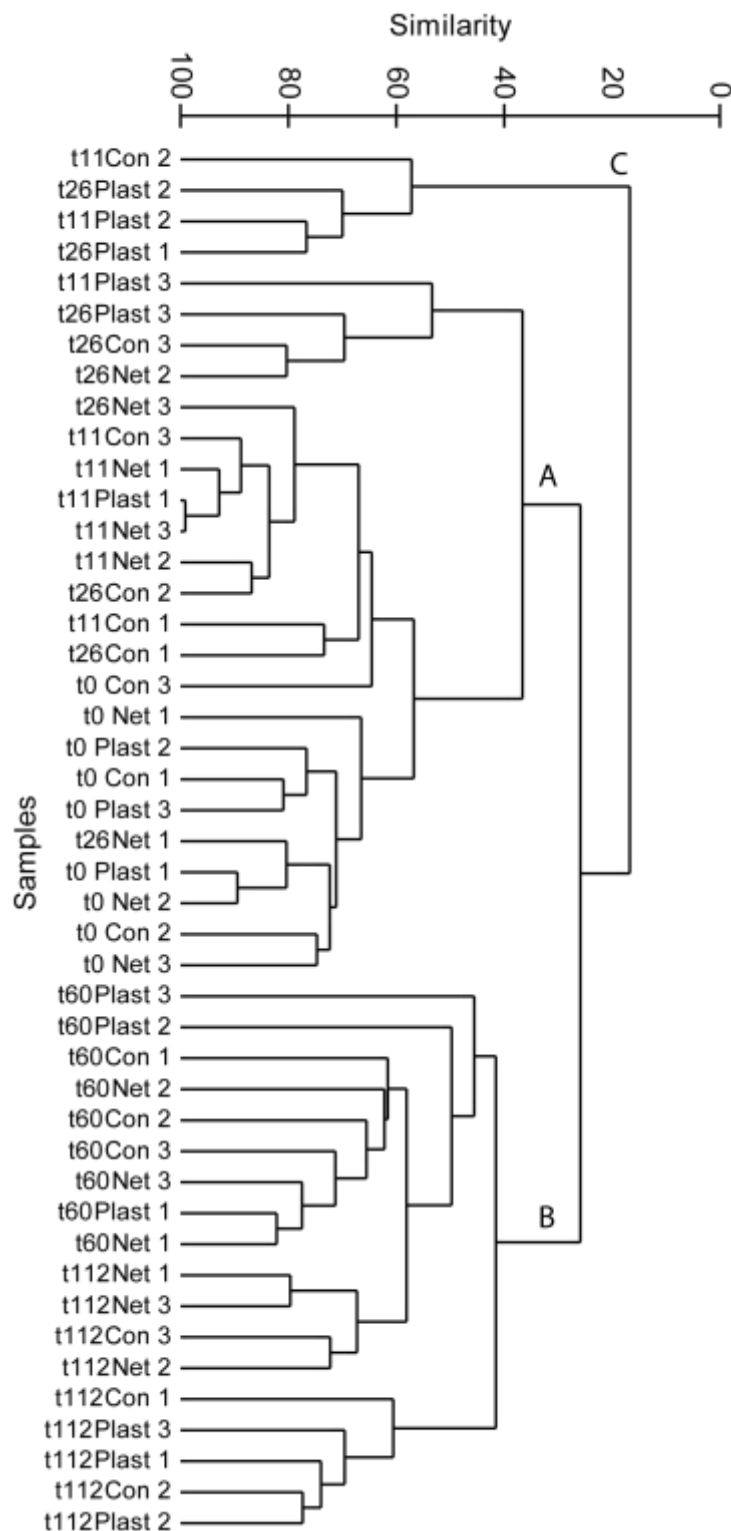
Nevertheless, the following differences between treatments were observed (Figure 5.1 and Table 5.1). In the control treatment the bacterial-feeding/predators already appeared on day 11, while in the soil cover and net treatment their occurrence was postponed to day 60 and day 112, respectively. Omnivores, i.e. the dorylaimid *Nygolaimoides* sp., were found on days 60 and 112 in control and on day 112 in the soil cover treatment but were absent from the net treatment. Rhabditidae sp.1 was found from day 11-112 in control and soil cover treatments but never in net treatments. Neodiplogastridae sp. was present exclusively on day 11 in the control treatment and *Acrostichus* sp.1 occurred from day 26-112 in the control and soil cover treatment but only on day 66 in the net treatment.

Only one nematode taxon could be retrieved from the Petri dishes with insects collected using insect-traps in the compost bins. The genus *Acrostichus* was isolated from insects (3) from the Sciaridae family (Order Diptera). However, this species was clearly different from the *Acrostichus* population in the compost.



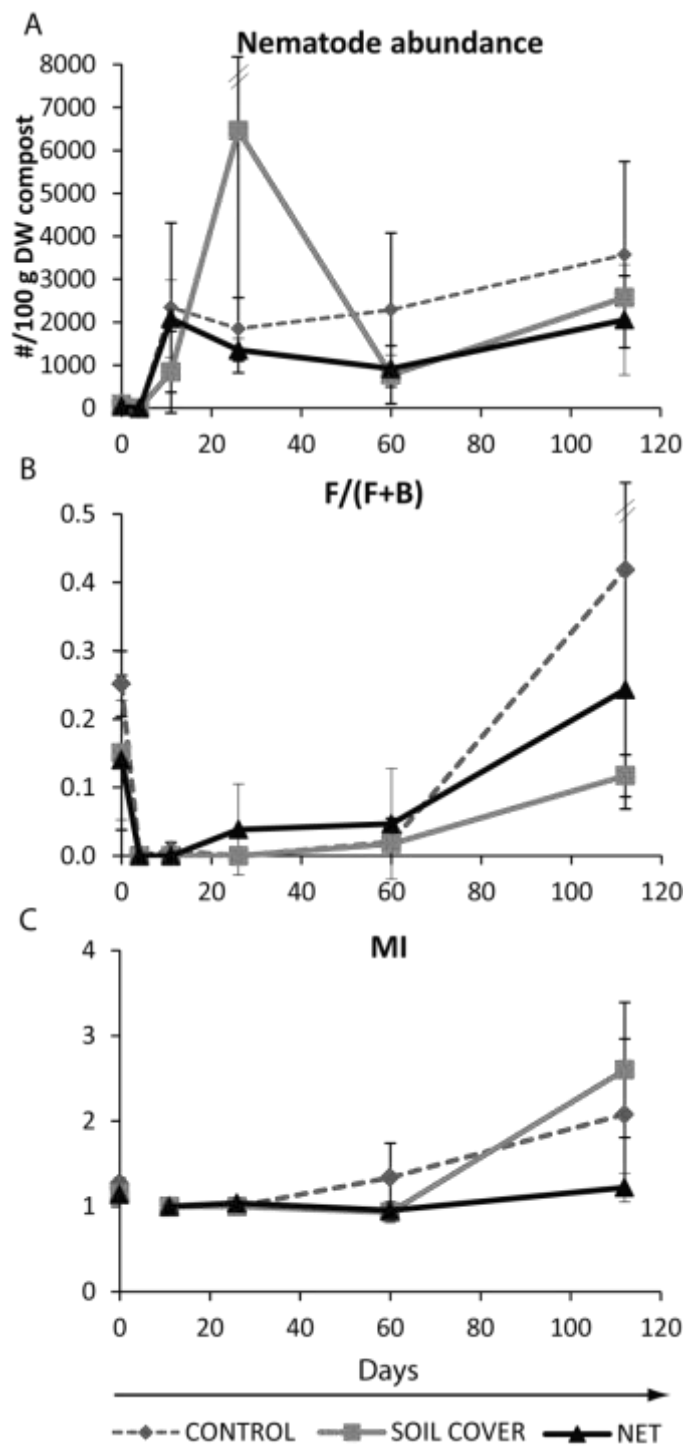
**Figure 5.4:**

The relative contributions of each nematode feeding type (bacterial-feeding, fungal-feeding, bacterial-feeding/predator and omnivores) at every sampling moment. Data are means of three replicates  $\pm$  SD. Mean temperature ( $^{\circ}$ C) at the time of sampling is indicated on the second Y-axis as a line.



**Figure 5.5:**

Hierarchical clustering of all nematode samples of all treatments, using group-average linking of Bray-Curtis similarities calculated on square-root transformed abundance data. The B cluster consists of samples of day 60 and 112 while the A and C cluster consist of earlier samples of days 0-26 (except for day 4 when nematodes were absent). In the labels of the samples “Con” refers to samples from the control group where no special manipulations were made to the compost barrel, “Plast” refers to samples from the soil cover treatment where the barrels were covered from the soil with plastic canvas, while “Net” refers to the net treatment samples where barrels were protected with a mosquito net and covered from soil with plastic canvas.



**Figure 5.6:**

Overview per treatment (control, soil cover and net) of (A) total nematode abundance (#/100 g DW compost) during composting and the nematode based indices: (B) F/F+B ratio based on the fungal- and bacterial-feeding (*s.s.*) densities, (C) Maturity Index (MI) based on the allocation of nematode taxa to cp-groups. In (C) MI could not be calculated for day 4 because of the absence of nematodes at this time. Values are means  $\pm$  SD based on three replicates.

**Table 5.1:**

Overview of the mean species abundance during the different composting phases, i.e. in the feedstock mixture (day 0), during cooling (day 11 + 26) and during maturation (day 60 +1 1). During the heat peak (day 4) no nematodes were found and therefore this phase is not included in the table. Data are means per composting phase  $\pm$  SD.

	Start (Day 0)			Cooling (Day 11 + 26)			Maturation (Day 60 + 112)		
	control	soil cover	net	control	soil cover	net	control	soil cover	net
<i>Acrostichus</i> sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	43 $\pm$ 53	160 $\pm$ 392	0 $\pm$ 0	160 $\pm$ 263	70 $\pm$ 96	25 $\pm$ 37
<i>Aphelenchoides</i> sp.	8 $\pm$ 5	6 $\pm$ 5	5 $\pm$ 4	13 $\pm$ 32	0 $\pm$ 0	20 $\pm$ 50	391 $\pm$ 446	75 $\pm$ 84	169 $\pm$ 214
<i>Bunonema</i> sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	10 $\pm$ 24	11 $\pm$ 19
Cephalobidae sp.	1 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0
Diplogasteridae juv.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	71 $\pm$ 173	1699 $\pm$ 3469	127 $\pm$ 311	0 $\pm$ 0	5 $\pm$ 12	38 $\pm$ 48
<i>Diploscapter</i> sp.	0 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	1321 $\pm$ 1540	391 $\pm$ 453	747 $\pm$ 890
<i>Ektaphelenchoides</i> sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	59 $\pm$ 144	37 $\pm$ 66
<i>Halicephalobus</i> sp.	0 $\pm$ 1	0 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	132 $\pm$ 234	10 $\pm$ 23	155 $\pm$ 179	181 $\pm$ 210	177 $\pm$ 98
<i>Mononchoides</i> sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	62 $\pm$ 74	52 $\pm$ 113
Neodiplogasteridae sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	91 $\pm$ 130	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0
Neotylenchidae sp.	1 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	10 $\pm$ 24	0 $\pm$ 0
<i>Nygolaimoides</i> sp.	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	380 $\pm$ 438	513 $\pm$ 691	0 $\pm$ 0
<i>Panagrolaimus</i> sp.	4 $\pm$ 4	24 $\pm$ 23	15 $\pm$ 14	13 $\pm$ 32	2 $\pm$ 5	61 $\pm$ 115	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0
<i>Pelodera</i> sp.	8 $\pm$ 6	21 $\pm$ 32	10 $\pm$ 6	952 $\pm$ 992	342 $\pm$ 553	411 $\pm$ 260	66 $\pm$ 103	49 $\pm$ 94	12 $\pm$ 28
Plectidae juv.	0 $\pm$ 0	0 $\pm$ 0	1 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0
<i>Prismatolaimus</i> sp.	0 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0
Rhabditidae	9 $\pm$ 3	35 $\pm$ 37	7 $\pm$ 3	881 $\pm$ 555	231 $\pm$ 524	1090 $\pm$ 703	380 $\pm$ 323	73 $\pm$ 92	220 $\pm$ 137
Rhabditidae sp. 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	17 $\pm$ 41	1084 $\pm$ 2206	0 $\pm$ 0	78 $\pm$ 121	169 $\pm$ 183	0 $\pm$ 0
Tylenchidae sp.	0 $\pm$ 0	0 $\pm$ 1	0 $\pm$ 1	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	0 $\pm$ 0	10 $\pm$ 24	0 $\pm$ 0

#### 5.4.2 Nematode survival

None of the tested species recovered from a 24 h temperature increase to 50 or 65 °C within 4 weeks (experiment 1). After the temperature increase to 40 °C only *Halicephalobus* cfr. *gingivalis* and *Procephalobus* sp. could be retrieved. However, when compost samples of day 0, comprising *Panagrolaimus* sp., *Aphelenchoides* sp., Tylenchidae sp. and Rhabditidae sp. (juveniles and dauer stages), were exposed to an experimental temperature peak (up to 60 °C), *Panagrolaimus* sp., *Aphelenchoides* sp. and Rhabditidae sp.1 were able to survive in respectively all, 5 and 5 out of 6 replicates. Hence, only Tylenchidae sp. did not survive the heating up to 60° of compost samples.

#### 5.4.3 Insect phoresy

After 48 hours, transfer of nematodes from donor to receptor plate (Figure 5.2) was observed for *Halicephalobus* cfr. *gingivalis*, *Diploscapter coronatus*, *Poikilolaimus* sp. (only second replicate), *Diplogasteritus* sp. and *Acrostichus* sp. Phoresy of *Mesorhabditis* sp. was first observed after 72 hours. *Poikilolaimus* sp. were never observed on the receptor plate in the first replicate, nor were any nematodes in both control experiments. For each species, the potential of phoresy was scored, based on the total number of transferred nematodes (T1 + T2 + T3), relative to the mean density of that species on the donor plate (Table 5.2). The successful

transportations of *Halicephalobus* cfr. *gingivalis* (in both replicates) and of *Mesorhabditis* sp. and *Poikilolaimus* sp. (in the second replicate) by the flies exceeded that of the other species by a factor 10 (except for *Diploscapter* sp. and *Diplogasteritus* sp. in the first replicate). Our observations indicated transfer by the flies of both adults and juveniles, except for *Diploscapter coronatus* and *Acrostichus* sp. where only juveniles were transported.

**Table 5.2:**

Table representing the potential of phoresy for tested compost nematodes by *Calliphora vomitoria* (blue bottle fly) for the first replicate (R 1) and the second replicate (R 2). Transport by the flies was observed with the highest success rate for *Halicephalobus* cfr. *gingivalis*, *Poikilolaimus* sp. and *Mesorhabditis* sp. (in respectively both, R 2 and R 2) and also for *Mesorhabditis* sp., *Diploscapter coronatus*, *Diplogasteritus* sp. and *Acrostichus* sp. but never for *Poikilolaimus* sp. in the first replicate. In the two control treatments no nematodes were found on the receptor plates.

		R 1	R 2
<b>Controls</b>	Control 1	-	-
	Control 2	-	-
<b>Panagrolaimidae</b>	<i>Halicephalobus</i> cfr. <i>gingivalis</i>	++	++
<b>Rhabditidae</b>	<i>Mesorhabditis</i> sp.	+	++
	<i>Diploscapter coronatus</i>	+	+
	<i>Poikilolaimus</i> sp.	-	++
<b>Diplogasteridae</b>	<i>Diplogasteritus</i> sp.	+	+
	<i>Acrostichus</i> sp.	+	+
++ ≥ 1% transferred			
+ ≤ 0.5% transferred			
- no transfer			

## 5.5 DISCUSSION

The treatments with different possibilities for compost colonization had a limited effect on the overall nematode succession patterns. For some specific taxa, however, the soil cover and/or net treatment produced an effect, sometimes as a delayed colonization, i.e. taxa arrived later than in the control treatment. Some caution is due when interpreting these relatively minor differences between treatments. For instance, we noted very slight damages to the insect nets near the end of the experiment, so we cannot completely exclude that some small Diptera could have been able to enter the net treatment in the later stages of the experiment. Also, some insect eggs or larvae could have been present in the feedstock material at  $T_0$  and could have potentially contained and later released nematodes.

In spite of these small treatment differences, the overall nematode succession in all 9 barrels was remarkably comparable with that of previous studies focusing on considerably larger-scale outdoor composting processes with greatly different feedstock materials (Chapter 2, 4 and 6). However, in these former studies, the bacterial-feeding/predators were more prominently present in the early cooling phase, which was less pronounced in the control of the present experiment and delayed in the soil cover and net treatment (Figure 5.4). The recurrence of the nematode succession is a strong indication that the described nematode patterns are universal for compost, and are relatively independent of the environmental conditions of the composting process, since covering or closing from insects or soil has very little effect. The scale of composting, which was more than 10-fold smaller in the barrels compared to the large-scale processes of the previous studies, also did not really affect this typical nematode succession. In addition, feedstock composition did not show a pronounced effect on the nematode community in mature compost (Chapter 7), and the nematode succession was not influenced by the season of composting since processes were run from spring to summer in this study compared to in autumn-winter in chapter 2 and 4.

Nevertheless, in spite of the generally very similar nematode communities between treatments, differences were observed. These include complete absence of *Nygolaimoides* sp. and Rhabditidae sp.1, and, albeit only temporarily, of *Acrostichus* sp. (i.e. present in control and soil cover treatment for day 26-112 but only in net on day 66) in the net treatment, and of Neodiplogasteridae sp. in the soil cover and net treatment. The dorylaim *Nygolaimoides* sp. was found in consecutive samplings (i.e. day 60 and 112) in the control setup and in the three replicates of only the last time point (i.e. day 112) in the soil cover setup. In previous composting processes (Chapter 2, 4 and 6) dorylaims were only sporadically found. They are typical K-strategists and tend to be very sensitive to different types of disturbances (Bongers 1999). Here,



in the dynamic composting environment, they made up an important part of the community, between 4-32 and 24-61% respectively, during the second half of our experiment. *Nygolaimoides* sp. thus survived and reproduced in the compost environment, and their absence from the net treatment indicates that they are transported by (flying) arthropods. To the best of our knowledge, the only previous report of a dorylaim with a phoretic relationship with an arthropod vector is that of *Nygolaimoides borborphilus* transported by dung beetles (Sachs 1950) and Diptera (Chizhov 1996). Although dorylaims are highly abundant and diverse and have been suggested to play an important role in soil food webs (Peña-Santiago 2006; Khan and Kim 2007), their ecology has been far less studied compared to e.g. rhabditids, partly as a result of the difficulty at maintaining or culturing them under lab conditions. The absence of Neodiplogasteridae in both the net and the soil cover treatment indicates that also soil dwelling animals (e.g. a non-flying beetle) could be involved in nematode phoresy. For the diplogasterid *Acrostichus* sp., another taxon of which the colonization was temporarily retarded by the net treatment, we have demonstrated actual transport by an insect; albeit in this case a flying one. The experiments with *Calliphora vomitoria* confirmed that 5 out of 6 tested compost nematodes (i.e. *Halicephalobus* cfr. *gingivalis*, *Mesorhabditis* sp., *Diploscapter coronatus*, *Diplogasteritus* sp., *Acrostichus* sp.) were effectively able to reach a new habitat (i.e. culture plate) by hitching a ride on flies, with *Halicephalobus* cfr. *gingivalis* being the most efficient hiker. However, since colonization differences between our treatments could not be observed for *Halicephalobus* cfr. *gingivalis*, other dispersal mechanisms could also play a role. Our results are a confirmation that insect phoresy is widespread among opportunistic colonizers (Timper and Davies 2004; Bongers 1999) like diplogasterids (e.g. *Diplogaster corprophila* (Kiontke 1996), *Acrostichus rhynchophori* (Kanzaki et al. 2009b)), panagrolaimids (e.g. *Panagrellus leperisini* and *P. ludwigi* Massey 1974 in Stock and Nadler 2006) and rhabditids (e.g. several *Caenorhabditis* species (Sudhaus and Kiontke 1996), *Rhabditis stammeri* (Richter 1993) and *Poikilolaimus floridensis* (Kanzaki et al. 2009)). It is especially these groups that are prominently present during the composting process. Current study on a compost process demonstrated, based on both in vivo and in vitro experiments, that colonization by a relatively diverse nematode community is only a matter of weeks. Our experimental evidence thus indicates the potential of soil dwelling organisms such as nematodes to disperse over a relatively long distance in a very short time. This strongly endorses the ubiquity hypothesis for microscopic organisms, i.e. 'everything is everywhere, but the environment selects' (Fenchel and Finley 2004). This explains for instance the widespread distribution of some of the tested nematodes such as *Diploscapter coronatus*. This is also in agreement with Wardle et al. (2003) who stated, in the framework of island ecology, that the

physical distance of suitable habitats to sources of colonizing organisms is not an important factor for the structure of decomposer communities. In agreement with Kruitbos et al. (2009) our results demonstrated that nictation (i.e. waving behavior of nematodes) is not a prerequisite for phoresis, nematodes such as *Halicephalobus* cfr. *gingivalis* could be transported by the fly but did not nictate. However, in many cases the phoretic relation is much more complex as transport can be internal and external, passive or active, and very often associations between nematodes and insects are highly species-specific (e.g. Krishnan et al. 2010). Since phoretic relations between nematodes and insects are common in compost, and as it is considered an important evolutionary step towards parasitism (Dillman et al. 2012), compost might be the perfect habitat to find an undiscovered diversity of insect associated nematodes. Thus, as previously suggested for micro-organisms (Hoitink and Boehm 1999), compost might be used as an organic carrier for antagonists such as nematodes with bio-control properties.

Next to colonization of the compost by insects we have demonstrated that survival of nematodes during compost heat peaks is possible, even for temperature peaks up to 60°C. This is much higher than expected based solely on temperature limits of nematodes that are based on simple lab experiments. Since a lot of juveniles could be recovered directly after the induced heat peak, these nematodes may survive as dauer stages or eggs. The specific structure of compost material, including the presence of micro-niches, each with slightly different conditions, might provide a more protected environment compared to agar cultures, e.g., in maintaining adequate moisture levels at high temperatures. The precise mechanism responsible for nematode survival in compost, however, remains to be unraveled. For instance, controlling the moisture level in agar plates could indicate the importance of moisture in survival of compost nematodes. Both our field and lab experiment indicate that both *Aphelenchoides* sp. and *Panagrolaimus* sp. are able to survive higher temperatures in a compost environment, as they were present both before and immediately after the (induced) heat peak.

In conclusion, our results indicate that the rapidly changing nematode community in a compost process is the result of both differential survival and colonization capacities. For several taxa we could readily explain their presence in compost by evidence of survival of the heat peak (i.e. *Aphelenchoides* sp., *Panagrolaimus* sp. and Rhabditidae in general) or for colonization using insects as carriers (i.e. *Acrostichus* sp., Neodiplogasteridae sp., *Nygolaimoides* sp., Rhabditidae sp1.). Although no proof was found in the experiment with the compost barrels, the experiments with the blue bottle fly as possible carrier indicated that insects may also play an important role in the dispersal of *Diploscapter coronatus* and *Halicephalobus* cfr. *gingivalis*




whether it is to compost or to other habitats. However, the colonization of a compost process by several other taxa (Table 5.3) remains to be investigated.

**Table 5.3:**

Schematic overview of the nematode species during the composting process in the three treatments (C= control, SC= soil cover, N= net), with indication of experimental evidence for survival of the heat peak or colonization of the compost after the heat peak.

	Start Day 0			Cooling Day 11 + 26			Maturation Day 60 + 112			Evidence for survival	Evidence for colonization
	C	SC	N	C	SC	N	C	SC	N		
<i>Acrostichus</i> sp.											X
<i>Aphelenchoides</i> sp.										X	
<i>Bunonema</i> sp.											
Cephalobidae sp.											
Diplogasteridae juv.											
<i>Diploscapter</i> sp.											X*
<i>Ektaphelenchoides</i> sp.											X*
<i>Halicephalobus</i> sp.											X
<i>Mononchoides</i> sp.											X
Neodiplogasteridae sp.											
Neotylenchidae sp.											
<i>Nygolaimoides</i> sp.											X
<i>Panagrolaimus</i> sp.										X	
<i>Pelodera</i> sp.											
Plectidae juv.											
<i>Prismatolaimus</i> sp.											
Rhabditidae										X	
Rhabditidae sp. 1											X
Tylenchidae sp.											

\* only evidence for possible transport by the blue bottle fly but not from the experiment with the different treatments in the barrels

-  only in feedstock
-  both before and after heat peak
-  only after heat peak

## 5.6 SUPPLEMENTARY MATERIAL

**Table 5.S1**

Overview of the insect families that frequent the compost barrels during the course of the experiment. A distinction was made between insects caught with pitfalls and insects collected with sticky strips.

	pitfall	sticky strip
Acari	X	
Anisopodidae	X	
Anthicidae	X	
<i>Calliphora vicina</i>		X
Chironomidae	X	
Chrysomelidae	X	
Collembola	X	
Coccinellidae		X
Cynipidae	X	
Dolichopodidae		X
<i>Drosophila</i> sp.		X
Dytiscidae	X	X
Formicidae	X	
Hybotidae	X	
Ichneumonidae	X	X
<i>Monotoma picipes</i>	X	
Muscidae		X
Phoridae	X	
Psilidae	X	
Sarcophagidae		X
Scatopsidae	X	
Sciaridae	X	X
Sphaeroceridae	X	
Sphecidae		X
Staphylinidae	X	X
Syrphidae		X
Tenthredinidae		X
Coleoptera larvae	X	
Muscidae larvae	X	
Diptera larvae	X	
Stratiomyidae larvae	X	

**Table 5.S2**

Overview of the nematode taxa found in compost and their feeding type mainly based on Yeates et al. (1993)

<b>TAXA</b>	<b>Feeding type</b>
<i>Achrostichus</i> sp.	3
<i>Aphelenchoides</i> sp.	2
<i>Bunonema</i> sp.	3
<i>Butlerius</i> sp.	3-5a
<i>Cephaloboides</i> sp.	3
<i>Cephalobus</i> sp.	3
<i>Choriorhabditis</i> sp.	3
<i>Crusthorhabditis</i> sp.	3
<i>Cruznema</i> sp.	3
<i>Diplogaster</i> sp.	3-5a
<i>Diplogasteritus</i> sp.	3
<i>Diplogasteroides</i> sp.	3
<i>Diploscapter coronatus</i>	3
<i>Ditylenchus filimus</i>	2
<i>Ektaphelenchoides</i> sp.	/
<i>Eucephalobus</i> sp.	3
<i>Fictor</i> sp.	3-5a
<i>Filenchus</i> sp.	2
<i>Halicephalobus</i> cfr. <i>gingivalis</i>	3
<i>Mesorhabditis</i> sp.	3
<i>Mononchoides composticola</i>	3-5a
Neotylenchidae unidentified sp.	2
<i>Nygolaimoides</i> sp.	8
<i>Panagrellus</i> sp.	3
<i>Panagrolaimus labiatus</i> sp.	3
<i>Parasitorhabditis</i> sp.	3
<i>Pelodera cylindrica</i>	3
<i>Pelodera teres</i>	3
<i>Poikilolaimus</i> sp.	3
<i>Procephalobus</i> sp.	3
<i>Protorhabditis</i> sp.	3
<i>Rhabditella axei</i>	3
<i>Rhabditophanes cobbi</i>	3
<i>Seinura</i> sp.	5
<i>Teratorhabditis</i> sp.	3

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6. Factors influencing the nematode community during composting: comparison between experimental farm compost and industrial green waste compost

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Publication in preparation.

## 6.1 ABSTRACT

According to pilot studies, shifts in the nematode species composition, life strategies and feeding behavior occur during the composting process. Although these shifts appear to be fairly consistent and therefore most promising as a potential tool to assess compost maturity, they are hitherto only based on a limited number of mainly non-replicated observations. In this study we tested if the nematode community succession patterns are recurrent for similar but independent processes and assess the relation between the changes in the nematode community and potential important variables (i.e. temperature, duration of composting and the microbial community). Therefore the nematode and microbial community of three simultaneously running controlled farm composting processes were analyzed through time and compared with a single industrial green waste composting process. Persistent high temperatures in this standard industrial process resulted in very low nematode abundances and aberrant nematode succession patterns, including the virtual absence of a fungal-feeding population. The general patterns of the controlled and well balanced farm compost were largely similar to the previous studies, i.e. during and directly after the heat peaks bacterial-feeding enrichment opportunists are most important. Subsequently, the bacterial-feeding/predator community dominated and during maturation the fungal-feeding nematodes became more important. However, the timing of the nematode succession in the farm compost processes was different compared to previous studies, with a greater fluctuation of fungivorous/bacterivorous indices. This is likely due to the fact that temperature in these processes did not show a simple decrease with time as in the other studies. This, however, allowed us to better distinguish between the effect of time and temperature in a generalized linear mixed model. The nematode abundances were significantly related with temperature; the amount of fungal-feeding nematodes was significantly related with both duration of composting and temperature, and the F/F+B ratio was only significantly related with duration of composting. Addition of PLFA based data (i.e. fungal PLFA or PLFA based F/B ratio) as a variable in the appropriate models did not significantly add to the explanation of the observed data. As shown, the nematode succession in monitored compost processes follows a repeatable and predictable pattern and especially the nematode based F/F+B holds promise as a reliable indicator of compost maturity since it was not significantly affected by temperature fluctuations but mainly related with duration of composting.

## 6.2 INTRODUCTION

Composting is an aerobic, heat producing and controlled process in which microorganisms convert a mixed organic substrate into carbon dioxide (CO<sub>2</sub>), water, inorganic nutrients and stabilized organic matter. Compost can be used as a fertilizer (Cogger 2005; Zvomuya et al. 2008) and is also known as a suppressive agent against plant diseases (e.g. Akhtar and Malik 2000; Kuo et al. 2004). The taxa that are most important to the composting process are bacteria, algae, fungi, isopoda, acari, nematoda and protozoa (Cooperband 2000; Young et al. 2005). This wide spectrum of organisms forms a complex and rapidly changing community. Of all these taxa only nematodes (Chapter 2 and 4) and bacteria (Ryckeboer et al. 2003; Chapter 4) are ubiquitous in all stages of the compost process, making them the most important groups to analyze during the composting process. Furthermore the nematode community is considered to feed mainly on the microbial community and shows several advantages over the latter rendering nematodes more suitable bio-indicators of ecosystem processes and quality (Neher 2001). For example nematodes are more integrated in the food web by being one or two steps higher and their response to changes are more significant on a stable temporal scale because of their longer generation time.

According to pilot studies (Chapter 2 and 4) a shift in nematode species composition, life strategies and feeding behavior occurs during the composting process. At the beginning of the process, during the thermophilic phase, the nematode population is primarily built by bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae, Diplogasteridae), followed by the bacterial-feeding general opportunists (cp-2) (Cephalobidae) and the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, via a community with increasing numbers and dominance of bacterial-feeding/predators (Neodiplogasteridae mainly *Mononchoides composticola*) in the cooling phase, finally the fungal-feeding general opportunists (Anguinidae and Aphelenchoididae) become more important during the maturation phase. And this increasing proportion of fungal-feeding nematodes during the compost process was proposed as a potential indicator of compost maturity<sup>6</sup> (see Chapter 2 and 4). Compared to nematode community, the microbial community, as revealed by phospholipid fatty acids (PLFA), showed an earlier shift towards higher proportions of fungi during both cooling and maturation phases. The delay of fungal-feeding nematodes with respect to the microbial community was mainly ascribed to the dominance of the bacterial-feeding/predators during cooling and to the relatively long generation time of most fungal-feeding nematodes.

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<sup>6</sup> For more information on and definition of compost maturity see 1.3.

Although the nematode community shifts appear to be fairly consistent and most promising as a potential tool to assess compost maturity, these patterns are hitherto only based on a limited number of observations (single case non-replicated processes) and based on the same method of composting (i.e. on farm Controlled Microbial Composting (CMC), referred to as farm compost). More or less similar community patterns as in the large scale farm composting systems were observed in short term, small scale processes in compost barrels (Chapter 5). Furthermore, although it is suggested that these remarkable nematode composition shifts are related to processing time, compost temperature and/or microbial community (Chapter 2 and 4), a replicate design is warranted to have a better insight in the underlying factors that might be related with the changing nematode community in compost.

In this study, the nematode and microbial community of three simultaneously running controlled farm compost processes, with different proportions of feedstock materials, were analyzed through time. In addition, a single industrial green waste composting process was sampled on a limited number of time points. We aimed to: (1) clarify if the nematode community succession patterns are recurrent for similar but independent processes (2); assess the relation of nematode community changes, i.e. nematode abundances, number of fungal-feeding nematodes, and the F/F+B ratio, with potentially important variables, i.e. temperature, duration of composting and the microbial community, and (3) compare the nematode and microbial community of the experimental farm composts with commercial green waste compost.

## **6.3 MATERIALS AND METHODS**

### **6.3.1 Composting sites and sampling**

The three farm composts (using the CMC-method) were produced simultaneously in open air windrows on a concrete floor at the experimental farm of the Institute for Agricultural and Fisheries Research (ILVO at Merelbeke, Belgium). Three compost piles (50 m long, 3 m wide and 1.5 m high with 3 m<sup>3</sup> feedstock materials per lineal meter) were set up with different ratios of a) grass hay and straw of clover and b) ground poplar bark, i.e. 25/75% (vol/vol), 50/50% (vol/vol) and 75/25% (vol/vol), respectively. The amount of grass hay in the three compost piles was 0%, 23% and 46% (vol/vol), respectively. We will further refer to these composting processes as Farm 1, Farm 2 and Farm 3. Each composting process is monitored individually and management practices are only executed if on a given moment these practices are required for this particular process. In all three composts urea was added at the start to correct the C/N content of the

feedstock towards 30/1, which is generally considered an ideal starting ratio for composting (Zorpas 2009), and cane molasses plus spoiled ensilaged maize were mixed in the feedstock as a compost starter. The heaps were turned on day 3, 10 and on day 83, after which the heap was stored for maturation. The water content was managed by a combination of placing and removing the canvas cover depending on the precipitation and temperature forecast and by manually adding water (2000 L added to Farm 1 on day 10). Samples were taken from the feedstock (day 0) and on day 3, 7, 10, 17, 24, 35, 49, 63, 77, 105, 119, 133, 147, 175, 203. On each of these 16 consecutive sampling events, three composite samples were taken for each of the three compost processes.

The non-experimental industrial green waste compost was produced by the Inter-municipal Society of Public Health in Moen, Belgium. At this site, the integrated processing of household wastes takes place, of which the aerobic composting of green waste materials is an important part. Every year, about 30,000 ton green waste is processed into 'VLACO' labeled compost. This label is provided by the Flemish Compost Organization and guarantees high quality compost with a lot of nutrients, high levels of organic matter and absence of diseases and weeds. In contrast, with the CMC-method the green waste composting uses standardized procedures for all processes with predetermined time schedules for management practices and duration of the process. The used composting method consisted of 5 phases. During the first phase a mixture of available feedstock materials was made (in this case: 35% grass, 15% mixed green waste, 40% wood chips, 10% roots of trees). These materials ( $\pm 700 \text{ m}^3$ ,  $450 \text{ kg/m}^3$ ) were then placed into a long heap (50 m long, 8 m wide and 3 m high) and covered with a membrane for four weeks. Afterwards, the cover was removed, water was added (25,000 L) and the heap was turned mechanically (phase 2). Then the heap was covered again and turned after two weeks (phase 3). After this the heap was kept uncovered and turned with a three-week interval (phase 4) to mature. Finally the compost is sieved and the fraction  $< 15 \text{ mm}$  is sold as compost (phase 5). Sampling took place from the freshly mixed materials (day 0) and during every turning event in each phase (respectively on day 33, 39, 61 and 83). Per sampling event, three composite samples were taken.

Each composite sample consisted of 20 thoroughly mixed randomly chosen samples (50 ml each in the farm processes and 1 L each in the green waste process), and of this total volume (respectively 1 L and 20 L), a subsample of 400 ml was taken for nematode extraction. A mathematical justification of taking a subsample from a bulk sample to estimate nematode population densities is given by Been and Schomaker (2006). A part of the composite samples ( $\pm$

600 ml) were freeze dried (Christ, Gamma 1-20, Osterode am Harz, Germany), grinded and stored at -4 °C for carbon nitrogen and PLFA analyses.

### **6.3.2 Abiotic variables**

Temperature and CO<sub>2</sub> content of the farm composts were measured at 3 random locations in the heap using specialized equipment (respectively, Digital Thermometer GTH 1150 and Brigon Messtechnik D-63110 Rodgau). Temperature of the green waste compost was continuously measured at a depth of 50 cm using a 5 probe thermocouple (Thermibel, Belgium). At every sampling moment moisture content (%), pH and C/N ratio were measured in three replicates. Extractions of 20 g compost in 100 ml distilled water were shaken by hand three times every two hours and the pH was measured with standard electrodes (Consort P400, Turnhout, Belgium). The moisture content was calculated by determining the dry weight of 50 ml compost after incubation for 48 h at 120 °C. Total C and N contents were measured with a Variomax CNS element analyzer (Elementar GmbH, Hanau, Germany) applying the Dumas method (EN<sup>7</sup> 13654-2).

### **6.3.3 Nematode community analyses**

The nematode communities of all samples (day 0, 3, 7, 10, 17, 24, 35, 49, 63, 77, 105, 119, 133, 147, 175, 203) of the farm composts and all samples (day 0, 33, 39, 61, 83) of the industrial green waste compost were analyzed (see 4.3.3 in Chapter 4 for a detailed description).

### **6.3.4 Microbial community analyses**

Phospholipid fatty acids (PLFAs) were analyzed from all sampling days (except for days 119, 133 and 147) of the farm composts and from all sampling days of the industrial green waste compost (see 4.2.4 in Chapter 4 for a detailed description).

### **6.3.5 Statistical analysis**

Nematode density changes during the compost processes were analyzed using one-way ANOVA on double square root transformed data and subsequent post hoc Tukey HSD tests in Statistica 6.0 (Statsoft Inc.). Nematode community compositions during the farm processes were compared using non-metric Multi-Dimensional Scaling (nMDS) based on Bray-Curtis similarity matrices of square-root transformed abundance data (numbers/100 g dry weight compost) using Primer 6 (Clarke and Warwick 2001). A stepwise BIOENV procedure was run in Primer 6 to

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<sup>7</sup> EN: European Standard. European Standards are developed by CEN, the European Commission for Standardization. Numbers refer to the specific protocols.

select the best explaining abiotic variables (duration of composting, C/N ratio, pH, moisture content, CO<sub>2</sub>).

Total PLFA concentrations and the relative concentrations of the functional groups of the green waste compost (i.e. Gram-positive, Gram-negative, Fungi, total bacteria, AMF and Actinomycetes) were compared between sampling days using one-way ANOVA and subsequent post hoc Tukey HSD tests in Statistica 6.0. Changes in the concentrations of the marker fatty acids (mol%) in the farm composts were analyzed using Principal Component Analysis (PCA) in Primer 6. Since assumptions for one-way ANOVA of normality and homogeneity of variances could not be fulfilled, the functional group concentrations of Gram-positive and Gram-negative bacteria, fungi, AMF (Arbuscular Mycorrhizal Fungi) and Actinomycetes of the different composting phases (based on the shifts in the nematode community, indicative delineation of composting phases was performed, see 6.4.2) were compared using non-parametric Kruskal-Wallis and Mann-Whitney U pairwise tests in Statistica 6.0. with Bonferroni corrections ( $\alpha=0.013$ ).

The relationship between the explanatory variables and the nematode abundance or the absolute number of fungal-feeding nematodes or the proportion of fungal-feeding nematodes to the total number of fungal- plus bacterial-feeding nematodes was modeled by means of a generalized linear mixed model with a normal, Poisson and binomial distributed error, respectively. The explanatory variables were temperature, the amount of fungal PLFA, day and a quadratic day effect to account for a possible non-linear relationship between the dependent variable and time. Given that the time intervals at which nematode numbers were assessed were shorter at the beginning of the experiment, variable day was log transformed before analysis. As nematode densities were measured repeatedly on each of the three farm compost heaps, we also accounted for temporal autocorrelation in all models by fitting a first order autoregressive variance structure to the residual errors. Compost heap was further included as a random effect. Degrees of freedom were adjusted by means of the Kenward-Roger approximation. Models with the absolute number of fungal- feeding nematodes or the proportion of fungal-feeding nematodes to the total number of fungal- plus bacterial- feeding response variables were fitted by means of the GLIMMIX procedure and the model with nematode abundance as response variable was fitted to the log transformed values by means of the MIXED procedure in SAS v.9.3. (SAS Institute Inc., Cary, NC, USA).

## 6.4 RESULTS

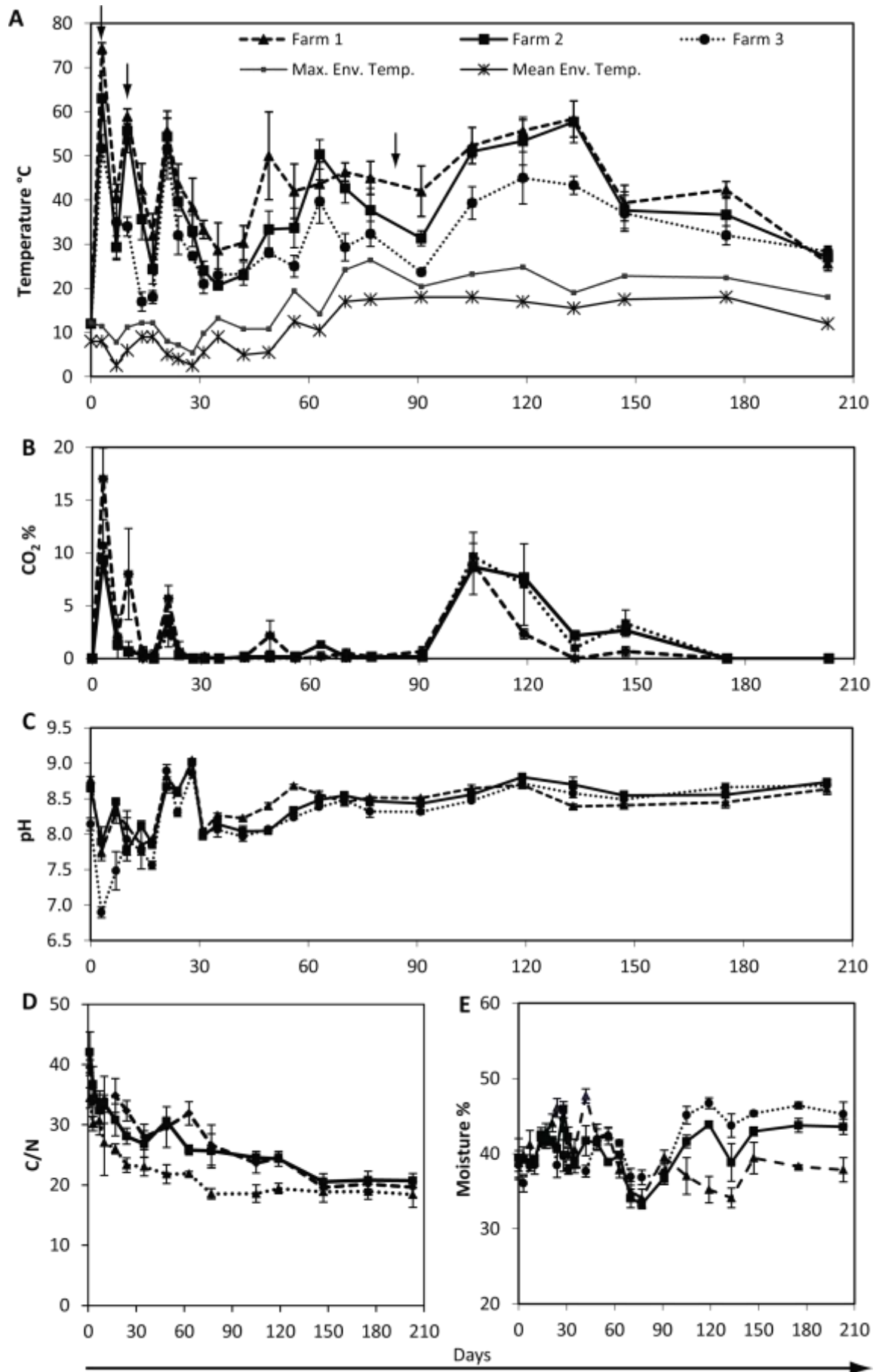
### 6.4.1 Abiotic variables

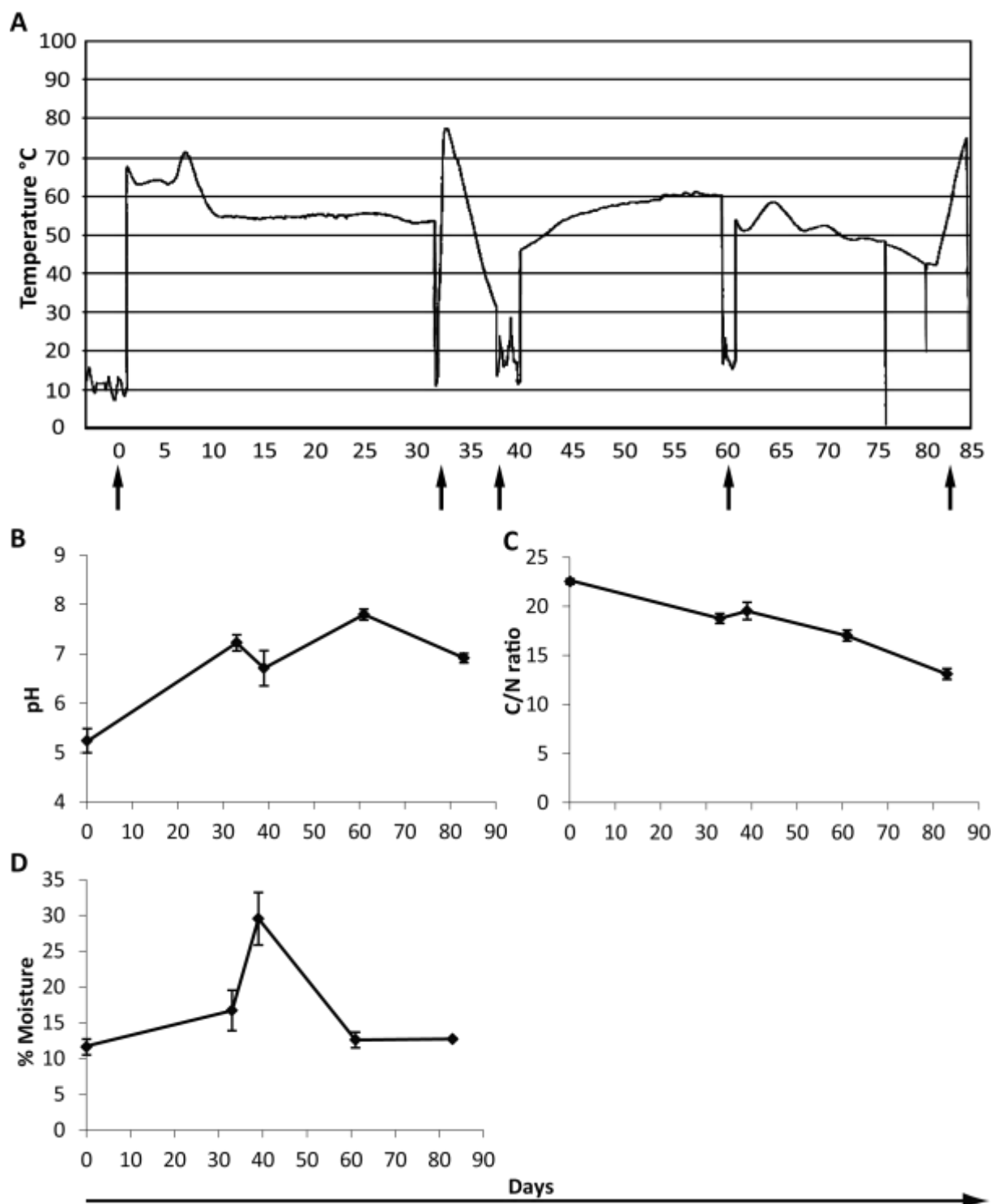
The abiotic variables of Farm 1, Farm 2 and Farm 3 exhibited very similar trends with time (Figure 6.1). Given the considerable temperature fluctuations the compost process cannot be categorized in the typical temperature related compost phases, i.e. thermophilic, cooling and maturation, as described in Chapters 2 and 4. However, since temperature did not simply decrease with time, a differentiation between the temperature and the time effect on the nematode community was still possible (see 6.2.5). The processes started with characteristic heat peaks where temperatures reached up to  $75 \pm 1.3$  °C in Farm 1,  $63 \pm 5.1$  °C in Farm 2 and  $52 \pm 3.1$  in Farm 3 (Figure 6.1A). The turning of the compost heaps on day 10 caused a temporary temperature drop (arrow in Figure 6.1A). Afterwards, from day 24 - 62, the temperatures decreased ( $< 40$  °C), increased (up to 50, 35 and 30 °C in farm 1, 2 and 3 respectively) and decreased again. From day 91 a distinct gradual increase of temperatures was observed, with maxima on day 119 - 133. These maxima (i.e.  $58 \pm 4.1$ ,  $58 \pm 4.7$  and  $43 \pm 2.1$  °C in Farm 1-3, respectively) were only slightly lower than the maxima during the primary heat peaks. The increased temperatures coincided with a period of increased carbon dioxide (CO<sub>2</sub>) production (Figure 6.1B). From day 133 - 203 the temperatures gradually decreased to near ambient levels. The pH fluctuated during the first month with maximum levels (8.8-9) on day 28. Afterwards the pH first decreased and then increased again to remain more or less constant (Figure 6.1C). The C/N ratio gradually decreased with time from 35-40 to approximately 20 on day 105 and afterwards remained stable (Figure 6.1D). The moisture content was always higher than 30% but never exceeded 47% (Figure 6.1E).

In the green waste compost process no heat peaks could be distinguished because temperatures were always very high (between 50 and 80 °C), except for the short periods of time after the heap was turned when temperatures reached more or less ambient levels (arrows in Figure 6.2A). The pH increased from  $5.3 \pm 0.24$  to levels between  $6.7 \pm 0.36$  and  $7.8 \pm 0.11$  (Figure 6.2B). The C/N ratio gradually decreased from  $22.5 \pm 0.27$  to  $13.1 \pm 0.56$  (Figure 6.2C) and the moisture content hardly exceeded 10% except for day 33 when water was added and the moisture content increased to 30%.

**Figure 6.1:** Abiotic variables measured during the three farm composting processes (Farm 1, Farm 2 and Farm 3) including: (A) Temperature of the compost (°C) and mean and maximum ambient temperatures (°C) per day (24h), (B) CO<sub>2</sub> content (%), (C) pH values, (D) C/N ratio, (E) moisture content (%). Error bars indicate SD based on three replicates. Arrows indicate turning events of the heaps.





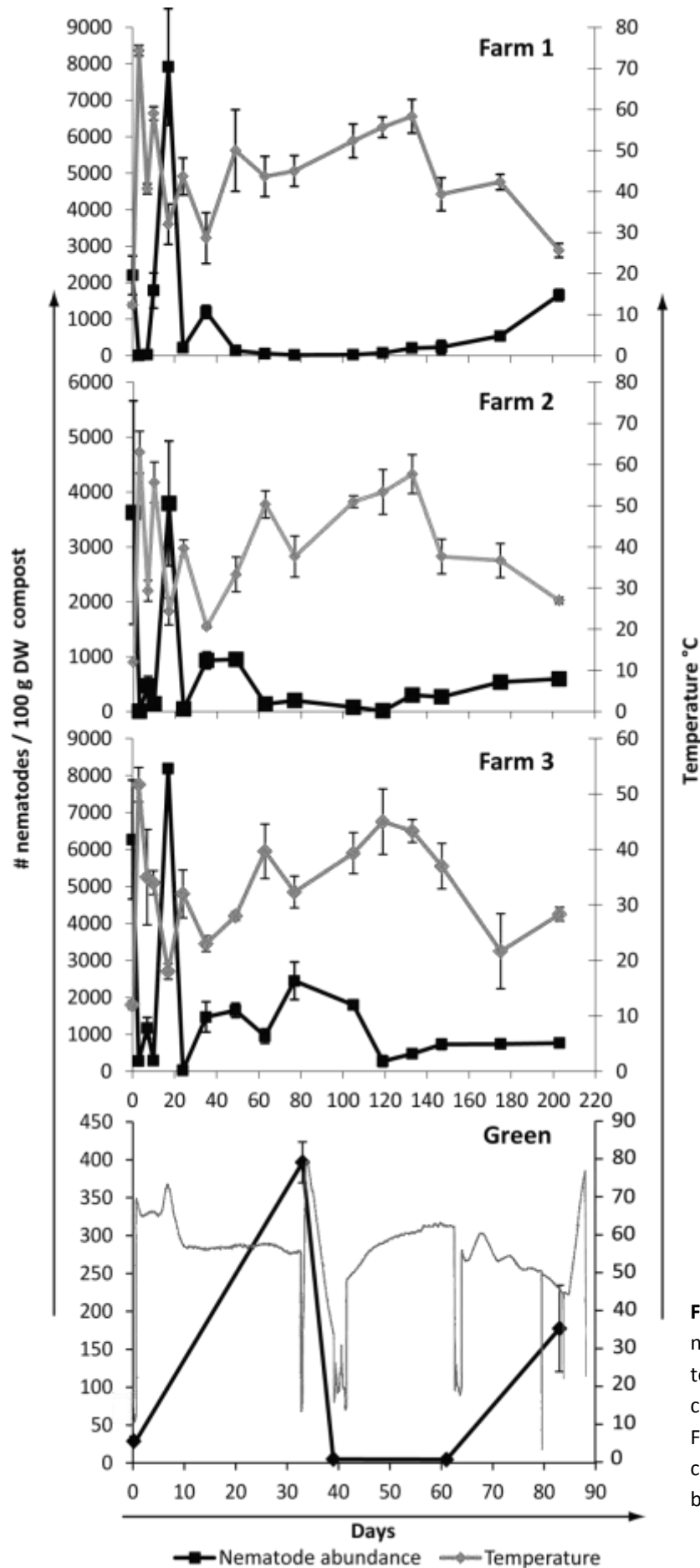


**Figure 6.2:** Abiotic variables measured during the green waste composting processes including: (A) Temperature of the compost (°C), arrows indicating turning and sampling events, (B) pH values, (C) C/N ratio, (D) moisture content (%). Error bars indicate SD based on three replicates.

### 6.4.2 Nematode community

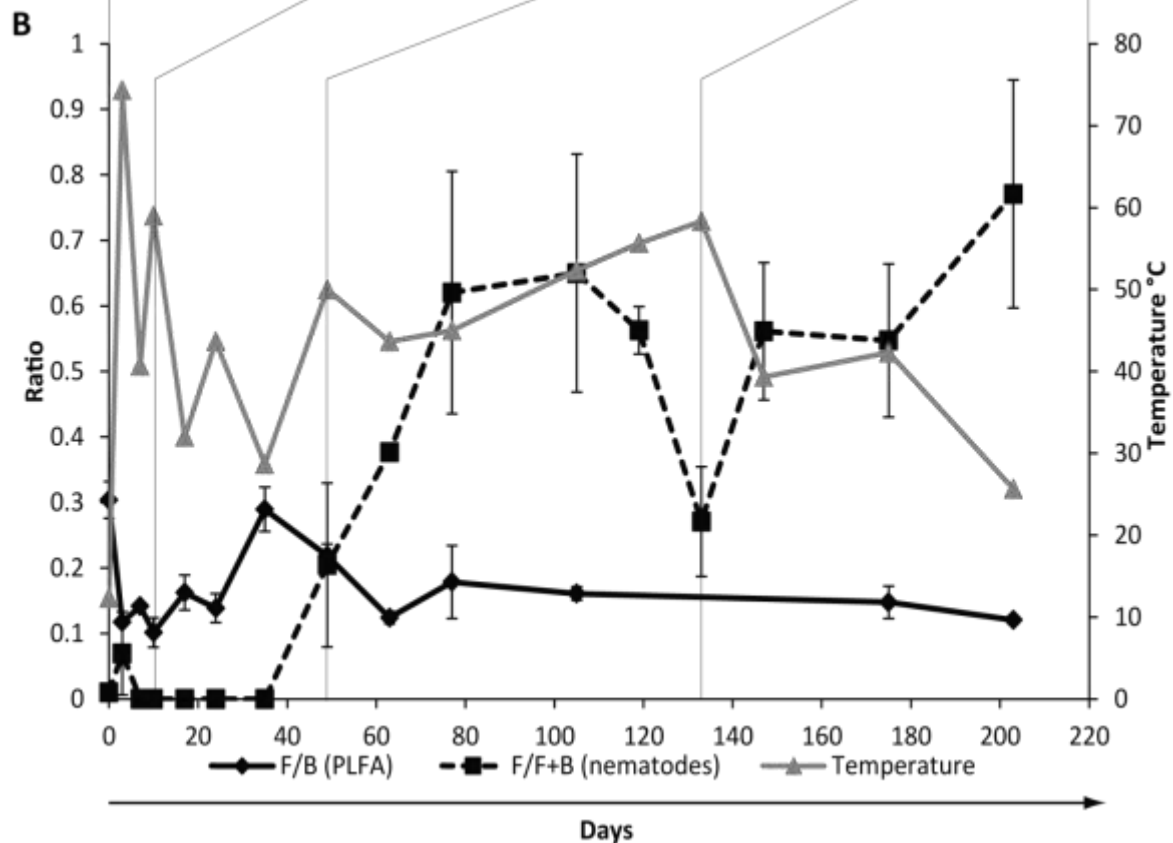
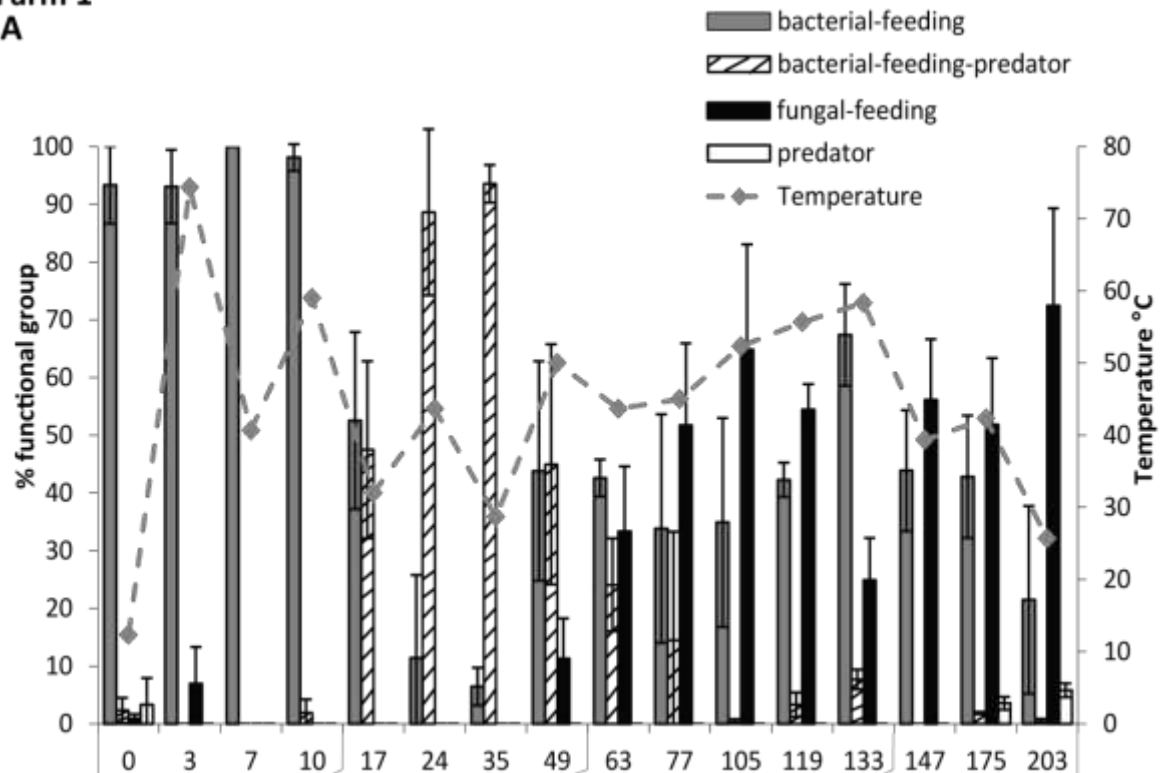
In the farm compost processes nematode numbers sharply increased on day 17, shortly after turning the heaps when the temperature dropped ( i.e.  $7920 \pm 1603$ ,  $3792 \pm 1137$  and  $9575 \pm 2407$  nematodes/100 g DW compost in Farm 1, Farm 2 and Farm 3, respectively) (Figure 6.3 and Table 6.1). Also in the continuation of the process the nematode densities were virtually inversely related with temperature: when the latter increased the nematode densities decreased and *vice versa*. Around 40 °C appeared to be the threshold for nematode densities to decrease or increase. For nearly all sampling moments above 40 °C, nematode densities were significantly lower except for day 7 where both low nematode abundance and low temperature were measured. The nematode abundances were significantly negatively related with temperature ( $p < 0.001$ ) but not with duration of composting (day) (MIXED procedure in SAS).

Thirty-one genera belonging to 14 families were identified from the farm processes (see also Supplementary Tables 6.S1, 6.S2, 6.S3), the most common taxa being *Aphelenchoides* sp., *Mononchoides composticola*, *Poikilolaimus* sp., *Pelodera* sp. and *Halicephalobus* cfr. *gingivalis*. Remarkably similar patterns were present in the three farm processes (Farm 1: Figure 6.4A, Farm 2: Figure 6.5A, Farm 3: Figure 6.6A). During days 0 - 10, the bacterial-feeding enrichment opportunists (cp-1) dominated the nematode community. The most prominent species in this phase were *Rhabditella axei*, *Pelodera teres*, *Pelodera cylindrica* and *Poikilolaimus* sp., including a high number of Rhabditidae that were found in dauer phase. Afterwards, from day 17 - 49, the bacterial-feeding/predators (*Mononchoides composticola*) became dominant, although this dominance was less pronounced for Farm 3, especially for day 24 where their proportion accounted only for  $7 \pm 4.1\%$ . The proportion of fungal-feeding nematodes, especially *Aphelenchoides* sp., increased from day 49 but decreased again with persistent high temperatures. Around day 119 the nematode community in farm 1 and 2 again changed towards a dominance of bacterial-feeding enrichment opportunists (mainly *Poikilolaimus* sp.). From day 147 to day 203 the relative share of the fungal-feeding nematodes increased again, including other taxa than *Aphelenchoides* sp., such as *Ditylenchus* sp., Neotylenchidae spp. and Tylenchidae spp. (cp-2). Other general opportunists, such as *Eucephalobus* sp. (bacterial-feeding) and *Seinura* sp. (predator)(in Farm 1 and 2), also became numerically more important during this phase. The F/F+B ratio (Figure 6.4B, 6.5B and 6.6B; Table 6.1) and the MI (Table 6.2) index values generally increased during the process but with considerable fluctuations.



**Figure 6.3:** Nematode abundances (# nematodes/100 g DW compost) and temperature (°C) during the three farm composting processes (Farm 1, Farm 2 and Farm 3) and during the green waste composting (Green). Error bars indicate SD based on three replicates.

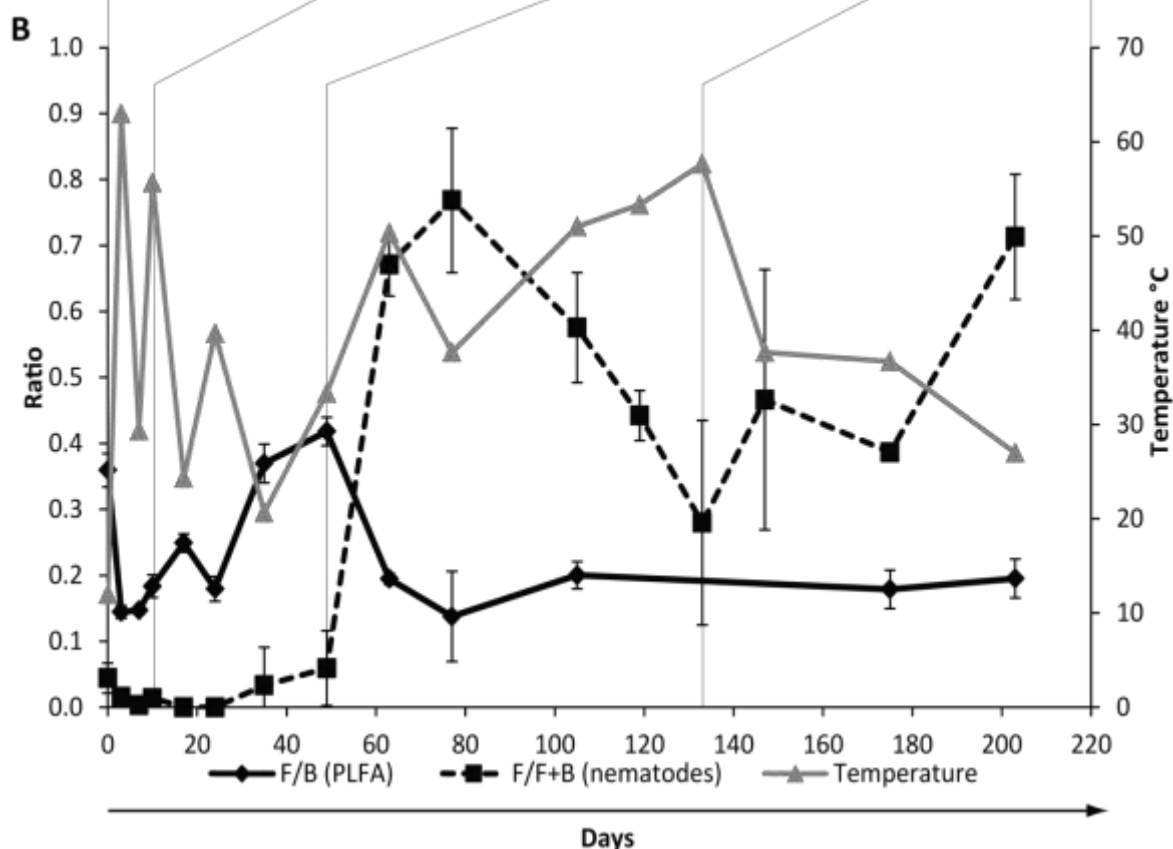
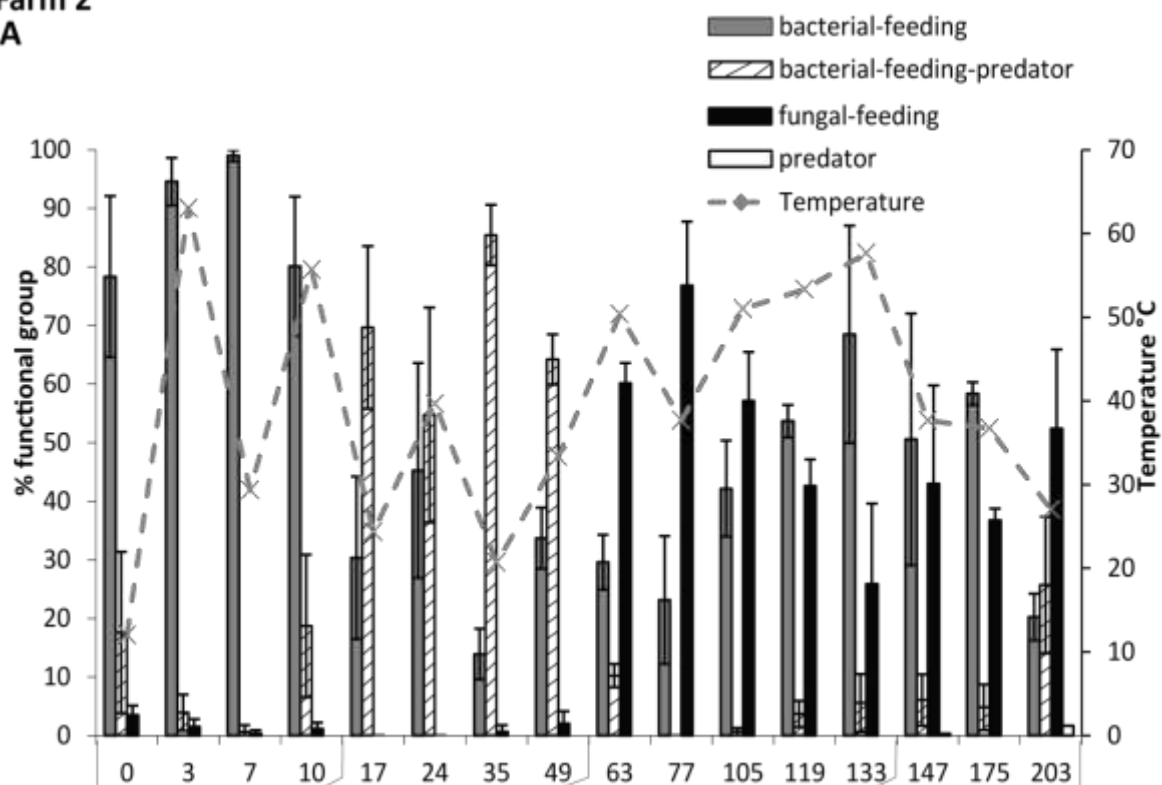
**Farm 1**  
**A**



**Figure 6.4:** Farm 1. (A) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator) at every sampling moment. Omnivores (low in abundance) are not represented in the graph. (B) F/B ratio based on fungal and bacterial PLFAs and F/F+B ratio based on the fungal- and bacterial-feeding nematode densities. Standard deviations are indicated as error bars. Vertical lines represent phases which were indicatively delineated based on key-point changes in the nematode community.

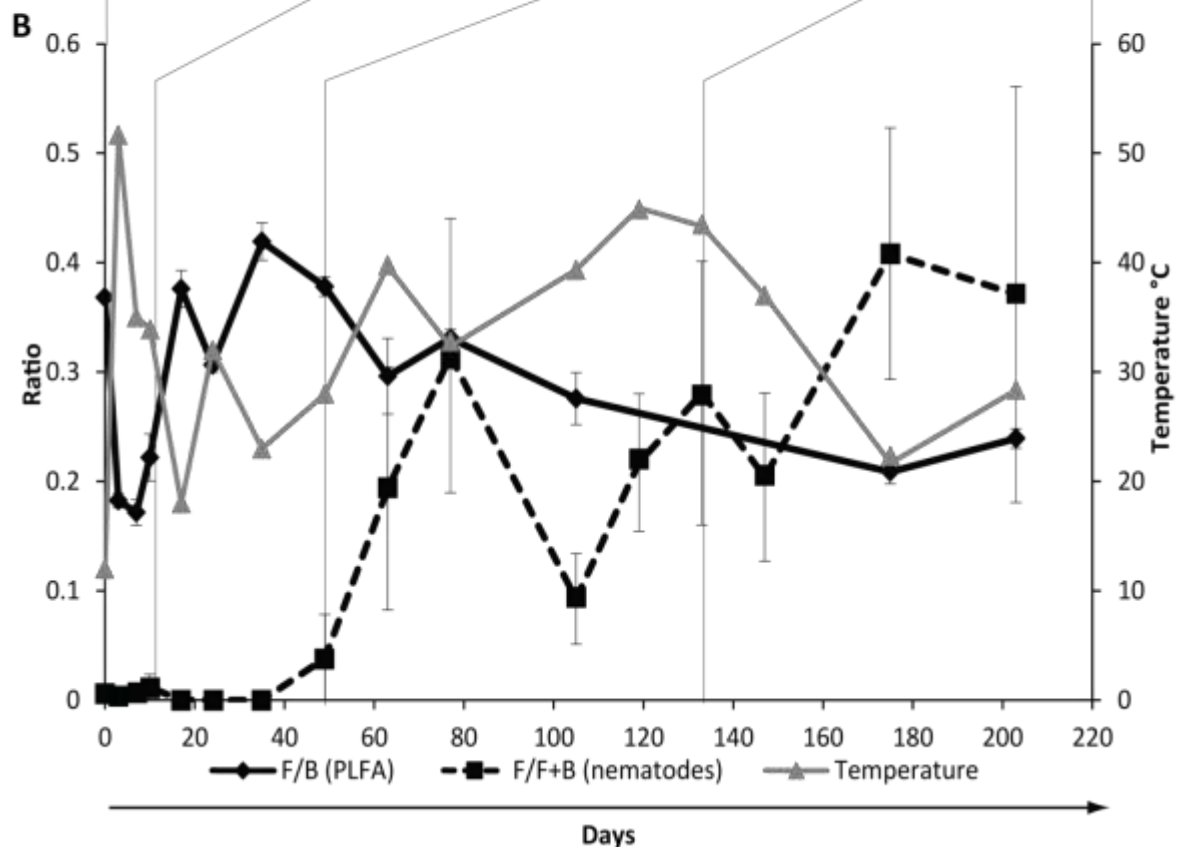
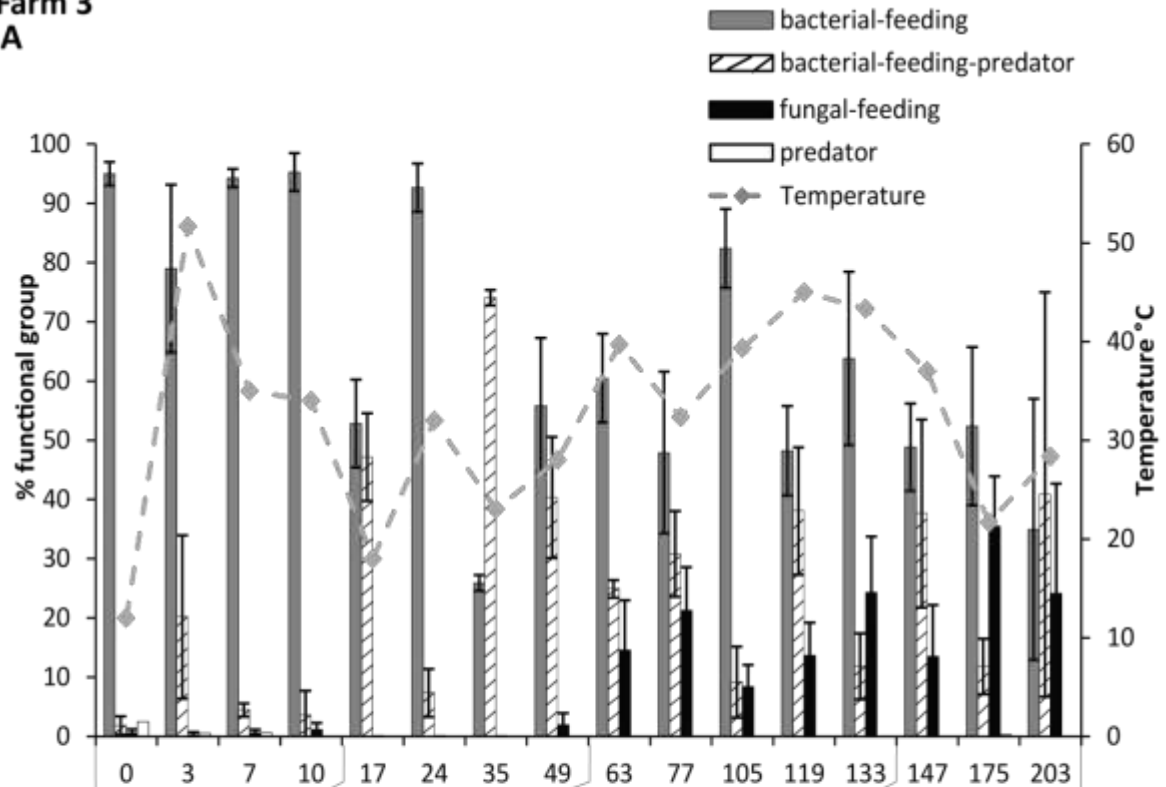
## Farm 2

### A



**Figure 6.5:** Farm 2. (A) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator) at every sampling moment. Omnivores (low in abundance) are not represented in the graph. (B) F/B ratio based on fungal and bacterial PLFAs and F/F+B ratio based on the fungal- and bacterial-feeding nematode densities. Standard deviations are indicated as error bars. Vertical lines represent phases which were indicatively delineated based on key-point changes in the nematode community.

**Farm 3**  
**A**

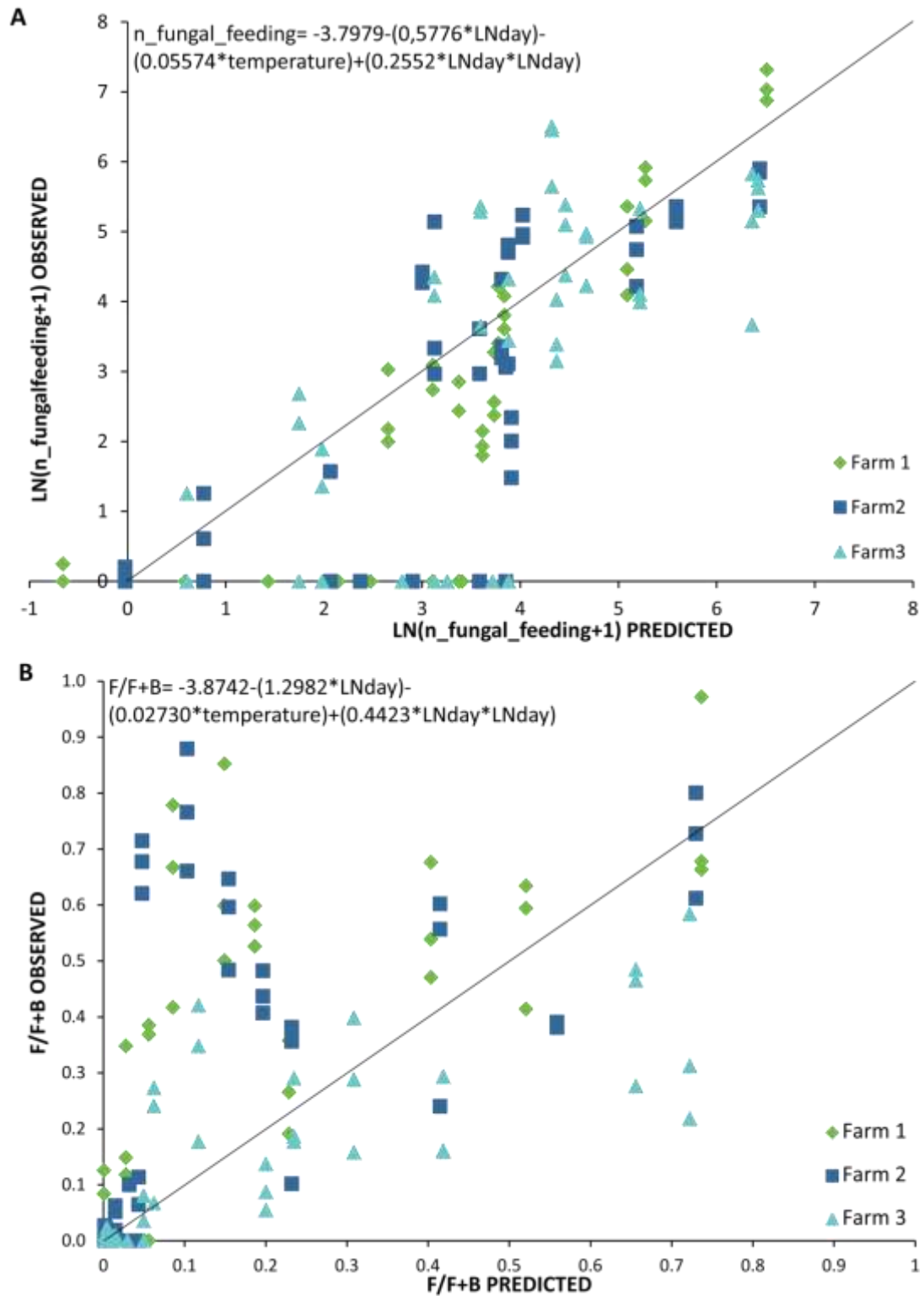


**Figure 6.6:** Farm 3. (A) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator) at every sampling moment. Omnivores (low in abundance) are not represented in the graph. (B) F/B ratio based on fungal and bacterial PLFAs and F/F+B ratio based on the fungal- and bacterial-feeding nematode. Standard deviations are indicated as error bars. Vertical lines represent phases which were indicatively delineated based on key-point changes in the nematode community.

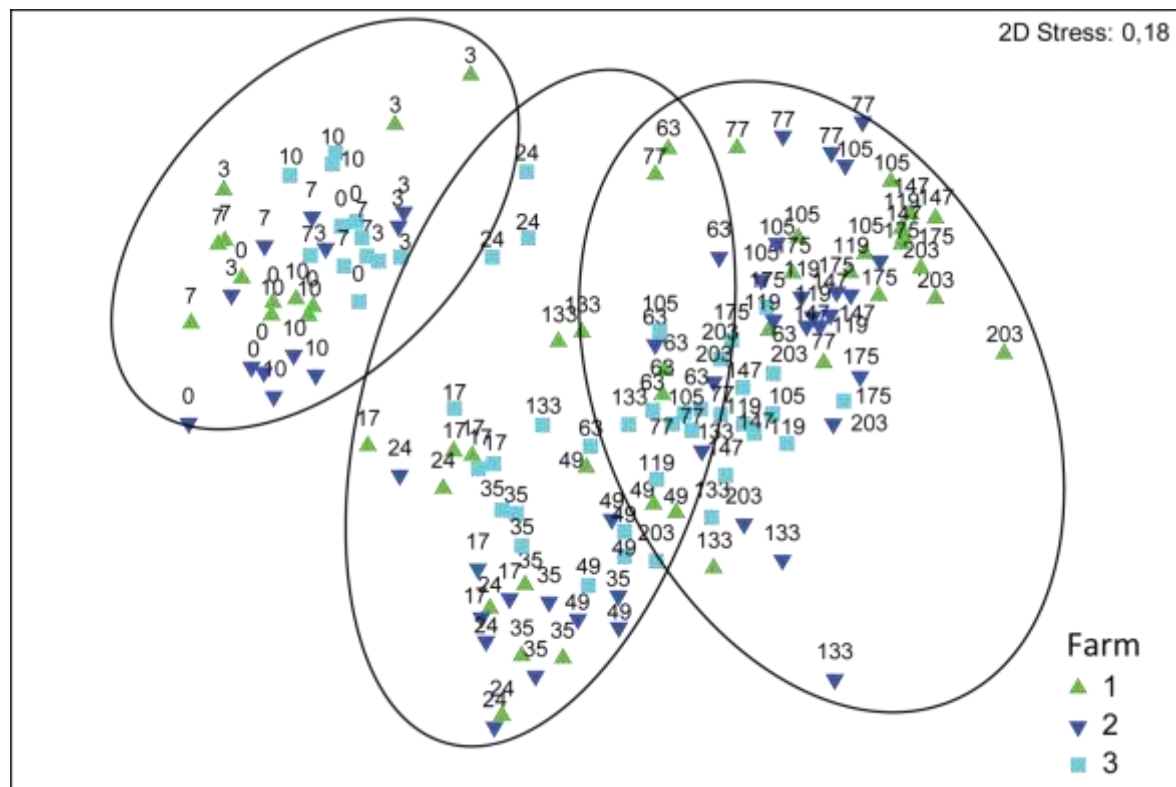
The absolute number of fungal-feeding nematodes was significantly negatively related with temperature ( $p=0.001$ ) and positively with duration of composting (day) (quadratic effect of time, GLIMMIX procedure in SAS,  $p=0.029$ ). Plotting the predicted against the observed number of fungal-feeding nematodes revealed that both variables explained the number of fungal-feeding nematodes fairly well (Figure 6.7A). In the samples dominated by the bacterial-feeding/predators (day 17-35), none or very few fungal-feeding nematodes were found while the model predicted higher numbers. The ratio F/F+B was also strongly positively related with duration of composting (quadratic day effect  $p<0.001$ , day effect  $p=0.029$ ) but not with temperature (GLIMMIX procedure in SAS). Figure 6.7B displays the observed F/F+B ratio against the predicted F/F+B ratio based on the estimated model parameters.

The nMDS of the farm composts clearly confirms that the nematode communities were primarily grouped according to duration of composting rather than to the compost process (i.e. Farm 1, Farm 2 and Farm 3) they originated from (Figure 6.8). The species composition in the compost was best explained by a combination of duration of composting and C/N ratio ( $r= 0.53$ , stepwise BIOENV).





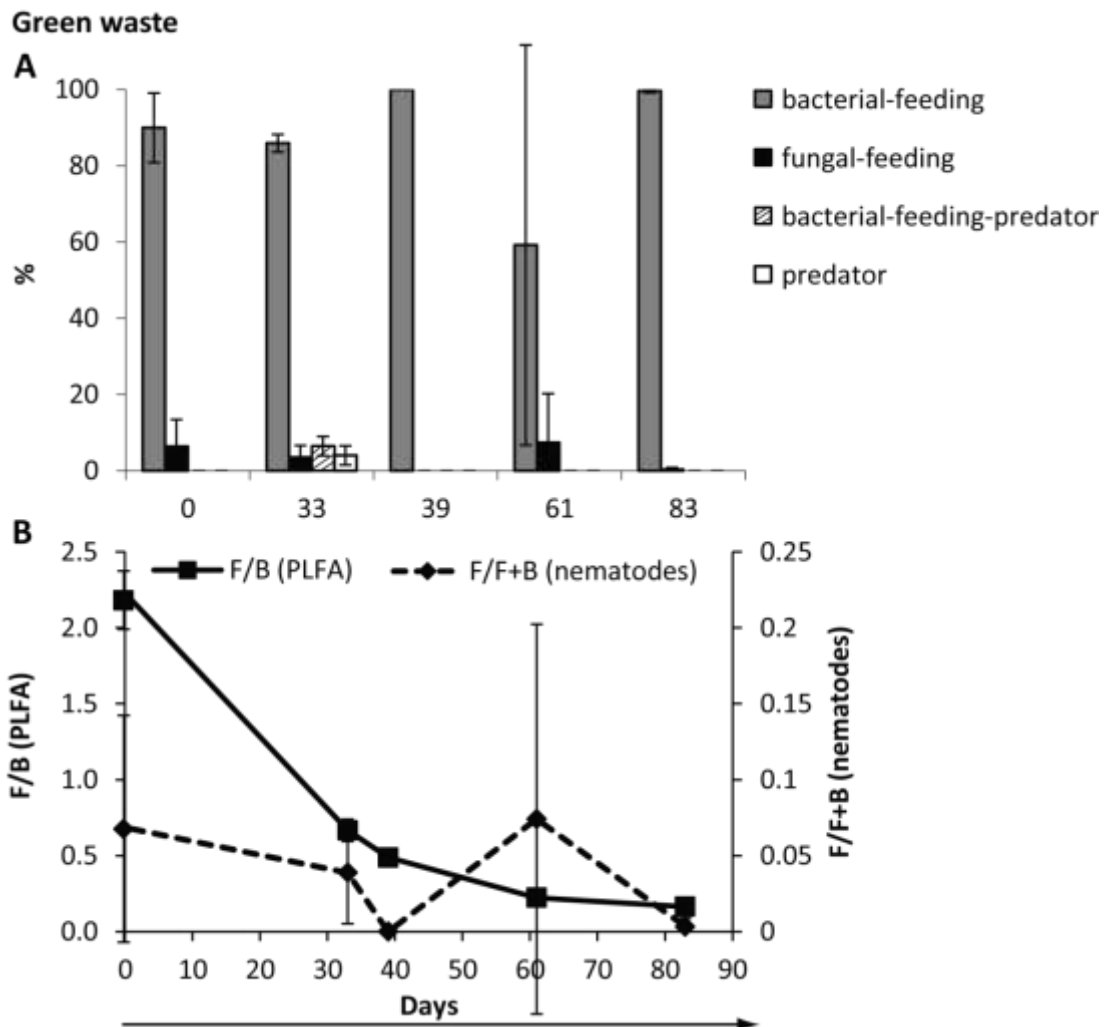
**Figure 6.7:** (A) The predicted against the observed numbers of fungal-feeding nematodes for Farm 1, 2 and 3. (B) The predicted against the observed F/F+B ratio for Farm 1, 2 and 3.



**Figure 6.8:** MDS ordination of square root transformed nematode species abundances of every sampling moment of the three farm composts. Duration of composting (days) is indicated as a number next to the mark of the sample.

Compared to the farm processes the nematode densities and the nematode community structure of the green waste process were completely different. Nematode densities were very low, from  $3 \pm 5$  nematodes/100 g DW to maximum 400 nematodes /100 g DW (Figure 6.3 and Table 6.2), compared to up to  $9575 \pm 2407$  nematodes /100 g DW in farm compost (Figure 6.3 and Table 6.1). Nematodes were even absent in 2 replicas of day 39 and 1 replica on day 61. Especially at the end of the compost process there was a pronounced difference in nematode numbers, with only  $177 \pm 57$  in the green waste compost compared to  $1008 \pm 572$  in the farm composts. Only 13 genera belonging to 7 families were detected (see also Supplementary Table 6.S4) and all taxa found in the green waste process were also found in the farm processes, except for *Procephalobus* sp. which was pre-eminently the most common genus in the industrial green waste compost (64% of the nematode community). The bacterial-feeding enrichment opportunists, such as *Procephalobus* sp., were omnipresent and made up more than 80% of the community in all samples (except for day 61) (Figure 6.9A). Of the fungal-feeding nematodes, only *Aphelenchoides* sp. was found; it was present on all days, except for day 39, but never reached proportions higher than 8%. The bacterial-feeding/predator *Mononchoides composticola* occurred solely on day 33 and made up only 7% of the community. In contrast with the farm processes, the nematode based indices (F/F+B and MI) hardly changed during the

green waste process. The F/F+B ratio was more or less zero (Figure 6.9B) while the MI was constantly close to one (Table 6.2).



**Figure 6.9:** (A) The percent contribution of each feeding type (fungal-feeding, bacterial-feeding, bacterial-feeding/predator) at every sampling moment of the green waste process. Omnivores are not represented in the graph because they only occurred in one sample. (B) F/B ratio based on fungal and bacterial PLFAs and F/F+B ratio based on the fungal- and bacterial-feeding nematode densities during the green waste process. Standard deviations are indicated as error bars based on three replicates.

**Table 6.1:** Overview of the means  $\pm$  SD (based on three replicates) of the abundance of nematodes (per 100g dry weight compost), number of genera and the values of the indices: F/F+B (fungivorous/ (fungivorous+bacterivorous) ratio), MI (Maturity Index) at every sampling moment during the farm processes.

Day	#					#					#			
	Abundance	Genera	F/F+B	MI		Abundance	Genera	F/F+B	MI		Abundance	Genera	F/F+B	MI
<b>0</b>	2203 $\pm$ 531	9 $\pm$ 2	0 $\pm$ 0.01	1.1 $\pm$ 0.07		3628 $\pm$ 2034	8 $\pm$ 1	0 $\pm$ 0.02	1.2 $\pm$ 0.06		6266 $\pm$ 1604	9 $\pm$ 1	0 $\pm$ 0.01	1 $\pm$ 0
<b>3</b>	6 $\pm$ 5	3 $\pm$ 1	0.1 $\pm$ 0.06	1.1 $\pm$ 0.06		10 $\pm$ 2	9 $\pm$ 2	0 $\pm$ 0.01	1 $\pm$ 0.01		282 $\pm$ 27	12 $\pm$ 3	0 $\pm$ 0.01	1 $\pm$ 0.02
<b>7</b>	28 $\pm$ 3	4 $\pm$ 1	0 $\pm$ 0	1 $\pm$ 0		469 $\pm$ 170	5 $\pm$ 2	0 $\pm$ 0.01	1 $\pm$ 0.02		1170 $\pm$ 287	13 $\pm$ 1	0 $\pm$ 0.01	1 $\pm$ 0.01
<b>10</b>	1784 $\pm$ 485	5 $\pm$ 1	0 $\pm$ 0	1 $\pm$ 0		141 $\pm$ 41	6 $\pm$ 1	0 $\pm$ 0.01	1 $\pm$ 0.01		292 $\pm$ 52	11 $\pm$ 2	0 $\pm$ 0.01	1 $\pm$ 0.01
<b>17</b>	7920 $\pm$ 1603	7 $\pm$ 2	0 $\pm$ 0	1 $\pm$ 0		3792 $\pm$ 1137	4 $\pm$ 0	0 $\pm$ 0	1 $\pm$ 0		9575 $\pm$ 2407	8 $\pm$ 1	0 $\pm$ 0	1 $\pm$ 0.01
<b>24</b>	214 $\pm$ 114	4 $\pm$ 2	0 $\pm$ 0	1 $\pm$ 0		47 $\pm$ 10	4 $\pm$ 2	0 $\pm$ 0	1 $\pm$ 0		33 $\pm$ 20	5 $\pm$ 2	0 $\pm$ 0	1 $\pm$ 0
<b>35</b>	1199 $\pm$ 176	4 $\pm$ 1	0 $\pm$ 0	1 $\pm$ 0		933 $\pm$ 153	4 $\pm$ 2	0 $\pm$ 0.06	1 $\pm$ 0.01		1470 $\pm$ 408	5 $\pm$ 1	0 $\pm$ 0	1 $\pm$ 0
<b>49</b>	140 $\pm$ 35	8 $\pm$ 3	0.2 $\pm$ 0.13	1.1 $\pm$ 0.07		951 $\pm$ 78	7 $\pm$ 3	0.1 $\pm$ 0.06	1 $\pm$ 0.02		1650 $\pm$ 193	6 $\pm$ 2	0 $\pm$ 0.04	1.1 $\pm$ 0.01
<b>63</b>	54 $\pm$ 14	5 $\pm$ 5	0.4 $\pm$ 0.01	1.3 $\pm$ 0.01		137 $\pm$ 20	6 $\pm$ 1	0.7 $\pm$ 0.05	1.6 $\pm$ 0.03		957 $\pm$ 195	7 $\pm$ 1	0.2 $\pm$ 0.11	1.1 $\pm$ 0.08
<b>77</b>	17 $\pm$ 3	5 $\pm$ 1	0.6 $\pm$ 0.18	1.5 $\pm$ 0.17		203 $\pm$ 19	4 $\pm$ 1	0.8 $\pm$ 0.11	1.9 $\pm$ 0.01		2446 $\pm$ 509	6 $\pm$ 0	0.3 $\pm$ 0.13	1.2 $\pm$ 0.07
<b>105</b>	26 $\pm$ 16	6 $\pm$ 1	0.7 $\pm$ 0.18	1.8 $\pm$ 0.15		80 $\pm$ 67	5 $\pm$ 1	0.6 $\pm$ 0.08	1.7 $\pm$ 0.13		1797 $\pm$ 130	7 $\pm$ 1	0.1 $\pm$ 0.04	1.1 $\pm$ 0.04
<b>119</b>	73 $\pm$ 34	8 $\pm$ 1	0.6 $\pm$ 0.04	1.7 $\pm$ 0.05		15 $\pm$ 8	8 $\pm$ 1	0.4 $\pm$ 0.04	1.5 $\pm$ 0.03		278 $\pm$ 144	6 $\pm$ 1	0.2 $\pm$ 0.06	1.1 $\pm$ 0.05
<b>133</b>	206 $\pm$ 80	10 $\pm$ 1	0.3 $\pm$ 0.08	1.2 $\pm$ 0.07		302 $\pm$ 81	6 $\pm$ 2	0.3 $\pm$ 0.15	1.3 $\pm$ 0.14		479 $\pm$ 71	6 $\pm$ 2	0.3 $\pm$ 0.12	1.2 $\pm$ 0.09
<b>147</b>	229 $\pm$ 191	6 $\pm$ 1	0.6 $\pm$ 0.1	1.9 $\pm$ 0.01		268 $\pm$ 53	8 $\pm$ 2	0.5 $\pm$ 0.2	1.7 $\pm$ 0.04		734 $\pm$ 138	7 $\pm$ 2	0.2 $\pm$ 0.08	1.2 $\pm$ 0.1
<b>175</b>	537 $\pm$ 80	9 $\pm$ 0	0.5 $\pm$ 0.12	1.8 $\pm$ 0.06		538 $\pm$ 68	8 $\pm$ 0	0.4 $\pm$ 0	1.5 $\pm$ 0.1		740 $\pm$ 45	8 $\pm$ 2	0.4 $\pm$ 0.12	1.4 $\pm$ 0.08
<b>203</b>	1662 $\pm$ 157	7 $\pm$ 1	0.8 $\pm$ 0.17	1.8 $\pm$ 0.15		596 $\pm$ 52	9 $\pm$ 1	0.7 $\pm$ 0.09	1.5 $\pm$ 0.15		768 $\pm$ 113	8 $\pm$ 1	0.4 $\pm$ 0.19	1.3 $\pm$ 0.2

**Table 6.2:** Nematode community during green waste composting with means  $\pm$  SD based on three replicates of the abundance of nematodes (per 100g dry weight compost), number of genera and the values of the indices: F/F+B (fungivorous/ (fungivorous+bacterivorous) ratio), MI (Maturity Index) during the green waste process. Microbial community during green waste composting with means  $\pm$  SD based on three replicates of total PLFA (nmol/g dry soil), F/B ratio and main biomarker concentrations (mol%).

	DAY				
	1	33	39	61	83
<i>Nematode community</i>					
<b>Abundance</b>	34 $\pm$ 1.4	397 $\pm$ 27	3 $\pm$ 5.5	4 $\pm$ 4.12	177 $\pm$ 56.93
<b>F/F+B</b>	0.07 $\pm$ 0.07	0.04 $\pm$ 0.03	0	0.07 $\pm$ 0.13	0.003 $\pm$ 0.01
<b>MI</b>	1.2 $\pm$ 0.14	1.1 $\pm$ 0.06	1	0.8 $\pm$ 0.65	1 $\pm$ 0.01
<i>Microbial community</i>					
<b>Gram +</b>	16.7 $\pm$ 1.10	38.9 $\pm$ 1.67	46.5 $\pm$ 0.79	59.1 $\pm$ 2.31	62.3 $\pm$ 0.49
<b>Gram -</b>	11.3 $\pm$ 0.74	15.5 $\pm$ 1.97	13.6 $\pm$ 0.71	12.7 $\pm$ 0.36	13.7 $\pm$ 0.19
<b>Actinomycetes</b>	0.8 $\pm$ 0.02	2.2 $\pm$ 0.11	2.4 $\pm$ 0.20	3.3 $\pm$ 0.36	3.2 $\pm$ 0.04
<b>Total Bacterial</b>	31.2 $\pm$ 1.90	58.7 $\pm$ 2.51	65.6 $\pm$ 1.47	79 $\pm$ 2.37	83.2 $\pm$ 0.44
<b>Fungi</b>	67.9 $\pm$ 1.92	39.1 $\pm$ 2.51	32.0 $\pm$ 1.65	17.6 $\pm$ 2.02	13.7 $\pm$ 0.42
<b>Total PLFA</b>	1963 $\pm$ 125	1565 $\pm$ 153	822 $\pm$ 108	995 $\pm$ 34	995 $\pm$ 51
<b>F/B</b>	2.2 $\pm$ 0.19	0.7 $\pm$ 0.07	0.5 $\pm$ 0.04	0.2 $\pm$ 0.03	0.2 $\pm$ 0.01

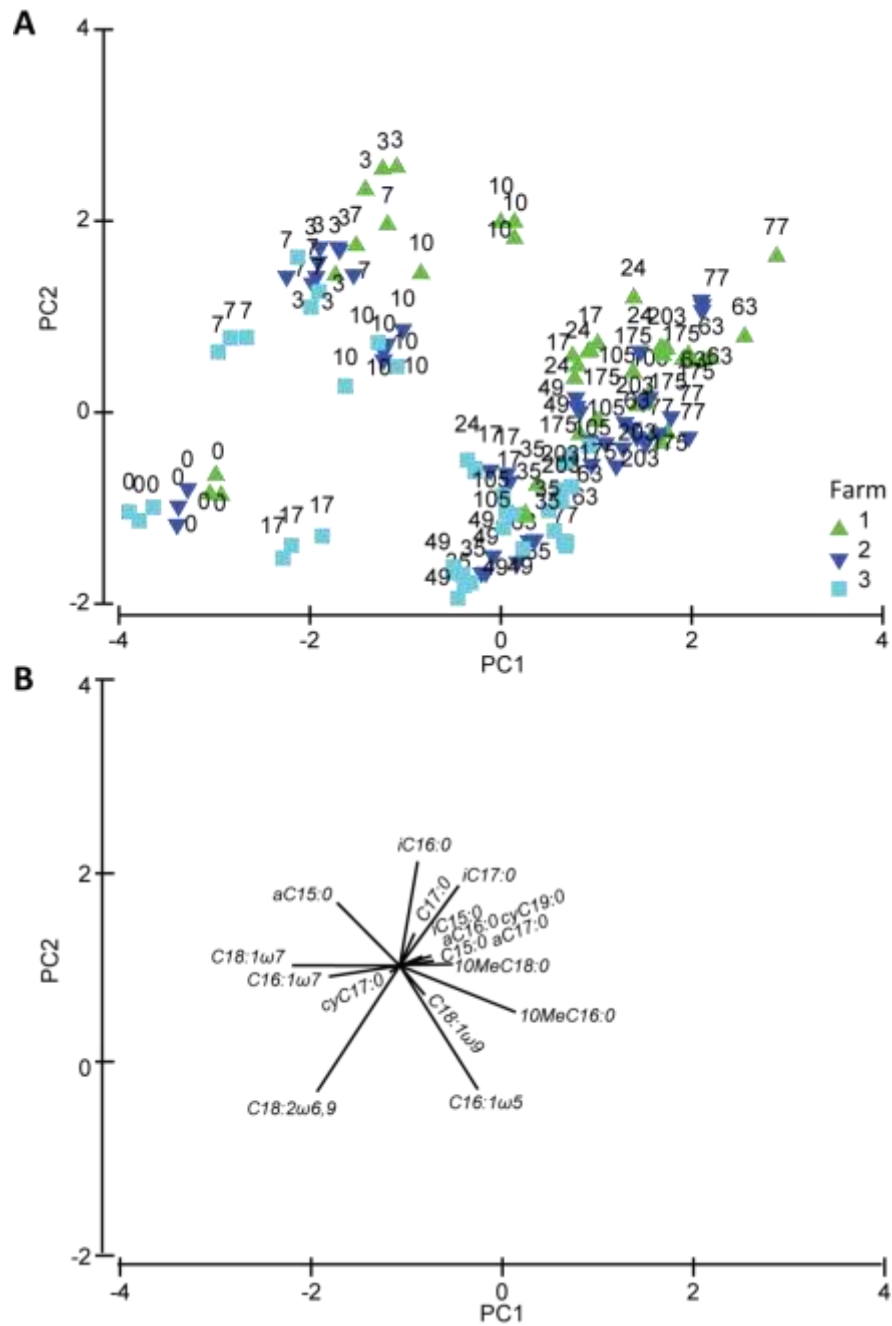
#### 6.4.3 Microbial community

According to the PLFA data, the microbial community of the farm composts, changed mainly during the first weeks of composting while afterwards the PLFA based patterns were remarkably stable (Table 6.3). This is confirmed by the PCA of the relative biomarker concentrations which resulted in a clear discrimination, mainly along the first axis, between early (until day 17) and later compost stages (Figure 6.10A) independent of the compost process (i.e. Farm 1, Farm 2 and Farm 3). The increasing 10Me16:0 (Actinomycetes) and decreasing 18:1 $\omega$ 7 (Gram-negative) biomarkers contributed most to the first axis (explains 56% of the variation), while the second axis (26% of the variation) was defined most importantly by decreasing fungal and AMF (18:2 $\omega$ 6,9 and 16:1 $\omega$ 5C respectively) biomarkers and the increasing Gram-negative biomarker i16:0 (Figure 6.10B).

The total PLFA was highest after the heat peaks on day 35 and/or day 49 and afterwards decreased again (Table 6.3). Except for day 0 in all farm processes and day 7 and 17 in Farm 3, all samples showed a distinct dominance of Gram-positive bacteria. Comparison of the relative contributions of the functional groups to the microbial community between indicatively delineated composting phases based on the changes in the nematode community (i.e. day 0-10, day 17-49, day 63-133, day 147-203) (see 6.4.2) revealed similar differences in all farm processes mainly between the first phase (day 0-10) and the other phases. The Gram-negative bacteria

were highest during the first 10 days of composting and their concentrations were significantly lower during days 17-49 and days 63-133 compared to days 0-10. The Actinomycetes gradually increased during the process, which is confirmed by significantly higher concentrations during days 63-133 and days 147-203 compared to days 0-10. The fungal PLFA decreased in the beginning of the process as temperatures increased but peaked on day 35 in Farm 1 and on day 35 and day 49 in Farm 2 and 3, and afterwards decreased again with significantly lower concentrations during days 147-203 compared to days 17-49. In accordance, the F/B ratio initially decreased with increasing temperatures and peaked on days 35-49, with significantly higher values on day 35 (Farm 1 & 2;  $p < 0.04$ ,  $< 0.001$ ) and day 49 (Farm 3  $p < 0.05$ ) compared to all later stages, except between day 49 and 77 in Farm 3. Unlike the steadily increasing proportions of fungal-feeding nematodes, the fungal PLFA remained remarkably stable and relatively low after day 63 even when temperatures reached near ambient levels. The amount of fungal PLFA had no significant effect ( $p \geq 0.05$ ) in the models (GLIMMIX procedure in SAS) of the absolute number of fungal-feeding nematodes and thus no additional information was explained by adding this variable in the model.

In the green waste compost process, the total PLFA on day 0 and day 33 was significantly higher ( $p < 0.001$ ) compared to days 39, 61 and 83. During the process, the fungal PLFA significantly ( $p < 0.001$  between all samples) decreased with time, while the share of the Gram-positive bacteria increased with time ( $p < 0.03$  between all samples). On day 0 the most contributing fungal PLFA was 18:1 $\omega$ 9, but afterwards on day 39 18:1 $\omega$ 9 and 18:2 $\omega$ 6,9 contributed equally. The most prominent Gram-positive biomarker was i16:0 and for the Gram-negative bacteria first (day 0 and 33) both 16:1 $\omega$ 7 and 18:1 $\omega$ 7 and later (day 39, 61, 83) cy17:0 and cy19:0 were dominant. According to the decreasing fungal PLFA, the F/B ratio also sharply decreased from  $2.2 \pm 0.19$  on day 0 to  $0.2 \pm 0.01$  on day 83 (Figure 6.10B).



**Figure 6.10:** (A) Two-dimensional PCA ordination of biomarker fatty acids (mol%) of the three farm composting processes (Farm 1, Farm 2, Farm 3). (B) Vector loading plot with all individual marker fatty acids.

**Table 6.3:** Total PLFA (nmol/g dry soil), F/B ratio and main biomarker concentrations (mol%)  $\pm$  standard deviation, during the farm processes. \* The used biomarker for AMF is questionable in a compost environment (see 4.3.4). For completeness the concentrations of this group are provided but not used in further community analyses

Day	Gram +	Gram -	Total Bact	Actinomycetes	Fungi	AMF*	Total PLFA	F/B
<b>Farm 1</b>								
0	30 $\pm$ 0.69	40.1 $\pm$ 0.88	72.6 $\pm$ 1.58	2.1 $\pm$ 0.05	22 $\pm$ 1.57	3.31 $\pm$ 0.05	1287 $\pm$ 95.9	0.3 $\pm$ 0.03
3	61.5 $\pm$ 1.79	22.9 $\pm$ 1.38	87.9 $\pm$ 0.43	1.1 $\pm$ 0.01	10.3 $\pm$ 0.39	0.63 $\pm$ 0.06	2103 $\pm$ 152.6	0.1 $\pm$ 0.01
7	53.2 $\pm$ 3.95	28.6 $\pm$ 3.8	85 $\pm$ 0.55	1.4 $\pm$ 0.08	12 $\pm$ 0.38	1.58 $\pm$ 0.25	1767 $\pm$ 238.4	0.1 $\pm$ 0.01
10	55.4 $\pm$ 0.86	21.5 $\pm$ 2.01	83.4 $\pm$ 0.42	5.4 $\pm$ 2.09	8.5 $\pm$ 1.89	2.77 $\pm$ 0.19	1921 $\pm$ 250.7	0.1 $\pm$ 0.02
17	51.7 $\pm$ 1.95	17.7 $\pm$ 1.01	73.2 $\pm$ 2.11	7.1 $\pm$ 0.13	11.8 $\pm$ 1.58	7.92 $\pm$ 0.42	1724 $\pm$ 110.4	0.2 $\pm$ 0.03
24	54 $\pm$ 2.98	16.8 $\pm$ 1.98	75 $\pm$ 1.62	6.7 $\pm$ 0.74	10.4 $\pm$ 1.48	7.86 $\pm$ 1.53	1674 $\pm$ 527.6	0.1 $\pm$ 0.02
35	42.1 $\pm$ 1.64	20 $\pm$ 0.26	64.4 $\pm$ 1.9	7.6 $\pm$ 0.16	18.6 $\pm$ 1.67	9.31 $\pm$ 0.23	3182 $\pm$ 126.9	0.3 $\pm$ 0.03
49	47.4 $\pm$ 0.57	18 $\pm$ 0.5	69 $\pm$ 0.74	8.3 $\pm$ 0.15	15.1 $\pm$ 1.04	7.6 $\pm$ 0.32	2452 $\pm$ 112.1	0.2 $\pm$ 0.02
63	50.6 $\pm$ 1.63	15.9 $\pm$ 2.7	70.5 $\pm$ 0.87	13.5 $\pm$ 0.68	8.8 $\pm$ 0.64	7.3 $\pm$ 1.23	1906 $\pm$ 173.4	0.1 $\pm$ 0.01
77	48.9 $\pm$ 8.68	15.3 $\pm$ 4.61	68.1 $\pm$ 4.65	10.6 $\pm$ 0.85	12 $\pm$ 3.19	9.32 $\pm$ 2.29	2208 $\pm$ 337.4	0.2 $\pm$ 0.06
105	47.5 $\pm$ 0.58	19.1 $\pm$ 0.32	70.1 $\pm$ 0.61	10.1 $\pm$ 0.2	11.3 $\pm$ 0.62	8.47 $\pm$ 0.1	2204 $\pm$ 158.1	0.2 $\pm$ 0.01
175	49.4 $\pm$ 3.18	17.9 $\pm$ 3.88	70.5 $\pm$ 2.05	11.2 $\pm$ 0.63	10.4 $\pm$ 1.48	7.87 $\pm$ 1.24	1667 $\pm$ 231.7	0.1 $\pm$ 0.02
203	49.1 $\pm$ 0.4	20.2 $\pm$ 0.32	72.3 $\pm$ 0.29	11.8 $\pm$ 0.21	8.7 $\pm$ 0.42	7.15 $\pm$ 0.19	1985 $\pm$ 140	0.1 $\pm$ 0.01
<b>Farm 2</b>								
0	27.9 $\pm$ 1.49	39.7 $\pm$ 0.56	70.2 $\pm$ 1.4	1.7 $\pm$ 0.03	25.2 $\pm$ 1.28	2.88 $\pm$ 0.12	1297 $\pm$ 60.7	0.4 $\pm$ 0.03
3	52.5 $\pm$ 1.19	29.1 $\pm$ 0.92	85.1 $\pm$ 0.71	1.5 $\pm$ 0.17	12.3 $\pm$ 0.71	1.17 $\pm$ 0.12	1811 $\pm$ 310.2	0.1 $\pm$ 0.01
7	49.8 $\pm$ 1.73	31.8 $\pm$ 1.74	84.6 $\pm$ 0.62	1.5 $\pm$ 0.19	12.4 $\pm$ 0.43	1.47 $\pm$ 0.17	2056 $\pm$ 199.2	0.1 $\pm$ 0.01
10	46.6 $\pm$ 1.24	28.9 $\pm$ 0.6	78.7 $\pm$ 1.16	3.2 $\pm$ 0.13	14.4 $\pm$ 1.14	3.6 $\pm$ 0.15	2136 $\pm$ 286.1	0.2 $\pm$ 0.02
17	39.9 $\pm$ 1.07	22.8 $\pm$ 0.86	65.8 $\pm$ 1.85	6 $\pm$ 0.23	16.4 $\pm$ 0.44	11.83 $\pm$ 1.19	2342 $\pm$ 133.7	0.2 $\pm$ 0.01
24	50.9 $\pm$ 2.75	17.7 $\pm$ 2.65	72.2 $\pm$ 0.74	7.8 $\pm$ 0.06	13 $\pm$ 1.26	7.02 $\pm$ 0.64	2841 $\pm$ 259.4	0.2 $\pm$ 0.02
35	38.1 $\pm$ 0.69	19.2 $\pm$ 0.33	59.7 $\pm$ 0.94	7.1 $\pm$ 0.25	22 $\pm$ 1.42	11.16 $\pm$ 0.72	3581 $\pm$ 86.4	0.4 $\pm$ 0.03
49	36.8 $\pm$ 0.71	20 $\pm$ 0.29	59.4 $\pm$ 0.89	6.2 $\pm$ 0.27	24.8 $\pm$ 0.92	9.62 $\pm$ 0.25	3128 $\pm$ 257	0.4 $\pm$ 0.02
63	46.9 $\pm$ 1.27	16.3 $\pm$ 1.89	66.8 $\pm$ 0.59	9.6 $\pm$ 0.32	13 $\pm$ 0.69	10.52 $\pm$ 1.46	2641 $\pm$ 346.1	0.2 $\pm$ 0.01
77	51.4 $\pm$ 3.94	15.5 $\pm$ 2.07	71.3 $\pm$ 5.99	12.3 $\pm$ 2	9.5 $\pm$ 3.64	6.96 $\pm$ 4.35	1855 $\pm$ 296.6	0.1 $\pm$ 0.07
105	44.2 $\pm$ 1.23	21.4 $\pm$ 1.25	68.8 $\pm$ 1.29	8 $\pm$ 0.46	13.8 $\pm$ 1.2	9.34 $\pm$ 0.45	2494 $\pm$ 751.5	0.2 $\pm$ 0.02
175	45.2 $\pm$ 0.61	18.4 $\pm$ 2.88	67.1 $\pm$ 2.88	12.2 $\pm$ 0.84	11.9 $\pm$ 1.44	8.81 $\pm$ 2.44	2105 $\pm$ 227.6	0.2 $\pm$ 0.03
203	41.9 $\pm$ 2.13	20.7 $\pm$ 0.48	65.6 $\pm$ 1.61	12.4 $\pm$ 0.35	12.8 $\pm$ 1.61	9.24 $\pm$ 0.33	2265 $\pm$ 17.1	0.2 $\pm$ 0.03
<b>Farm 3</b>								
0	26.2 $\pm$ 0.29	41.9 $\pm$ 0.15	70.4 $\pm$ 0.23	1.2 $\pm$ 0.06	25.9 $\pm$ 0.21	2.48 $\pm$ 0.13	2055 $\pm$ 178.8	0.4 $\pm$ 0
3	52.6 $\pm$ 1.78	26.8 $\pm$ 1.2	82.5 $\pm$ 0.58	1 $\pm$ 0.18	15.1 $\pm$ 0.5	1.47 $\pm$ 0.71	2698 $\pm$ 84	0.2 $\pm$ 0.01
7	39.7 $\pm$ 0.27	40.6 $\pm$ 0.97	83 $\pm$ 0.7	1.1 $\pm$ 0.11	14.2 $\pm$ 0.84	1.73 $\pm$ 0.04	2986 $\pm$ 707.1	0.2 $\pm$ 0.01
10	43.7 $\pm$ 2.41	29.6 $\pm$ 1.43	76.8 $\pm$ 1.41	2.9 $\pm$ 0.18	17 $\pm$ 1.35	3.25 $\pm$ 0.53	2625 $\pm$ 137.7	0.2 $\pm$ 0.02
17	30.5 $\pm$ 0.95	32.1 $\pm$ 0.37	65.1 $\pm$ 0.66	2.5 $\pm$ 0.18	24.5 $\pm$ 0.85	7.88 $\pm$ 0.07	3108 $\pm$ 487.9	0.4 $\pm$ 0.02
24	44.1 $\pm$ 0.38	21.1 $\pm$ 0.74	68.1 $\pm$ 0.77	5.4 $\pm$ 0.31	20.9 $\pm$ 0.26	5.68 $\pm$ 0.3	4123 $\pm$ 66	0.3 $\pm$ 0.01
35	35.5 $\pm$ 0.24	20.8 $\pm$ 0.48	58.6 $\pm$ 0.59	5.3 $\pm$ 0.33	24.5 $\pm$ 0.76	11.57 $\pm$ 0.31	4773 $\pm$ 324.1	0.4 $\pm$ 0.02
49	37.5 $\pm$ 0.42	21.7 $\pm$ 0.49	61.7 $\pm$ 0.6	4.8 $\pm$ 0.23	23.3 $\pm$ 0.46	10.27 $\pm$ 0.6	4689 $\pm$ 68.9	0.4 $\pm$ 0.01
63	39.8 $\pm$ 1.72	20.3 $\pm$ 0.59	62.8 $\pm$ 1.82	6.9 $\pm$ 0.53	18.6 $\pm$ 1.69	11.81 $\pm$ 0.21	3713 $\pm$ 171.5	0.3 $\pm$ 0.03
77	38.4 $\pm$ 0.4	18.7 $\pm$ 0.3	59.9 $\pm$ 0.15	7 $\pm$ 0.18	19.8 $\pm$ 0.43	13.31 $\pm$ 0.45	3107 $\pm$ 75.1	0.3 $\pm$ 0.01
105	39.5 $\pm$ 0.8	23.2 $\pm$ 0.4	65.7 $\pm$ 1.01	5.6 $\pm$ 0.27	18.1 $\pm$ 1.35	10.62 $\pm$ 1.25	3178 $\pm$ 362	0.3 $\pm$ 0.02
175	42.1 $\pm$ 0.71	21.9 $\pm$ 1.44	67 $\pm$ 0.9	8.7 $\pm$ 0.45	14 $\pm$ 0.86	10.32 $\pm$ 1.98	2294 $\pm$ 381.5	0.2 $\pm$ 0.01
203	39.4 $\pm$ 0.49	22.8 $\pm$ 0.2	64.8 $\pm$ 0.55	8.9 $\pm$ 0.16	15.5 $\pm$ 0.48	10.74 $\pm$ 0.48	2427 $\pm$ 53.6	0.2 $\pm$ 0.01



## 6.5 DISCUSSION

### 6.5.1 Microbial succession

In agreement with Chapter 4 and several other studies (e.g. Herrmann and Shann 1997; Klamer and Bååth 1998; Steger et al. 2003), the Gram-positive bacteria were most prominent during the heat peaks, while the proportion of fungi clearly decreased with increasing temperature and the Gram-negative bacteria peaked during the intermediate temperature drop (day 7) in the thermophilic phase. Increased proportions of Actinomycetes in the later compost stages were also found by Hellmann et al. (1997), Klamer and Bååth (1998), Bolta et al. (2003) and Steger et al. (2003), and might be explained by their slower development compared to most bacteria and fungi and their ineffectiveness as competitors when nutrient levels are high at the beginning of the process (Beffa et al. 1996). However, unlike in chapter 4 and several other studies (e.g. Herrmann and Shann 1997; Klamer and Bååth 1998; Steger et al. 2003; Ryckeboer et al., 2003), but similar to Bolta et al. (2003) and recurrent in all three heaps studied here, the proportions of the fungal PLFA did not increase but rather decreased at the end of the process, even when near ambient temperature levels were reached. It is highly unlikely that this could be completely attributed to the possible effects of previous elevated temperatures on fungal growth or suppressive (top-down) control of the abundant fungal-feeding nematodes on the fungi. Alternatively, the variable outcome of our PLFA study could be partly ascribed to the technique to characterize the fungal community. The amount of reliable fungal biomarkers is rather limited: only two reliable markers were detected and analyzed by the GCMS (i.e. 18:1 $\omega$ 9c and 18:2 $\omega$ 6,9) compared to 15 bacterial biomarkers (Joergensen and Wichern 2008). Although the applied technique does not provide any information on this matter, diversity might also be an important factor here. The fungal diversity is known to increase with duration of composting (Ryckeboer et al. 2003) and it is not impossible that some forms or species of fungi appearing more at the end of the process are not detected with current PLFA techniques.

### 6.5.2 Nematode succession

Clear shifts in the nematode community structure were found in the farm compost processes. These shifts are not clearly delineated according to the three typical successive temperature related composting phases, i.e. thermophilic, cooling and maturation phase, as previously described in Chapters 2 and 4. Hence, although the nematode patterns in the three processes are remarkably similar, the nematode succession is less straightforward compared to previous studies. But most importantly, the absence of a linear relation of temperature and time in

current study facilitated to distinguish between the effect of temperature and duration of composting. Although the timing of the nematode succession is different compared to previous studies, the general patterns are largely similar. The nematode successions are largely represented by the same functional groups and nematode taxa, i.e. during and directly after the heat peaks (day 0-10) bacterial feeding enrichment opportunists are most important, including *Pelodera* sp. together with *Rhabditella axei*. Subsequently, the bacterial-feeding/predator community (days 17-49) became dominant. Then, from day 63-133, the proportion of the fungal-feeding general opportunists initially increased. However, with increasing temperatures this ratio decreased again resulting in a less unambiguous positive linear relation with compost time compared to former studies (Chapters 2 and 4).

Since an increasing share of fungal-feeding nematodes was suggested as a potential tool to assess compost maturity (Chapters 2 and 4), the relation of fungal-feeding nematodes with time, temperature and microbial community was better elaborated here. The density of fungal-feeding nematodes is, like the total density of nematodes, significantly related to temperature, but also to duration of composting. A model including these parameters predicts the observed fungal-feeding nematodes fairly well (Figure 6.8A), except for the moments after the thermophilic phase (i.e. days 17-35). These are the samples where the bacterial-feeding/predators (i.e. *Mononchoides composticola*) were dominant and possibly outcompeted fungal-feeding nematodes due to their ability to feed on bacteria, other compost nematodes (Chapter 3) and most likely also fungi (note that a fungal-feeding behavior has also been reported for *Pristionchus pacificus* of the same nematode family (Fürst von Lieven and Sudhaus 2000)). Nematode densities were highly dependent on temperature. In contrast, the F/F+B ratio was only significantly positively related with duration of composting. Hence, our results show that this ratio, previously proposed as an indicator of compost maturity, is effectively related to the duration of a compost process and is less affected by temperature fluctuations. Nevertheless, the model that included duration of composting and temperature predicted higher F/F+B values than observed at sampling moments with relatively high temperatures resulting in low nematodes densities (Figure 6.8B). This is due to the fact that the ratio, being a proportion, is not sensitive to densities per se. Compared to the changes in the nematode data, the PLFA data are more or less stable, especially towards the second half of the process. Thus, when the amount of fungal PLFA or the PLFA based F/B ratio were added as explanatory variables in the models of the abundances of fungal-feeding nematodes and of the F/F+B ratio, no additional information was explained. Surprisingly, during maturation, the increased levels of fungal-feeding nematodes did not coincide with increased levels of fungal PLFA. Similarly,

Sánchez-Moreno et al. (2006) reported that in soil the fungal-feeding nematodes were not related as strongly with ergosterol as expected. Despite the different proxies used for fungal biomass, i.e. ergosterol vs. PLFA, these two findings suggest that fungal biomass may not be determining the size of the fungal feeder populations (Sánchez-Moreno et al. 2006).

### **6.5.3 Green waste compost versus farm compost**

The farm composts were well balanced replicated processes that allowed a founded modeling of nematode parameters, whereas the green waste compost represents a standardized industrial process. Both abiotic (i.e. temperature) and biotic (i.e. nematode and microbial community succession) data were manifestly different. The persistent high temperatures during the industrial green waste composting can be partly related to the feedstock material. The green waste compost was composed of less ligneous materials (i.e. grass hay, straw of clover) and more fresh materials (i.e. fresh grass, mixed green waste), and the latter contain more readily degradable carbon which causes prolonged periods of very high temperatures as a result of decomposition by mainly thermophilic bacteria (Steger et al. 2005). The nematode abundances and diversity were significantly lower and the nematode community of the “finished” green waste compost hardly contained fungal-feeding nematodes. Both the amount of fungal-feeding nematodes and the F/F+B ratio are clearly lower than predicted by the models based on more balanced composts (Figure 6.7), respectively 1 fungal-feeding nematode vs. 41 predicted in 100g DW compost and a ratio of 0.003 vs. 0.1 predicted. The very low F/F+B ratio is an indication that the composting process has not yet been able to mature towards a balanced biological community. This is quite evident given the persistently high temperatures. We endorse that in such extreme situations nematode based in indices appear somewhat superficially, they could be of more relevance for more subtle different situations. Nevertheless, especially compared to the farm composts, the green waste compost is extremely poor in nematode biology. In addition, since both the abundance and (functional) diversity of the nematode community together with the availability of an adequate resource are important for the continuity of their ecosystem services in soil (Ferris 2010), the structure and quality of the nematode community in the finished composts may be an important issue for the beneficial effects of compost when added to the soil.

#### **6.5.4 Conclusion**

In conclusion several features of the nematode community during composting (i.e. nematode abundances, total amount of fungal-feeding nematodes and the F/F+B ratio) showed a clear and consistent pattern in all three independent farm processes. This made it possible to design models for each of these features. Especially the nematode based F/F+B holds promise as a reliable indicator of compost maturity since it was not affected by temperature fluctuations but only related with duration of composting. The next step is to improve the obtained models based on other compost methods and validate their universal use as an effective indicator of compost maturity.

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## 6.6 SUPPLEMENTARY MATERIAL

Supplementary Table 6.S1

Nematode species list with indication of relative abundance of the species during the Farm 1 composting process (averages of 3 replicates). The feeding type (FT) of each species is also provided (3= bacterial-feeding, 2= fungal-feeding, 3-5a= bacterial-feeding/predator, 5= predator).

Taxa	FT	Day of compost duration															
		0	3	7	10	17	24	35	49	63	77	105	119	133	147	175	203
<i>Cylindrocorpus</i> sp.	3																
<i>Pelodera teres</i>	3																
<i>Rhabditella axei</i>	3																
<i>Rhabditis</i> sp.	3																
<i>Pelodera</i> sp.	3																
<i>Choriorhabditis</i> sp.	3																
juv. Rhabditidae	3																
<i>Acrostichus</i> sp.	3																
<i>Halicephalobus</i> cfr. <i>gingivalis</i>	3																
juv. Diplogasteridae	3																
<i>Panagrolaimus</i> sp.	3																
<i>Pelodera cylindrica</i>	3																
<i>Protorhabditis</i> sp.	3																
<i>Mesorhabditis</i> sp.	3																
<i>Diplogasteritus</i> sp.	3																
Fam. Bunonematidae	3																
<i>Cephaloboides</i> sp.	3																
Fam. Panagrolaimidae	3																
<i>Diploscapter coronatus</i>	3																
<i>Poikilolaimus</i> sp.	3																
<i>Eucephalobus</i> sp.	3																
juv. Rhabditidae /P	3																
<i>Teratorhabditis</i> sp.	3																
<i>Teratocephalus</i> sp.	3																
Fam. Tylenchidae	2																
<i>Aphelenchoides</i> sp.	2																
<i>Ditylenchus</i> sp.	2																
Fam. Neotylenchidae	2																
<i>Butlerius</i> sp.	3-5a																
<i>Fictor</i> sp.	3-5a																
<i>Mononchoides composticola</i>	3-5a																
juv. Diplogasteridae /M	3-5a																
<i>Seinura</i> sp.	5																
<i>Ektaphelenchoides</i> sp.	/																

<5%    5-30%    >30%

**Supplementary Table 6.S2**

Nematode species list with indication of relative abundance of the species during the Farm 2 composting process (averages of 3 replicates). The feeding type (FT) of each species is also provided (3= bacterial-feeding, 2= fungal-feeding, 3-5a= bacterial-feeding/predator, 5= predator, 8= omnivorous).

Taxa	FT	Day of compost duration															
		0	3	7	10	17	24	35	49	63	77	105	119	133	147	175	203
<i>Pelodera</i> sp.	3																
<i>Protorhabditis</i> sp.	3																
<i>Rhabditella axei</i>	3																
<i>Diplogasteritus</i> sp.	3																
<i>Teratorhabditis</i> sp.	3																
juv. Rhabditidae	3																
<i>Choriorhabditis</i> sp.	3																
juv. Diplogasteridae	3																
<i>Acrostichus</i> sp.	3																
<i>Mesorhabditis</i> sp.	3																
Fam. Panagrolaimidae	3																
<i>Pelodera cylindrica</i>	3																
<i>Halicephalobus</i> cfr. <i>gingivalis</i>	3																
<i>Poikilolaimus</i> sp.	3																
<i>Teratocephalus</i> sp.	3																
<i>Cephaloboides</i> sp.	3																
<i>Panagrolaimus</i> sp.	3																
juv. Diplogasteridae/M	3																
Fam. Bunonematidae	3																
<i>Crustorhabditis</i> sp.	3																
<i>Diploscapter coronatus</i>	3																
<i>Eucephalobus</i> sp.	3																
juv. Rhabditidae/P	3																
<i>Ditylenchus</i> sp.	2																
<i>Aphelenchoides</i> sp.	2																
Fam. Neotylenchidae	2																
Fam. Tylenchidae	2																
<i>Diplogaster</i> sp.	3-5a																
<i>Fictor</i> sp.	3-5a																
<i>Mononchoides composticola</i>	3-5a																
<i>Butlerius</i> sp.	3-5a																
<i>Seinura</i> sp.	5																
Fam. Qudsianematidae	8																
<i>Ektaphelenchoides</i> sp.	/																

<5% 5-30% >30%

**Supplementary Table 6.S3**

Nematode species list with indication of relative abundance of the species during the Farm 3 composting process (averages of 3 replicates). The feeding type (FT) of each species is also provided (3= bacterial-feeding, 2= fungal-feeding, 3-5a= bacterial-feeding/predator, 5= predator, 8= omnivorous).

Taxa	FT	Day of compost duration															
		0	3	7	10	17	24	35	49	63	77	105	119	133	147	175	203
<i>Crustorhabditis</i> sp.	3																
<i>Pelodera teres</i>	3																
<i>Choriorhabditis</i> sp.	3																
<i>Poikilolaimus</i> sp.	3																
juv. Rhabditidae	3																
juv. Diplogasteridae	3																
<i>Rhabditis</i> sp.	3																
<i>Rhabditella axei</i>	3																
<i>Acrostichus</i> sp.	3																
<i>Protorhabditis</i> sp.	3																
<i>Diplogasteritus</i> sp.	3																
<i>Mesorhabditis</i> sp.	3																
<i>Myolaimus</i> sp.	3																
<i>Pelodera cylindrica</i>	3																
<i>Pelodera</i> sp.	3																
<i>Plectus</i> sp.	3																
<i>Halicephalobus</i> cfr. <i>gingivalis</i>	3																
<i>Operculorhabditis</i> sp.	3																
<i>Cylindrocorpus</i> sp.	3																
<i>Diploscapter coronatus</i>	3																
<i>Eucephalobus</i> sp.	3																
<i>Ditylenchus</i> sp.	2																
Fam. Tylenchidae	2																
<i>Aphelenchoides</i> sp.	2																
Fam. Neotylenchidae	2																
<i>Diplogaster</i> sp.	3-5a																
<i>Butlerius</i> sp.	3-5a																
<i>Mononchoides composticola</i>	3-5a																
juv. Diplogasteridae /M	3-5a																
<i>Seinura</i> sp.	5b																
Fam. Qudsianematidae	8																

<5%    5-30%    >30%

**Supplementary Table 6.S4**

Nematode species list with indication of relative abundance of the species during the green waste composting process (averages of 3 replicates). The feeding type (FT) of each species is also provided (3= bacterial-feeding, 2= fungal-feeding, 3-5a= bacterial-feeding/predator, 5= predator, 8= omnivorous).

TAXA	FT	Day of compost duration				
		0	33	39	61	83
<i>Acrostichus</i> sp.	3					
<i>Teratorhabditis</i> sp.	3					
<i>Panagrolaimus</i> sp.	3					
<i>Rhabditella axei</i>	3					
<i>Oscheius</i> sp.	3					
juv. Rhabditidae	3					
<i>Pelodera</i> sp.	3					
juv. Panagrolaimidae	3					
juv. Diplogasteridae	3					
<i>Cephalobus</i> sp.	3					
<i>Diploscapter coronatus</i>	3					
<i>Halicephalobus</i> cfr. <i>gingivalis</i>	3					
Fam. Panagrolaimidae	3					
<i>Aphelenchoides</i> sp.	2					
<i>Mononchoides</i> sp.	3-5a					
<i>Seinura</i> sp.	5b					
Fam. Dorylaimidae	8					

<5%    5-30%    >30%

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# 7. Nematode communities and macronutrients in composts and compost-amended soils as affected by feedstock composition

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Modified from:

Steel H, Vandecasteele B, Willekens K, Sabbe K, Moens T and Bert W (2012). Nematode communities in composts and compost-amended soils as affected by feedstock composition. *Applied Soil Ecology* 61: 100-112.

## 7.1. ABSTRACT

Farm composts were produced from selected feedstocks and compared to one external farm compost and one green waste compost. Nematodes were omnipresent in the composts (on average 26 ind./g dry weight compost) and many taxa were common to all composts (i.e. *Mononchoides composticola*, *Diploscapter coronatus*, *Halicephalobus gingivalis*, *Ditylenchus* sp., *Diplogaster* sp., *Diplogastrellus* sp. and *Diplogasteritus* sp.) and occurred in similar proportions. Composts with a somewhat different species composition or proportion also displayed differences in the abiotic parameters, suggesting that compost maturity and status may be reflected by the nematode community. Significant differences (ANOSIM,  $p = 0.001$ ) in nematode community between the farm composts and the green waste compost were found. Nevertheless, despite largely different feedstock materials and proportions, and despite clear differences in chemical properties and stability of the composts, biologically very similar composts were produced. The 11 composts of different composition were further tested in an incubation experiment to investigate their short-term effect on the existent soil nematode community and on the soil chemical properties. Therefore, the nematode community together with several abiotic parameters (pH, EC, DM, OM, P<sub>tot</sub>, C/N, and NO<sub>3</sub>/NH<sub>4</sub>) of the used composts and the soils before and 12 weeks after compost amendment, were analyzed. All compost amendments resulted in a significant pH increase in the soil (one-way ANOVA,  $p < 0.01$ ), and differences in plant-available macronutrients in the soil between the applied composts were detected. The changes in soil chemical properties after compost addition were related to the compost type and could be linked to the properties of the used feedstock materials. After 12 weeks of incubation, the nematode numbers in the soil increased, except in soil amended with the green waste compost. In particular, the abundance of the fungal-feeding *Ditylenchus* increased significantly (one-way ANOVA,  $p < 0.03$ ) in all soils amended with farm compost. This increase may well be purely caused by the addition of nematodes present in the compost.

## 7.2. INTRODUCTION

Composting is an effective tool for the management of municipal and agro-industrial wastes by converting raw organic materials into a stabilized form, destroying human and animal pathogens and recycling valuable plant nutrients (Naidu et al. 2004). Multiple benefits of compost addition to the soil's physical and chemical characteristics have been reported and include increased soil organic matter content (Termorshuizen et al. 2004) and the subsequent improvement of soil

aeration, soil porosity, drainage, and water holding capacity (Cogger 2005; Kuo et al. 2004; Termorshuizen et al. 2004). Furthermore, compost can provide an important source of nutrients for plants by providing readily available nitrogen and by promoting mineralization of compost nitrogen in the soil (Cogger 2005; D'Hose et al. 2012; Zvomuya et al. 2008). Composts are also known for their disease-suppressive activity based on both physicochemical and biological mechanisms (Akhtar and Malik 2000; Bailey and Lazarovit, 2003; Kuo et al, 2004; Oka 2010; Reuveni et al. 2002). Another benefit of compost application is the suppression of weed seeds (De Cauwer et al. 2010, 2011). Therefore, truly functional compost should meet criteria for stability and maturity before application (Zorpas 2009).

The use of compost significantly impacts the soil fauna and flora (Pfozter and Schüler 1997). Application of compost enhanced the biological activity of the soil (i.e. higher microbial activity and higher numbers of protozoa and bacterial-feeding nematodes), resulting in enhanced turnover of organic matter and release of plant available nutrients (Forge et al. 2003). In translocating and transforming litter and soil organic matter and in changing the supply of nutrients to plant roots, soil fauna fulfill crucial roles in the nutrient supply and the conservation of the soil structure (Brussaard et al. 2004). Hence, compost application can strengthen the role of the living soil. However, current insight into the consequences of compost addition for the complex interactions in the soil is limited. In addition, soil biota can be considered important soil quality indicators. The nematode community in particular is strongly influenced by soil physical and chemical properties (Boag and Yeates 1998; Goralczyk 1998). Furthermore, there is considerable evidence that organic amendments cause changes to the whole soil nematode community, affecting the presence and abundance of different nematode groups (Bulluck et al. 2002; Nahar et al. 2006; Renčo et al. 2010). Recently a pilot study highlighted the potential of the nematode community as an indicator of compost status (Chapter 2). The soil nematode community, in turn, plays an important role in nutrient cycling because of its abundance, rapid life cycle and intricate interactions with soil microbes and predators (Ingham et al. 1985).

To date, only few studies have investigated the effect of compost on the soil food web (Bulluck et al. 2002; Leroy et al. 2007; Nahar et al. 2006; Renčo et al. 2010). To the best of our knowledge, in all these studies compost was treated as a black box, i.e. without or with little a priori knowledge on compost biotic properties, especially regarding the nematode community. Nevertheless, composts may vary significantly in chemical, physical and biological properties due to differences in feedstock composition, process and conditions of compost storage. The variation in compost composition, stability and maturity determines its effect on soil properties.

It is important to know to what extent effects of composts on soil biology are related to the communities living in the compost at the time of its application to soil.

In this study nematode abundance and community composition were analyzed together with chemical properties of different types of compost. Nine composts were produced on-farm from selected feedstock materials to obtain compost types with variable organic matter contents and concentrations of nutrients. These 9 composts, and 2 other composts obtained from other facilities, were thoroughly characterized chemically (especially concentrations of the macronutrients Ca, K, Mg and Na) and biologically (i.e. the nematofauna and fungal biomass). The overall objective of this study is to integrate a comprehensive picture of the factors determining nematode assemblage in compost and of how application of this compost with its associated nematodes affects soil nematode communities and their abiotic environment. To our knowledge, this study is the first to take into account the whole process, from the preparation of a compost to its effects on the soil biota. This main objective translates into the following specific hypothesis: (1) the selection of feedstock materials (e.g. wood chips vs. bark) would influence the nematode community and/or the chemical properties of composts; (2) the short-term (12 weeks long) effect of compost application on the macronutrients concentrations and the nematodes in the soil would be different for the different types of compost; and (3) the effects of compost application on the existent soil nematode community should be related to chemical compost properties.

### **7.3. MATERIALS AND METHODS**

The effect of feedstock composition on nematode community composition, nematode abundance and on compost chemical properties was investigated in a two-stage experiment consisting of composting trials (Section 7.2.1) and a soil incubation experiment (Section 7.2.2) using the composts obtained in the composting trials. The methods listed in Sections 7.2.3 and 7.2.4 were applied in both stages of the experiment.

#### **7.3.1. Compost trials**

Three separate compost trials were executed in open air on a concrete floor at the experimental farm of the Institute for Agricultural and Fisheries Research (ILVO at Melle, Belgium) (Figure 7.1). Each trial consisted of three different feedstock compositions. Selection of the feedstock materials for the compost trial treatments was based on the availability of on-farm waste materials (e.g. manure, hay, crop residues) and on the approximation of the proportion of 60%

brown and 40% green material as ideal starting point ([http://compost.css.cornell.edu/OnFarmHandbook/onfarm TOC.html](http://compost.css.cornell.edu/OnFarmHandbook/onfarm%20TOC.html)).

For the first trial, three compost windrows were set up (3-5 January 2007) with 31.5% on a volume to volume base (% v/v) grass hay and 63.5% (v/v) ground tree bark. Three types of tree bark were compared in these piles: oak (*Quercus robur*), poplar (*Populus* sp.) and Norway spruce (*Picea abies*), respectively. Additionally, 5% of poultry manure, mixed with wood shavings, was added. After 17 weeks of composting, the composts were further stored in piles for another 35 weeks.

For the second trial, three compost piles were set up (11-13 February 2008) with different ratios of grass hay and straw of clover on one hand, and ground poplar bark on the other, i.e. 25/75% (v/v), 50/50% (v/v) and 75/25% (v/v), respectively. The amount of grass hay in the three compost piles was 0, 23 and 46% (v/v), respectively. Additionally, urea was added after 2 weeks to correct the C/N content of the feedstock towards 30/1, which is generally considered an ideal starting ratio for composting (Zorpas 2009). After three weeks, cane molasses and spoiled ensilaged maize were mixed in the feedstock as a compost starter. After 16 weeks of composting, the composts were further stored in piles for another 16 weeks.

For the third trial, three compost piles were set up (2-4 March 2009) with 7% (v/v) crop residues of leek, 27% (v/v) of straw of grass, 16% (v/v) of spoiled ensilaged maize (as compost starter) and 50% (v/v) of ground tree bark or wood chips. Wood chips of willow, wood chips of poplar and ground poplar bark were used in the first, second and third windrow, respectively. The wood chips were harvested at the short rotation plantation at ILVO. No storage period was included in this trial.

In all trials, the feedstock materials were mechanically mixed with a windrow turner and composted in a windrow system with a length of 10 m per compost type. Temperature and CO<sub>2</sub> levels in the composts were monitored and when necessary, the composts were mixed with a Tractor-pulled Sandberger ST300 windrow compost turner and covered (with Top tex compost fleece) or rewetted.

After 52, 32 and 24 weeks respectively (cf. Figure 7.1), three bulk samples were taken from each trial treatment. Each bulk sample consisted of 10 individual samples ( $\pm 3$  l) which were lumped together. These were then sieved over a 20 mm mesh and the fraction <20 mm was stored in the refrigerator at 4 °C.

In addition to the 3 × 3 trial treatments, we also examined nematode composition of two additional composts: i.e. commercially available green waste compost and farm compost from another research station (i.e. external farm compost).

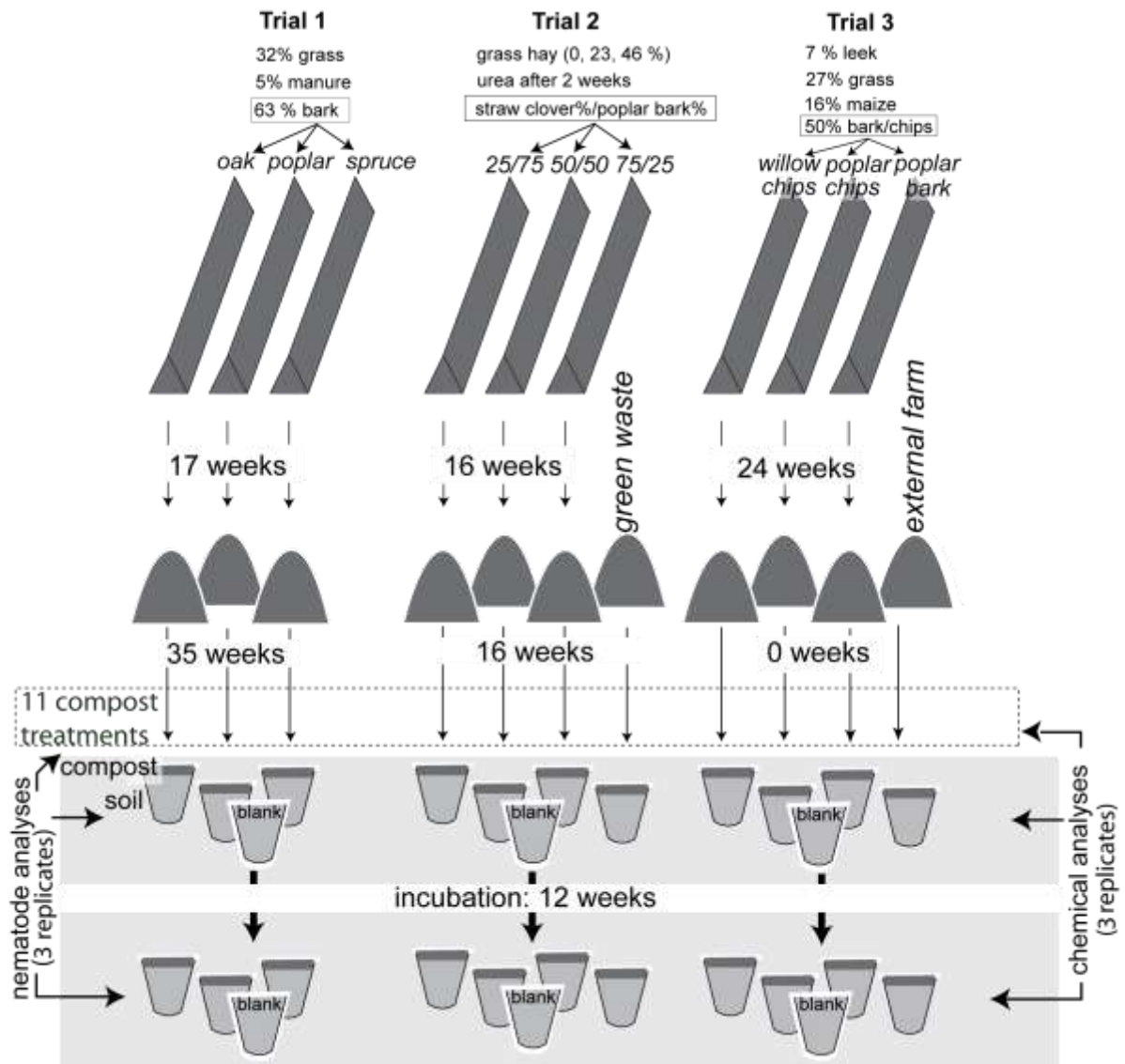
### 7.3.2. Incubation experiments

For each compost trial treatment with finished composts, an incubation experiment was set up (Figure 7.1) in which agricultural top soils were mixed with the different composts. Incubation experiments were performed in 5 l vessels with 4 replicates per treatment. Top layer material from soils under agricultural practice was used. For these initial soils both the chemical properties (Table 7.1) and the nematode community (except for trial 1) (Table 7.2) were characterized. Per vessel the equivalent of 50 tons fresh compost per ha was applied on a surface basis: 0.117 kg fresh compost was mixed with

1.64 kg dry mass of soil after adjusting the soil moisture content to 50% water-filled pore space. Soil bulk density after filling the vessels was  $1.4 \text{ kg dm}^{-3}$ . The vessels were closed with a cover provided with a small split for exchange of air. The vessels were kept for 12 weeks at  $17 \pm 2 \text{ }^\circ\text{C}$ , and the soil water content was adjusted every two weeks.

In addition, the green waste and farm compost (see Section 7.2.1) were included in the incubation experiments performed in 2008 (expt. 2) and 2009 (expt. 3) respectively.





**Figure 7.1:**

Experimental setup of the two-stage experiment. The upper level indicates which feedstock materials were used in which proportion and gives information about the time interval between the phases of the three composting trials. The lower level (in gray) displays the set up of the three incubation experiments. Arrows indicate which analyses were done on which samples.

**Table 7.1:**

Chemical properties of the soils used in the incubation trials (PAL: ammonium lactate extractable P, OC: organic carbon). Values illustrated are means ( $\pm$  SD) of 4 replicates.

	PAL (mg/100g dry soil)	pH-KCl	NO <sub>3</sub> -N (mg/kg dry soil)	NH <sub>4</sub> -N (mg/kg dry soil)	OC (%/dry soil)
Incubation 1	16.2 (0.9)	5.28 (0.07)	15.5 (0.9)	1.9 (0.3)	1.1 (0.1)
Incubation 2	51.3 (8.7)	6.44 (0.02)	11.5 (0.6)	1.8 (0.1)	1.6 (0.02)
Incubation 3	8.8 (0.9)	5.00 (0.04)	60.6 (6.3)	3.5 (0.3)	0.9 (0.02)

**Table 7.2:**

Nematode community of soils used in incubations with compost of trials 2 and 3 (Incubation 2 and Incubation 3 respectively). Average percentage of 3 samples per taxa with standard deviation in parentheses.

%	Incubation 2	Incubation 3
Fam. Rhabditidae	8.3 (0.8)	11.8 (3.6)
Fam. Cephalobidae	28.2 (3.8)	13.6 (2.7)
Fam. Aphelenchidae	0	18.4 (2.9)
Fam. Tylenchidae	4 (0.4)	22.9 (6.8)
Fam. Neotylenchidae	0	4.3 (1.7)
Ordo Dorylaimida	26.7 (2)	0.1 (0.1)
<i>Tylenchorhynchus</i> sp.	6.5 (3.4)	0
<i>Pratylenchus</i> sp.	15 (1.4)	0
<i>Ditylenchus</i> sp.	4.6 (1.7)	27.5 (4)
<i>Rotylenchus</i> sp.	4.7 (2)	0
<i>Mononchoides</i> sp.	0.9 (0.9)	0.6 (1)
<i>Steinernema</i> sp.	1.2 (0.58)	0
<i>Diplogasteritus</i> sp.	0	0.4 (0.6)

### 7.3.3. Nematode community analyses

The nematode communities of the compost (Section 7.2.1) and incubation (Section 7.2.2) experiments were analyzed. From each of the 33 (3 × 11) compost bulk samples (Section 7.2.1), 300 ml subsamples were taken and analyzed. For the incubation experiments, 200 ml of each of the three replicates of the initial soils (incubations 2 and 3 with compost of trials 2 and 3 respectively, see Figure 7.1), the soils after the incubation experiments and the untreated soils (Section 7.2.2), were analyzed. We used a modified Baermann funnel method (tray 49 cm × 37.5 cm, basket 38.5 cm × 19.5 cm) (Hooper 1986) for nematode extraction. Total nematode numbers were counted using a stereomicroscope (Leica MZ95). For light microscopy observations the specimens were collected in a very small drop of water in a staining block. Formaldehyde (4% with 1% glycerol) was heated to 70 °C and an excess (4-5 ml) was quickly added to the specimens to kill and preserve the nematodes (Seinhorst 1966). The preserved nematodes were processed to anhydrous glycerol following the glycerol-ethanol method (Seinhorst 1959, as modified by De Grisse 1969) and mounted on mass glass slides (slide 40 mm × 76 mm; cover glass 34 mm × 60 mm). Measurements and identification were done manually with a camera lucida on an Olympus BX 51 DIC microscope (Olympus Optical, Tokyo, Japan). For each subsample at least 100 nematodes were identified to family and genus whenever possible. The abundance (individuals/gram dry weight compost or soil) of each taxon in each sample was calculated based on the density and moisture content of the compost or soil. Nematode genera were assigned to the “coloniser-persister” cp-scale according to their *r* vs. *K* life-strategy characteristics (Bongers 1990, 1999) and were also classified according to their feeding type

(Yeates et al. 1993). These allocations were, respectively, used to calculate the sum Maturity Index (MI) (Bongers 1990, 1999), the f/b (fungal to bacterial-feeder) ratio and the Channel Index (CI). The f/b ratio and CI were used as indicators of the dominant decomposition pathway (Ferris et al. 2001; Ruess 2003).

#### **7.3.4. Chemical analyses of compost, blank soil and incubated soil**

Chemical analyses were performed for the compost trial treatments (3 subsamples for each of the 11 bulk samples, corresponding with the samples taken for the nematode analyses, cf. Section 7.2.3) and all replicates of the incubation experiments.

Sample preparation of composts for chemical analyses, determination of dry matter content (DM), moisture content and laboratory compacted bulk density were performed according to EN<sup>8</sup> 13040. Electrical conductivity (EC) (EN 13038) and pH<sub>H2O</sub> (EN 13037) in the compost samples were measured in a 1:5 soil to water suspension. Determination of organic matter (OM) and ash content in the composts was done according to EN 13039. Extraction of water-soluble nutrients and elements was performed according to EN 13652, and bulk elemental concentrations were measured with a Dionex DX-600 IC ion chromatograph (Dionex, Sunnyvale, CA). Ca, K, Mg and P were extracted in ammonium acetate and measured by simultaneous Inductively Coupled Plasma Optical Emission Spectrometry (ICP-OES, VISTA-PRO, Varian, Palo Alto, CA). Compost samples were dried for 4 days at 70 °C, mechanically ground in a cross beater mill (SK100, Retsch, Haan, Germany) equipped with heavy-metal-free grinding tools. Determination of organic matter (OM) and ash content in the composts was done according to EN 13039. Total N concentration in the compost samples was determined according to the modified Kjeldahl method (EN 13654-1). Pseudo-total element concentrations are measured by simultaneous ICP-OES, following ashing and digestion with HNO<sub>3</sub> (p.a. 65%).

As an indicator of compost stability, oxygen uptake rate (OUR) at 20 °C was calculated from the oxygen consumption due to microbial activity of 20 g compost (<1 cm fraction) in 200 ml buffered nutrient solution during 5 days of shaking in a closed Oxitop respirometer. OUR is expressed as mmol/kg OM/h. Ergosterol as a proxy for fungal biomass in the freeze-dried compost samples was measured with a Thermo Finnigan Surveyor HPLC with UV-VIS detector and a Waters Nova-Pak C18 4-µm column, after extraction with methanol based on physical disruption (Gong et al. 2001).

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<sup>8</sup> EN: European Standard. European Standards are developed by CEN, the European Commission for Standardization. Numbers refer to the specific protocols.

After twelve weeks the soils in the incubation vessels were sampled destructively and mineral nitrogen content (both NO<sub>3</sub>-N and NH<sub>4</sub>-N) was extracted in a 1 M KCl solution according to ISO<sup>9</sup> 14256-2 and measured with a Foss Fiastar 5000 continuous flow analyzer. Soil moisture content (expressed on a fresh weight basis) was determined as the weight loss at 105 °C after (at least) 24 h. pH was measured in a 1 M KCl solution according to ISO 10390. Ammonium lactate extractable P (PAL), K, Mg, Ca and Na were determined by shaking 5 g air-dried soil in 100 ml ammonium lactate for 4 h (Egnèr et al. 1960), and measured with a simultaneous ICP-OES (VISTA-PRO, Varian, Palo Alto, CA). The blank soil at the start of the incubation experiment was analyzed similarly, and the organic carbon content was measured with a Skalar Primacs SLC TOC-analyzer according to ISO 10694.

### **7.3.5. Statistical analyses**

#### Compost trials

Differences in abiotic parameters, nematode densities and nematode-based indices ( $\Sigma$ MI, CI and f/b ratio) between different composts were analyzed using one-way ANOVA in Statistica 6.0 (Statsoft Inc.); differences in their nematode community composition were analyzed using Analysis of Similarities (ANOSIM) and Similarity Percentages analysis (SIMPER) in Primer 6 (Clarke and Warwick 2001). The relationship between variation in nematode community composition and the measured abiotic parameters was analyzed using ordination techniques in Canoco for Windows, version 4.5 (ter Braak and Smilauer 1998).

ANOVA assumptions were tested using the Kolmogorov-Smirnov statistic for normality and Levene's test for homogeneity of variances. To fit the assumptions the nematode densities and the CI data were square-root transformed while the f/b ratio data were log-transformed. All one-way ANOVA analyses were followed by post hoc pair wise comparisons using Tukey's HSD. However, it should be noted that because of the scale of the compost heaps and the duration of the composting process in the on-farm composting trials (Section 7.2.1), proper replication of compost types and trials was not feasible. Hence, replicate samples were taken from single compost heaps and are thus essentially pseudoreplicates. Furthermore, although the duration of composting in the different trials was not identical, we analyzed data of the three different trials in one analysis to be able to compare all composts, which was one of the prime goals of this study.

The ANOSIM analyses were performed comparing green vs. farm composts, trials and used feedstock materials, and were based on Bray-Curtis similarity matrices of square-root

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<sup>9</sup> ISO: International Organization for Standardization. Numbers refer to specific approved protocols by ISO.

transformed abundance data. SIMPER was used to identify which species were primarily responsible for the differences between nematode assemblages.

For the ordination analysis a preliminary Detrended Correspondence Analysis (DCA) using detrending by segments revealed a weak turnover in species composition between the samples (length of gradient < 2.5 SD, cf. Jongman et al. 1995). Hence, we used a linear constrained technique, viz. Redundancy Analysis (RDA), for our analyses. The data set consisted of the  $\log(x + 1)$  transformed abundances (numbers of individuals/gDM) of 11 nematode taxa in 28 samples. Only one replicate sample of the external farm compost was retained and the green waste compost was excluded due to missing values. The forward selection procedure in RDA was used to select only those variables that contributed significantly to the variation in the nematode data using Monte Carlo permutation tests (4999 permutations). The remaining, non-selected abiotic variables were introduced as supplementary (passive) variables.

Spearman rank correlations between mean relative bacterial-feeding nematode abundances, fungal-feeding nematode abundances and ergosterol concentrations in the composts were calculated in Statistica 6.0.

#### Incubation experiments

Differences in the effect of compost addition on abiotic soil properties (mineral nitrogen content (Nmin), pH-KCl and ammonium lactate extractable P, K, Mg, Ca and Na), nematode densities and nematode based indices ( $\Sigma$ MI, CI and f/b ratio) were analyzed using one-way ANOVA in Statistica 6.0 (Statsoft Inc.); the effects on the soil nematode community were analyzed using MANOVA in PERMANOVA (PRIMER).

Separate analyses were performed for each incubation experiment. One-way ANOVA analyses and subsequent post hoc Tukey HSD tests were performed on log-transformed data for K, Na, P, Nmin and total nematode numbers and on square-root transformed data for  $\Sigma$ MI, CI and f/b ratio. Due to the small sample size (i.e. 3 replicates per treatment for the nematode data), ANOSIM was not able to locate the significant differences in nematode communities of the overall test using pair-wise tests. Therefore, a one-way permutational MANOVA (PERMANOVA) with compost as a fixed factor was performed. Monte Carlo p-values were used to indicate significant differences in the pair-wise comparisons. PERMDISP (distances to centroid) in PRIMER was used to test homogeneity of multivariate dispersions among a priori groups (i.e. compost). When PERMDISP indicates that the homogeneity requirement is fulfilled, an observed significant effect can be confidently attributed to a real difference between groups and not to differences in variances between groups.

## 7.4. RESULTS

### 7.4.1. Chemical compost properties

In general, the farm composts were rich in OM (values between  $43.4 \pm 4.3$  and  $75 \pm 3.3\%$ /DM) (Table 7.3), due to the choice of feed-stock materials with a relatively low soil particle load and high amount of lignin-rich materials. The green waste compost is characterized by a significantly (one-way ANOVA,  $p < 0.001$ ) higher dry matter (DM) content (i.e.  $56.1 \pm 3.05\%$  compared to values between  $23.1 \pm 0.5$  and  $38.3 \pm 0.5\%$  in the farm compost), significantly (one-way ANOVA,  $p < 0.001$ ) higher EC value (i.e.  $1254 \pm 53.1 \mu\text{S}/\text{cm}$  compared to values between  $284 \pm 9.9$  and  $984.5 \pm 93.2 \mu\text{S}/\text{cm}$  in the farm compost) and a significantly (one-way ANOVA,  $p < 0.02$ ) lower C/N ratio ( $13 \pm 2.3$  compared to values between  $17.4 \pm 1.5$  and  $30.1 \pm 1.4$  in the farm compost) (Table 7.3). Within the farm composts, the Norway spruce bark compost and the willow wood chips compost had a significantly (one-way ANOVA,  $p < 0.03$ ) lower pH ( $7.3 \pm 0.1$  and  $7.2 \pm 0.5$  respectively) (Table 7.3). Large differences of Ca, Na, K and Mg concentrations between the composts were found, for both total (tot) (Table 7.4) and plant-available (plant) (Table 7.5) concentrations, and high concentrations in the feedstock materials (Table 7.4) resulted in high concentrations in the final compost. For instance, in trial 1, oak bark and Norway spruce had the highest and lowest Ca concentration respectively and this resulted in the highest and lowest Ca concentrations in finished oak bark and Norway spruce composts, for both total and plant-available concentrations. When considering compost stability, all composts, except for the willow wood chips compost and the poplar wood chips compost, had a low OUR, as values were lower than  $10 \text{ mmol}/\text{kg OM}/\text{h}$ , values typical for stable composts (Veeken et al., 2003) (Table 7.6). Ergosterol contents (Table 7.6) were significantly (one-way ANOVA,  $p < 0.001$ ) higher for the willow wood chips compost ( $72 \pm 3.4 \mu\text{g}/\text{g DM}$ ) and the external farm compost ( $50.8 \pm 4.8 \mu\text{g}/\text{g DM}$ ).

**Table 7.3:**

P concentration, organic matter (OC) content and dry matter (DM) content in composts during the 3 composting trials and for external composts (E). Values are averages of 3 samples per compost with standard deviations in parentheses. For the external farm compost, only 1 replicate was analyzed for NO<sub>3</sub>-N, NH<sub>4</sub>-N, pH and EC, and only 2 replicates were measured for the other properties.

Compost and trial		N-NO <sub>3</sub> mg/l compost	N-NH <sub>4</sub> mg/l compost	pH-H <sub>2</sub> O -	EC μS/cm	DM %	Total N %/DM	C/N -	P <sub>tot</sub> mg/kg DM	OM % /DM
Oak bark	1	82.1 (3.8)	<5	8.7 (0.2)	718.8 (76.4)	29.3 (0.9)	1.7 (0.1)	19.2 (1.2)	4895 (224.3)	59.6 (0.7)
Poplar bark 1	1	81.7 (9.5)	<5	8.2 (0.1)	519.8 (33)	22.8 (0.3)	1.9 (0.1)	19.7 (1.5)	6958.2 (1277.1)	65.7 (1.7)
Norway spruce bark	1	29.1 (3)	<5	7.2 (0.5)	294.8 (19)	24.2 (0.2)	1.6 (0.1)	25.6 (0.6)	4546.8 (875)	71.9 (1.6)
75% poplar bark	2	93.5 (5.8)	7.5 (3.25)	9.4 (0.6)	901.3 (58.1)	23.1 (0.5)	2 (0.1)	19 (1.1)	3335.6 (524.7)	69.7 (2.3)
50% poplar bark	2	94.9 (11.3)	<5	9 (0.1)	984.5 (93.2)	29.5 (1.9)	1.9 (0.1)	17.4 (1.5)	3872.8 (291)	60.5 (1.3)
25% poplar bark	2	70.6 (8.8)	<5	9.1 (0.1)	983.5 (49.5)	26.6 (1)	1.8 (0.1)	18.9 (1)	4277.4 (158.7)	62.1 (1.3)
Willow wood chips	3	<5	<5	7.3 (0.1)	284.3 (9.9)	34.1 (0.6)	1.4 (0.1)	30.1 (1.4)	2403.2 (123.1)	75 (3.3)
Poplar wood chips	3	0.3 (0.6)	<5	7.8 (0.1)	311.5 (27.5)	27.8 (0.4)	1.6 (0.1)	25.2 (0.3)	2926.4 (168)	71.4 (0.5)
Poplar bark 2	3	24 (2.1)	<5	8.2 (0.1)	615.3 (38.5)	38.3 (0.5)	1.2 (0.1)	19.6 (2.1)	1514.8 (128.6)	43.4 (4.3)
Green waste	E	235.9 (4.9)	<5	7.8 (0.1)	1254.3 (53.1)	56.1 (3.1)	1.2 (0.1)	13 (2.3)	3159.5 (144.1)	28.4 (4.7)
External farm	E	78.4	<5	8.3	868	38.5 (1.1)	1.5 (0.01)	24.6 (0.1)	2063.4 (88.1)	66.2 (0.8)

**Table 7.4:**

Total macronutrient concentrations in the feedstock materials (F) and the composts (C). Values are averages of 3 samples per compost. Values in parentheses are standard deviations of three replicates.

Material	Type	Ca (g/kg DM compost)	Na (g/kg DM compost)	K (g/kg DM compost)	Mg (g/kg DM compost)
Poultry manure	F	20.4 (2.8)	3.06 (0.43)	30.2 (3.6)	4.8 (0.5)
Straw of grass 1	F	2.5 (0.2)	0.1 (0.02)	4.2 (0.9)	0.9 (0.2)
Oak bark	F	17.6 (2.7)	0.15 (0.01)	2.4 (0.1)	0.6 (0)
Poplar bark 1	F	14.8 (1.2)	0.16 (0.01)	3.7 (0.4)	1 (0)
Norway spruce bark	F	7 (1.4)	0.08 (0.02)	1.6 (0.3)	0.9 (0.1)
Oak bark	C	47.1 (0.7)	0.95 (0.07)	10.5 (0.6)	3.8 (0.1)
Poplar bark	C	43.7 (0.2)	0.74 (0.02)	8.5 (0.1)	4.5 (0.1)
Norway spruce	C	31.2 (3)	0.69 (0.03)	7.7 (0.2)	3.8 (0.2)
Straw of grass 2	F	2.3 (0.6)	0.22 (0.13)	12.2 (1.3)	0.5 (0.1)
Straw of clover	F	16.2 (4.2)	0.5 (0.03)	37.2 (2.7)	3.3 (1.2)
Poplar bark 2	F	23.4 (3.1)	0.33 (0.05)	4.7 (0.2)	1.2 (0)
Ensilaged maize 1	F	4 (0.9)	0.37 (0.08)	20.9 (2.4)	3.1 (0.7)
75% poplar bark	C	44.3 (4.1)	0.75 (0.03)	16.6 (0.6)	4.3 (0.3)
50% poplar bark	C	51.6 (2.7)	0.69 (0.01)	17 (0.2)	4.4 (0.1)
25% poplar bark	C	40.5 (1.8)	0.63 (0.03)	18.7 (0.8)	4.2 (0.1)
Willow wood chips	F	5.3 (0.9)	0.13 (0.01)	2.9 (0.2)	0.5 (0)
Poplar wood chips	F	5.6 (1.7)	0.08 (0)	3.7 (0.1)	0.7 (0.1)
Poplar bark 3	F	26.1 (1.4)	0.71 (0.06)	6.1 (0.8)	1.3 (0.1)
Leek	F	6.8 (2.3)	0.39 (0.05)	11.9 (0.5)	1 (0.1)
Straw of grass 3	F	2.8 (0.5)	0.1 (0.02)	1.6 (0.4)	0.5 (0.1)
Ensilaged maize 2	F	1.8 (0.2)	0.09 (0.01)	10.5 (0.4)	1.2 (0.1)
Willow wood chips	C	10.3 (0.7)	0.38 (0.01)	9.7 (0.6)	1.4 (0.1)
Poplar wood chips	C	11.7 (0.4)	0.32 (0.01)	11.4 (0.4)	1.8 (0.1)
Poplar bark	C	20.9 (1.3)	0.58 (0.03)	7.4 (0.6)	1.8 (0.2)
Green waste	C	23.7 (1.6)	1.05 (0.07)	8.1 (1)	4 (0.2)
External farm	C	49 (2.4)	0.7 (0.01)	15.6 (0.4)	5.2 (0.1)

**Table 7.5:**

Plant-available element concentrations in the composts. Values are averages of 3 samples per compost. Values in parentheses are standard deviations of three replicates (except for \*where analyses were not replicated).

Compost	Trial	Ca (mg/l compost)	Na (mg/l compost)	K (mg/l compost)	Mg (mg/l compost)	P (mg/l compost)
Oak bark	1	4146 (225)	206 (36)	1731 (243)	356 (23)	598 (40)
Poplar bark 1	1	4622 (289)	176 (12)	1619 (120)	510 (35)	815 (46)
Norway spruce bark	1	2195 (124)	142 (8)	1216 (78)	347 (18)	373 (24)
75% poplar bark	2	3398 (355)	94 (5)	2428 (127)	388 (30)	234 (23)
50% poplar bark	2	3332 (280)	81 (5)	2290 (65)	343 (16)	220 (16)
25% poplar bark	2	2776 (162)	70 (3)	2497 (82)	343 (15)	280 (14)
Willow wood chips	3	746 (124)	37 (4)	1042 (137)	128 (21)	116 (20)
Poplar wood chips	3	958 (41)	35 (1)	1278 (24)	186 (8)	137 (10)
Poplar bark 2	3	2565 (105)	130 (10)	1844 (111)	307 (18)	155 (10)
Green waste	E	3919 (403)	395 (33)	2939 (242)	531 (16)	340 (9)
External farm*	E	2836	108	2349	360	292



**Table 7.6:**

Ergosterol concentration as indicator of fungal biomass in composts (values in parentheses are standard deviations of 3 samples per compost pile), oxygen uptake rate (OUR) as an indicator of compost stability (NA: not assessed), and fresh bulk density of the tested composts.

Compost	Trial	Ergosterol ( $\mu\text{g/g DM compost}$ )	OUR (mmol/kg OM/h)	Bulk density (g/l compost)
Oak bark	1	8.5 (1.2)	2.5	594.2
Poplar bark 1	1	7.9 (2.2)	2.3	604.2
Norway spruce bark	1	9.2 (1.0)	1.8	556.5
75% poplar bark	2	7.0 (0.9)	3.8	522.6
50% poplar bark	2	7.7 (3.4)	3.5	538.8
25% poplar bark	2	7.1 (1.1)	3.5	575.9
Willow wood chips	3	72 (3.4)	10.1	381.0
Poplar wood chips	3	13.3 (2.3)	9.4	433.6
Poplar bark 2	3	17.8 (3.6)	4.3	593.7
Green waste	E	NA	1.8	589.1
External farm	E	50.8 (4.8)	6.6	403.0

#### 7.4.2. Nematode community in composts

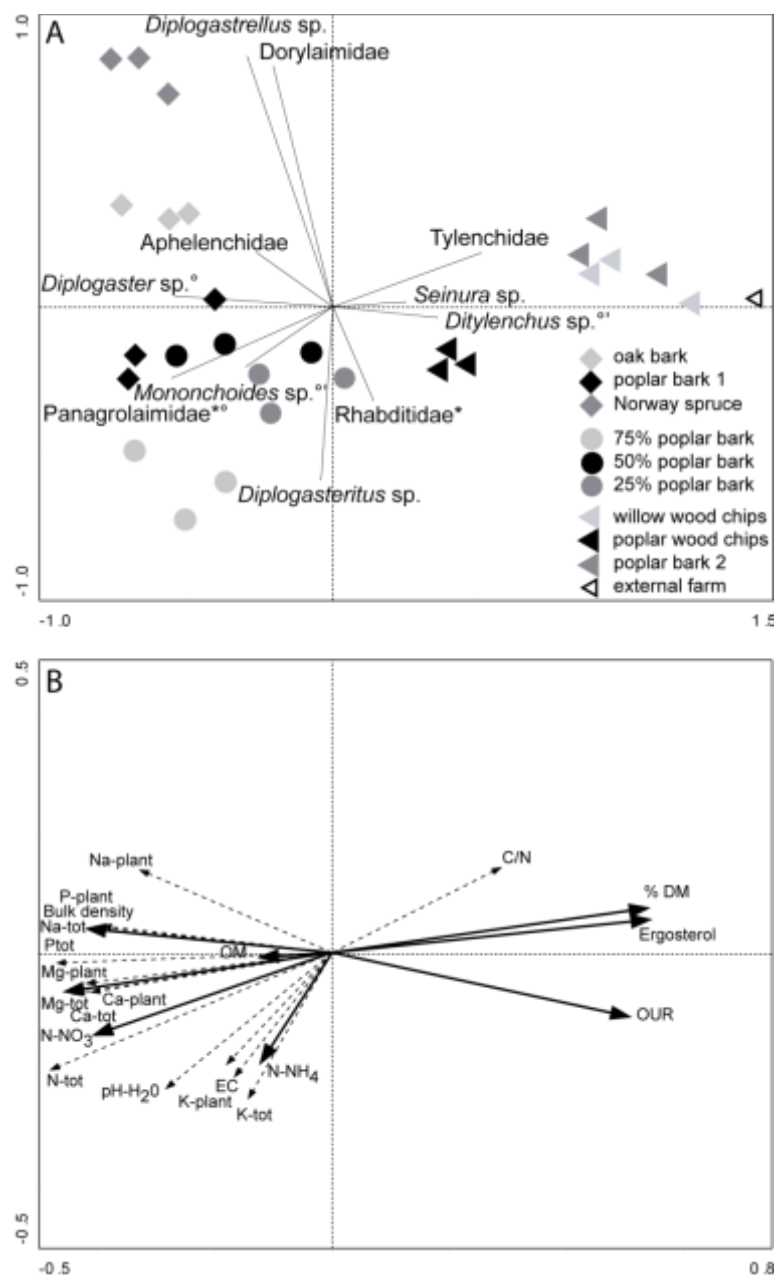
All analyzed composts contained a relatively high abundance and diversity of nematodes (Table 7.7). Total numbers of nematodes were significantly higher (one-way ANOVA,  $p < 0.02$ ) in farm composts (range  $9 \pm 1.1$  to  $44.3 \pm 6.6$ /g DM compost) compared to the green waste compost ( $3.3 \pm 0.4$ /g DM). The highest abundances of nematodes ( $>30$ /g DM compost) were found in the poplar wood chips compost ( $44.3 \pm 6.6$ /g DM), the willow wood chips compost ( $40 \pm 7.2$ /g DM), the compost with 25% poplar bark ( $34.3 \pm 3.8$ /g DM) and the poplar bark 1 compost ( $31 \pm 5.2$ /g DM). The fungivorous *Ditylenchus* sp. was present in all composts and was the most prominent species (42-80%), except for the compost with 75% poplar bark and the green waste compost, where, respectively, species from the bacterivorous families Panagrolaimidae ( $40.3 \pm 17.7\%$ ) and Rhabditidae ( $48.8 \pm 11.3\%$ ) were dominant. The second most common nematodes belonged to the bacterivorous family Rhabditidae (12-29%) in all composts except in the green waste compost where they were the most abundant taxon, in the external farm compost and in the poplar bark 1 compost. In the latter two composts the second most common taxa were, respectively, the putative fungivorous *Ditylenchus* sp. and Tylenchidae, and the bacterivorous Panagrolaimidae. All composts, except for the poplar wood chips compost, also contained the bacterial-feeding/predatory diplogasterids; in six out of eleven composts (i.e. the oak bark compost, the poplar bark 1 compost, the Norway spruce compost, the green waste compost and the composts with 75% and 50% poplar bark) they had a share of 10 to 20% in the total nematode community, prominent taxa being *Mononchoides composticola*, *Diplogaster* sp., *Diplogastrellus* sp. and *Diplogasteritus* sp. The species composition of the green waste compost

was significantly different (ANOSIM,  $p = 0.001$ ) from the average species composition of the farm composts.

The RDA forward selection procedure, executed with the farm composts, selected 8 abiotic variables (Mg-tot, Na-tot, N-NH<sub>4</sub>, N-NO<sub>3</sub>, ergosterol, %DM, %OM and OUR) which together significantly explain 80% of the variation in the nematode data. The first two RDA axes (Figure 7.2) capture more than half (56%) of the total variation in the nematode data. The first RDA axis represents the most important gradient (43%) in species composition and separates the composts of trial 3 (i.e. the willow wood chips, the poplar bark 2, the external farm compost and to a lesser degree the poplar wood chips compost) from the other composts from trial 1 and 2. These composts are characterized by higher abundances of *Seinura* sp., *Ditylenchus* sp. and Tylenchidae, and have significantly ( $p < 0.05$ ) higher values for OUR, ergosterol and %DM, and lower values for all other abiotic variables. Consistent with ergosterol as a proxy for fungal biomass, there was a significant ( $p = 0.0004$ ) positive correlation ( $R = 0.79$ ) between ergosterol content and the relative abundance of fungal-feeding nematodes, and a significant ( $p = 0.004$ ) negative correlation of ergosterol content with the relative abundance of bacterial-feeding nematodes ( $R = -0.87$ ). The composts with the highest ergosterol content also contained the highest proportion of fungal-feeders. Variation along the second RDA axis is less pronounced (13% of the variation in the nematode data). Along this axis, the oak bark and the Norway spruce compost (with higher *Diplogastrellus* sp. and Dorylaimida abundance) are separated from the poplar bark composts (i.e. the poplar bark 1 compost and the composts of trial 3), which have higher *Diplogasteritus* sp. and Rhabditidae abundance, and are characterized by significantly ( $p < 0.05$ ) higher ammonia values and also higher values for pH, K-plant, K-tot and EC.

As illustrated in Figure 7.2, the species composition of the composts differed significantly between all three composting trials (ANOSIM,  $p < 0.02$ ), suggesting that differences between trials were at least as large as between composts which partly differed in feedstock materials. The taxa responsible for the discrimination between the trials (SIMPER) are: Panagrolaimidae and Rhabditidae for trial 1 vs. 2; Panagrolaimidae, *Diplogaster* sp., *Ditylenchus* sp. and *Mononchoides composticola* for trial 1 vs. 3 and *Diplogaster* sp. and *M. composticola* for trial 2 vs. 3 (Figure 7.2). According to functional group composition (bacterial-feeding, fungal-feeding and bacterial-feeding/predators) trials 1 and 2 are both significantly different (ANOSIM,  $p = 0.001$ ) from trial 3. Nematode assemblages did not differ significantly between different selections of bark or chips except between poplar bark and the willow wood chips (ANOSIM,  $p = 0.02$ ). The oak bark, the 75% poplar bark and the green waste composts had a significantly lower (one-way ANOVA,  $p < 0.05$ )  $\Sigma$ MI compared to the other composts, while the compost of trial 3

showed significantly higher (one-way ANOVA,  $p < 0.05$ )  $\Sigma$ MI than all other composts except for the Norway spruce and the 25% poplar bark composts. The composts of trial 3 also tended to have a higher f/b ratio and CI (Table 7.7), with the highest overall f/b ratios and CI for the willow wood chips compost (i.e.  $6.53 \pm 1.23$  and  $61.6 \pm 4.8$  respectively) and the poplar bark 2 compost (i.e.  $6.30 \pm 4.32$  and  $57 \pm 15$  respectively), both with a significantly ( $p \leq 0.05$ ) higher f/b ratio and CI than all composts of trials one and two. The 75% poplar bark compost had a significantly lower (one-way ANOVA,  $p < 0.01$ ) f/b ratio and CI than all other composts except for the green waste compost.



**Figure 7.2:**

Species-sample (A) and environmental-supplementary environmental (B) biplots of a Redundancy Analysis summarizing the effects of compost composition on nematode composition. Sample symbols show the replicates of the compost trial treatments. Abiotic parameters selected in the FS procedure (see text) are indicated with solid arrows, supplementary abiotic variables are represented by dashed arrows. For more details, see text. Results of SIMPER, indicating taxa responsible for discrimination between trials are presented with \*for trial 1 and 2, °for trial 1 and 3 and °for trial 2 and 3 in (A).

### 7.4.3. Effect of compost on soil chemical properties

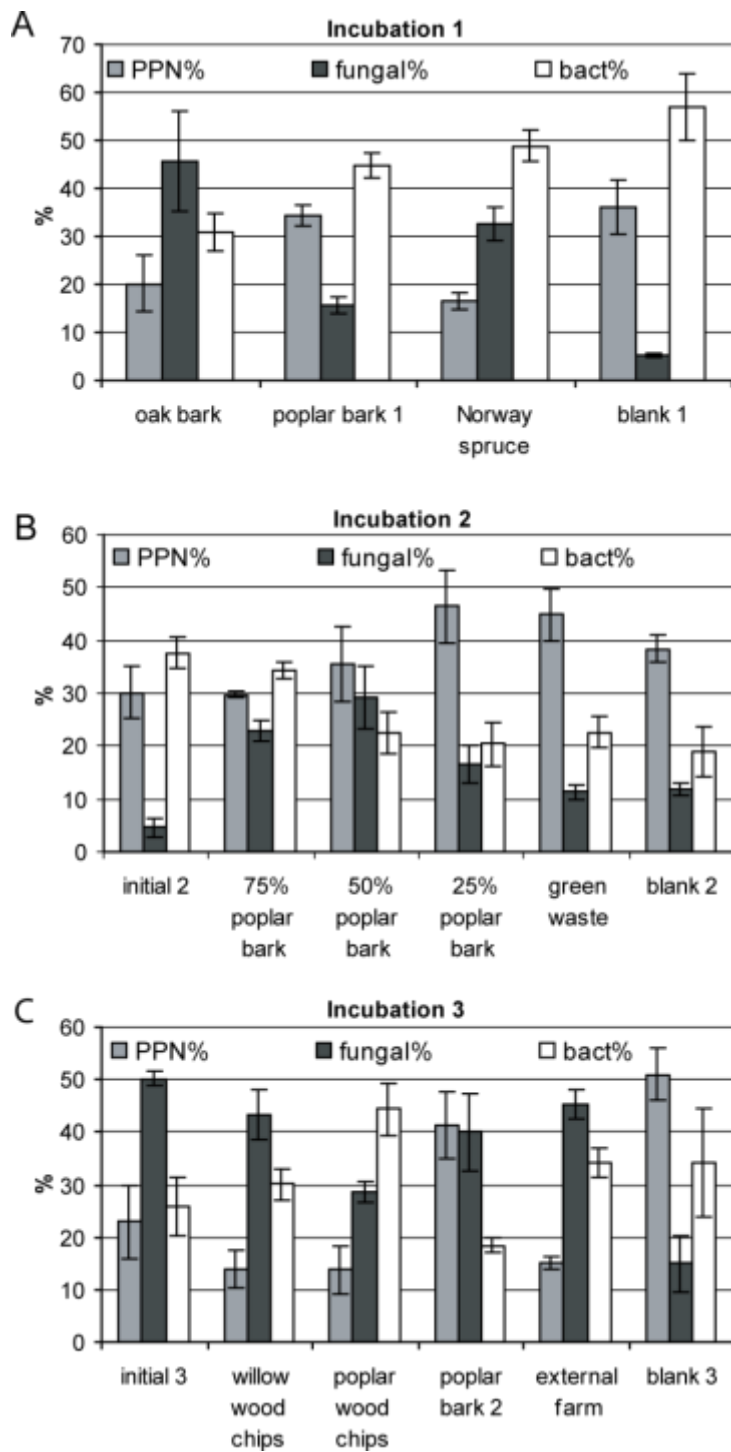
After 12 weeks of incubation, the main effect of compost on the soil properties was a significant increase in soil pH (one-way ANOVA,  $p < 0.01$ ) (Table 7.8), while in blank treatments the pH slightly decreased after 12 weeks of incubation when compared to the initial pH (Table 7.1). Another overall effect of compost application was a significant (one-way ANOVA,  $p < 0.01$ ) increase in ammonium lactate extractable K concentrations compared to blank treatments (Table 7.8). The other parameters (i.e. mineral N ( $N\text{-NO}_3 + N\text{-NH}_4$ ) and ammonium lactate extractable Mg, Ca, Na and P) did not show an overall trend compared to the blank treatments, although some significant changes within incubation experiments were detected (Table 7.8). N mineralization in the compost-amended soil was significantly higher (one-way ANOVA,  $p < 0.01$ ) compared to the blank treatments for incubation with composts of trials 1 and 2, except for the Norway spruce bark compost, but not for incubation with composts of trial 3. Both plant-available Mg and Ca concentrations significantly (one-way ANOVA,  $p < 0.01$ ) increased in the soil for all composts except for the poplar bark composts in incubation 2 and the willow wood chips and the poplar wood chips composts of incubation 3, respectively. Significantly higher Na concentrations were only detected after incubation with green waste compost (one-way ANOVA,  $p < 0.05$ ). For soils high in PAL, used in incubation experiment 2 (Table 7.1), no significant increases after incubation were detected (Table 7.8). High soil concentrations of plant-available Ca, Na, Mg and K (Table 7.8) after incubation with compost correspond to high plant available concentrations in the composts (Table 7.5), which were, as described above (see Section 7.3.1), the result of high concentrations in the feedstock materials. This might indicate that, from a chemical point of view, the fertilizing effect of compost on soil can be manipulated by feedstock selection.

### 7.4.4. Nematode community after 12 weeks of incubation

The average number of nematodes per g DM soil (Table 7.7) was higher after the compost treatments (5-23/g DM) compared to the treatments without amendment (3-6/g DM). In 6 of the 11 treatments this increase was significant (one-way ANOVA, all  $p \leq 0.03$ ). The latter was not the case for the treatments with poplar bark 1 compost, Norway spruce bark compost, compost with 75% and 25% poplar bark and green waste compost. With only one exception (i.e. the 25% poplar bark compost) the nematode species compositions of the compost treatments were significantly different from the control treatments in the corresponding incubation experiment (PERMANOVA,  $p(\text{MC}) < 0.015$  for incubation 1,  $p(\text{MC}) < 0.034$  for incubation 2 and  $p(\text{MC}) < 0.007$  for incubation 3). Compost treatment did not result in an unequivocal effect on the proportion

of plant-parasitic nematodes (Figure 7.3). In the first two incubations the proportions of plant-parasitic nematodes in compost treated soil remained stable or slightly increased, whereas in incubation 3 the proportion of plant-parasitic nematodes slightly decreased compared to the untreated soil. Similarly, compost amendment had a variable effect on the relative proportions of bacterial-feeding nematodes (Figure 7.3). However, species of the fungal-feeding genus *Ditylenchus* increased following all compost treatments, except for the green waste compost. This increase was significant (one-way ANOVA,  $p < 0.03$ ) for all compost treatments, except for the treatments with 75% and 25% poplar bark composts and was on average equivalent to 1.94 specimens of *Ditylenchus* sp. per g soil DM compared to treatments without compost. Note that all *Ditylenchus* sp. are considered as fungal-feeding here, since species that are known to be epidermal cell or root hair feeders were not identified. Survival of compost nematodes appeared possible, e.g. specimens of the invertebrate predator *Seinura* sp. were found in compost and in compost-amended soil after 12 weeks of incubation, but not in the initial soil 2 nor in the control treatment. However, the diplogasterid nematodes, bacterivorous (*Diplogasteritus* sp. and *Diplogastrellus* sp.) or bacterivorous-predatory (*Mononchoides composticola* and *Diplogaster* sp.) species were most likely not retained from the compost since they were only present in very low numbers (<3%) and in very few compost-amended soils (treated with oak bark compost, Norway spruce compost and the composts with 75% and 50% poplar bark) after 12 weeks of incubation.

No clear trend was observed for the  $\Sigma$ MI (Table 7.7) in compost-treated soils compared to the untreated soils. The  $\Sigma$ MI significantly increased after treatment with poplar bark 1 compost in incubation 1 (one-way ANOVA,  $p < 0.002$ ) but significantly decreased in treatment with willow wood chips and poplar wood chips compost in incubation 3. The f/b ratio and CI (Table 7.7) in farm compost treatments increased during all incubations compared to the treatment without compost. However, this increase was not significant ( $p > 0.05$ ) for treatments with poplar bark compost 1, composts with 75% and 25% poplar bark and the poplar wood chips compost.



**Figure 7.3:** Relative abundances of plant-parasitic nematodes (PPN%), fungal-feeding nematodes (fungal%) and bacterial-feeding nematodes (bact%) after 12 weeks of incubation. Treatments displayed per incubation experiment with blank treatments and composition of the initial soil when available.



**Table 7.8:**

Soil properties (mean based on 3 replica's and standard deviation in parentheses), of the soils after 12 weeks of incubation (Nmin = N-NO<sub>3</sub> + N-NH<sub>4</sub>). Treatments were compared with one-way ANOVA for each incubation trial separately. Means that are significantly different are denoted with different letters (one-way ANOVA and subsequent post hoc Tukey HSD tests on log-transformed data).

Compost	Incubation exp.	pH-KCl	Nmin (mg/kg DM)	P (mg/100g DM)	K (mg/100g DM)	Mg (mg/100g DM)	Mn (mg/100g DM)	Ca (mg/100g DM)	Na (mg/100g DM)
Oak bark	1	5.81 (0.06) c	61.7 (4.4) bc	22.3 (1.2) b	23.3 (0.6) c	11.2 (0.7) b	12.6 (0.7) b	85.4 (5.8) b	3.3 (1.1) a
Poplar bark 1	1	5.92 (0.06) c	54.1 (3.4) c	22.5 (1.0) b	21.0 (0.7) b	10.8 (1.1) b	11.3 (0.4) a	82.7 (6.4) b	1.9 (0.6) a
Norway spruce bark	1	5.49 (0.10) b	50.5 (4.1) ab	20.5 (1.3) b	23.4 (0.9) c	11.3 (0.3) b	14.1 (0.6) c	76.1 (5.3) b	3.4 (1.1) a
Blank 1	1	5.14 (0.01) a	42.3 (5.0) a	16.5 (1.3) a	13.7 (0.5) a	7.5 (0.3) a	10.8 (0.5) a	59.0 (1.2) a	1.7 (1.0) a
75% poplar bark	2	6.40 (0.01) b	48.1 (4.3) b	50.4 (3.3) a	57.0 (0.7) c	19.1 (0.1) a	8.5 (0.3) a	113.5 (0.7) ab	2.9 (0.4) a
50% poplar bark	2	6.46 (0.03) b	45.5 (11.6) b	50.1 (2.7) a	58.2 (0.8) c	19.8 (0.7) a	8.5 (0.4) a	118.9 (4.6) bc	2.7 (0.2) a
25% poplar bark	2	6.40 (0.04) b	54.1 (2.4) b	51.3 (1.9) a	59.6 (2.7) c	19.8 (0.8) a	8.6 (0.2) a	111.7 (4.5) ab	2.6 (0.3) a
Green waste	2	6.46 (0.09) b	56.9 (4.9) b	49.1 (8.0) a	53.1 (1.3) b	23.3 (0.4) b	9.0 (1.4) a	125.8 (2.4) c	6.6 (0.3) b
Blank 2	2	6.15 (0.01) a	30.0 (0.7) a	46.9 (4.0) a	30.2 (1.4) a	19.0 (0.6) a	8.5 (0.4) a	103.9 (2.7) a	2.1 (0.3) a
Willow wood chips	3	5.37 (0.05) b	93.2 (22.2) a	12.2 (0.6) b	36.6 (2.4) b	7.5 (0.5) b	2.2 (0.1) b	54.3 (4.4) a	7.4 (1.3) a
Poplar wood chips	3	5.36 (0.04) b	102.1 (17.1) a	12.0 (0.6) b	35.6 (1.6) b	7.7 (0.2) b	2.2 (0.1) b	53.7 (1.0) a	6.3 (0.5) a
Poplar bark 2	3	5.71 (0.04) c	117.1 (17.6) a	11.7 (0.4) a	34.2 (0.8) b	8.5 (1.0) b	2.3 (0.2) b	72.6 (8.2) b	6.8 (1.1) a
External farm	3	6.30 (0.01) d	107.3 (14.7) a	13.3 (0.2) b	47.6 (1.8) c	11.2 (0.5) c	3.0 (0.2) c	88.7 (4.5) c	5.8 (0.7) a
Blank 3	3	4.91 (0.01) a	82.8 (6.6) a	10.0 (0.8) a	23.7 (1.9) a	4.9 (0.2) a	1.5 (0.1) a	45.2 (2.0) a	5.9 (1.0) a



## 7.5. DISCUSSION

### 7.5.1. Omnipresence of nematodes in composts and their potential to reflect compost status

In all composts in this study, relatively high abundances of nematodes were found (on average 26 nematodes/g DM), the only exception being the green waste compost with only  $3 \pm 0.4$  nematodes/g DM, whereas for the farm compost densities from approximately 10-50 nematodes/g DM were found, which tends to be higher than previously described abundances for farm compost ( $9.3 \pm 1$  nematodes/g DM; Chapter 2), and which meets the standard of 20-100 beneficial nematodes/g DM of the Soil Foodweb Inc. company (except for the poplar bark 2 compost). These densities are comparable to nematode densities commonly found in soil under agricultural use, where between 1 and 250 nematodes/g DM are found (Freckman and Ettema 1993; Hu and Qi 2010a; Liang et al. 2005; Vikeft et al. 2011). However, these numbers all include also plant-parasitic nematodes while in compost only free living nematodes are found. The taxon composition for all analyzed composts in this study was remarkably similar to that described in Chapter 2 with *Mononchoides composticola*, *Diploscapter coronatus*, *Halicephalobus gingivalis*, *Ditylenchus* sp., *Diplogaster* sp., *Diplogastrellus* sp. and *Diplogasteritus* sp. being virtually omnipresent. The trophic group composition was also very similar: 40-85% fungal-feeding nematodes, 13-40% bacterial-feeding nematodes, and 5-20% bacterial-feeders/predators in the mature compost of this study, compared to, respectively,  $\pm 80\%$ ,  $\pm 10\%$  and  $\pm 5\%$  in that of Chapter 2. This similarity in density and trophic structure might be explained by the selective nature of a fast changing (succession of composting phases) though very specific compost habitat (in terms of organic materials, moisture levels and temperatures). The family Tylenchidae was recorded for the first time in compost in the present study, i.e. the genus *Filenchus* in the willow wood chips, the poplar bark 2 and the external farm compost. Generally, Tylenchidae are considered associates of algae, mosses, lichens and plant roots (Siddiqi 2000) and only recently *Filenchus* was shown to be capable of feeding on fungi (Okada et al. 2005). Current records confirm that at least some Tylenchidae (basal Tylenchomorpha/plant-parasitic nematodes) are independent of plants (Bert et al. 2011). When considering the nematode community structure, the differences between trials were larger than differences within trials (see also RDA plot in Figure 7.2). Hence, the trial effect is larger than the effect of the chosen feedstock material. This contrasts with the chemical compost properties where substantial differences were found between composts with different feedstock materials, in agreement with previous studies (Francou et al. 2005; Grigatti et al. 2011). For the green waste compost

significantly lower nematode abundances and different species were found. This might be explained by the lack of careful selection of the feedstock materials (in contrast with farm composts) or by repeated high temperature peaks and/or low moisture levels, but in the absence of regular measurements during composting, this explanation remains speculative. Nevertheless, although only one green waste compost was included in this study, the compost method appears to have a considerable effect on the nematode community. In contrast, the exact types and proportions of feedstock materials had only a moderate effect on the nematode community composition and abundance.

Results of the farm composts indicate that those composts that exhibit a species composition or distribution of functional groups that differs to some extent from the typical compost community as described above, also showed deviating values of one or more of the abiotic parameters. For example: for both the willow wood chips compost and the poplar wood chips compost values of oxygen uptake rate (OUR) were rather high (>8), indicating relatively low compost maturity (Grigatti et al. 2011; Kalamdhad et al. 2008), and the  $\text{NO}_3/\text{NH}_4$  ratio was very low (<1) indicating instability (Bernal et al. 1998). And, remarkably, the proportion of nematode feeding groups in these composts deviated from that in most other composts, with a lack or very low numbers of bacterial-feeders/predators like *Mononchoides composticola* and/or *Diplogaster* sp. and an unusually high proportion of fungal-feeding *Ditylenchus* sp. (75-85%). The latter agrees with the high ergosterol concentrations in these composts (Figure 7.2). The time span of the composting process may well be important here, since trial 3 only lasted 24 weeks and included no storage period, but resulted, based on a high OUR (>8) and low (<1)  $\text{NO}_3/\text{NH}_4$  ratio, in two out of three immature composts. The external farm compost also showed high ergosterol concentration along with a high proportion of fungal-feeding nematodes (65% on average) but no signs of instability. When nematode communities between composts based on used feedstock were compared (see Section 7.3.2), only a significant difference between the poplar bark based composts and the willow wood chips compost was detected. However, as mentioned above, the willow wood chips compost is not completely mature, which may explain the difference in nematode communities rather than this being an effect of the chosen feedstock material. Thus, despite the largely different feedstock materials and proportions and the clear differences in chemical properties (Section 7.3.1), biologically very similar composts were produced, the only major difference in nematode assemblages being between immature (i.e. willow wood chips and poplar wood chips) and mature composts. In conclusion, since the nematode community structure appears to be linked with the ergosterol content and the abiotic parameters (C/N ratio, DM and OUR) of the composts (Figure 7.2), nematodes can potentially be

valuable potential candidates as indicators of compost status regarding stability and maturity, but seem not to be related to the type and proportions of the feedstock materials. The overall quality of the feedstock materials (i.e. accurate selection or merely unselected waste material) combined with the composting process (i.e. for example time span of composting phases, height and duration of temperature peaks, approximation of the proportion of 60% brown and 40% green material) appears to be more crucial for nematode populations in the final product than the proportion or specific mix of the feedstock material.

### **7.5.2. Effects of compost addition: compost nematodes vs. existent soil-nematode communities**

In terms of available macro-nutrients, compost treatments did not significantly increase mineral N or plant-available P (Table 7.8) for soils initially high in mineral N and PAL (Table 7.1), i.e., in incubation trials 3 and 2, respectively. Hence, our results indicate that the distinctiveness of the compost effect on the soil properties (Table 7.8) depends on the initial elemental or nutrient concentrations in the soil (Table 7.1). Regarding soil chemical properties, the main effect of incubation with compost was a significant increase in soil pH. Organic amendments have previously been reported to serve as a buffer against acidification (Koopmans et al., 2007). An increased pH in soil is known to stimulate the growth of bacteria and Actinomycetes (see also D'Hose et al. 2010) which favors bacterial-feeding nematodes and causes accelerated degradation of soil organic matter and release of nutrients such as nitrogen and phosphorus, while numbers of fungal-feeding nematodes decreased under conditions of increasing pH (Korthals et al. 1996). In this study however, compost addition generally resulted in an increase of the density of total nematodes and of fungal-feeding nematodes in soil, while the effects on bacterial-feeding nematodes were inconsistent. There is considerable though often conflicting evidence in recent literature on changes in the abundance and structure of the soil nematode community due to the addition of organic amendments (for a review see, Thoden et al. 2011). A marked increase in nematode population density after compost application was also found by Kimpinski et al. (2003), Yao et al. (2006), Langat et al. (2008), and Liang et al. (2009), but not by Garcia-Alvarez et al. (2004), Yeates et al. (2006) and Hu and Qi (2010a). Organic amendments were generally found to increase the density of bacterial-feeding nematodes (Bulluck et al. 2002; Hu and Cao, 2008; Hu and Qi 2010b; Porazinska et al. 1999), although Renčo et al. (2010) found that, as in this study, some composts suppressed bacterial-feeding nematodes while others increased them. The increase in bacterial-feeding nematodes, which was only rarely and inconsistently observed in this study, is usually attributed to the corresponding increase in bacterial populations (Bongers and Ferris 1999; Bulluck and Ristaino 2002; Ferris et al. 1997;

Forge et al. 2003). In our experiment, the most distinct increase in bacterial-feeding nematodes, compared to blank treatment, was observed following 75% poplar bark compost addition. This increase might indicate a stimulatory effect of compost addition (by stimulating bacterial populations) or might be explained by the actual addition of nematodes with the compost, since this compost also contained the highest relative abundance of bacterial-feeding nematodes. In line with the latter explanation, we found that the most pronounced effect of the composts (green waste excluded) on the existent soil nematode community was the increase in fungivorous nematodes. Such an increase was also described by Bulluck et al. (2002) and Leroy et al. (2009), while the reverse was described by Renčo et al. (2010). However, the presence of nematodes in compost amendments is often overlooked. To the best of our knowledge, this incubation experiment is the first where the nematode population of both the composts and the amended soils were analyzed. Since only a single genus, *Ditylenchus*, was responsible for this increase it is plausible that an increased number of fungivorous nematodes is only the result of inoculation with compost nematodes and not of any stimulatory effect of the compost. Taking into account the dilution effect, assuming nematode survival after 12 weeks, and using the control treatment soil as a reference, a hypothetical calculation indeed shows that the increased abundance of fungal-feeding nematodes may at least partly be a direct effect of inoculation. This was the case for *Ditylenchus* specimens in the compost with 25% poplar bark: an average of  $40.0 \pm 0.03$  individuals per 100 g dry weight were added with the compost, while after 12 weeks of incubation only an extra  $12.0 \pm 0.2$  individuals per 100 g dry weight soil were found compared to the untreated soil. This has critical implications for the interpretation of former studies on the effect of compost on the soil nematode community; in the latter, compost was treated as a black box devoid of nematodes. For example, Kimpinski et al. (2003) described a difference of 1560 nematodes/kg dry soil between compost amended and control plots. Theoretically, nematodes already present in the compost could have been completely responsible for this difference: if we assume a comparable nematode density in the applied compost as found in our study (on average 26/g dry weight), and taking into account the doses of compost added (i.e. 50 t/ha in our study and 16 t/ha in Kimpinski et al. (2003)), more than 8000 nematodes/kg dry soil were added with the compost, which greatly exceeds the observed increase. To test whether compost nematodes effectively survive and reproduce in soil and to prove that the observed increase is not only caused by the added effect of the compost, one might try to use appropriate molecular tracer methods like microsatellites (Selkoe and Toonen 2006), though it remains a highly complex transfer to prove. In the case of *Seinura* sp., an invertebrate predator which was not present in the initial and blank soil, inoculation with compost was successful for at least 12

weeks. This was probably not the case for the bacterial-feeder/predators since they were added in high numbers but could not be recovered from the soil after 12 weeks of incubation. This seriously hampers their biocontrol potentials as suggested in Chapter 3 (part 2) and by Bilgrami (2008).

In conclusion, the most important short-term effect of the used farm composts on the soil was an increase of total and fungal-feeding nematodes irrespective of the used feedstock materials used in the compost. However, we have demonstrated that such results should be interpreted with caution, i.e. that the addition effect of compost nematodes should not be neglected. In contrast to the nematode community, the soil chemical properties after incubation could be linked to the properties of the used feedstock materials. Future research should assess whether the populations added with compost actively survive and reproduce in soil, and whether the beneficial effects of compost amendment on soil chemical properties affects nematode communities in the longer run.

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## **7.6 REFERENCES**

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## 8. General Discussion

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In the framework of this PhD project, the diversity, structure and succession of the nematode community during composting were studied for the first time. In total 9, complete composting processes were examined: *i.e.* 5 farm composting processes (using the Controlled Microbial Composting method), 1 industrial green waste process, and 3 small-scale processes in compost barrels (each in three replicates, *cfr.* treatments in chapter 5). In addition, finished composts resulting from seven other compost processes were also analyzed.

Given their important relation with nematodes and because we aimed to compare their use as indicators of compost maturity with that of nematodes, the microbial community of 4 out of 5 farm composting processes and the industrial green waste process were examined, this based on phospholipid fatty acid (PLFA) extractions.

Current study is the first comprehensive study on the succession of nematode communities in compost and this resulted in several new findings and insights. First, repeatable patterns of nematode succession were observed in the monitored composting processes (Chapter 2, 4, 6). Second, the nematode community analyses proved to be more efficient in tracking the different composting stages compared to microbial PLFA patterns. Third, experimental evidence confirms the potential of soil-dwelling nematodes to disperse over a relatively long distance in a very short time and indicates insects as vector (Chapter 5). Additionally, we demonstrated that previously reported short-term effects of compost amendments on the soil nematode community may to a large extent have been caused by the addition of nematodes already present in the compost (Chapter 7).

## **8.1 MICROBIAL COMMUNITIES AS INDICATORS OF COMPOST MATURITY: METHODOLOGICAL CONSIDERATIONS**

Unlike the nematode community, the succession of the microbial community during composting has been more extensively studied and relatively well documented. This may be attributed to their role as main decomposers which directly contribute to the degradation process. However, only few studies have described the diversity of fungi during an entire composting process (Ryckeboer et al. 2003).

Compared to the nematode community succession, the changes in the microbial community as based on our PLFA analyses were mostly concentrated in the first month of composting and were less pronounced and not unequivocal among examined processes (Chapter 4 vs. 6). No distinct changes in the major microbial functional groups (gram-positive, gram-negative,

actinomycetes and fungi) related with compost maturity were found, and especially the absence of a clear pattern in the later compost stages hampers the use of the microbial community as a bio-indicator of compost maturity. There is only one exception: the abundance of actinomycetes generally increases during the process, as confirmed by our results, and the change of their assemblage composition may be a possible indicator of maturity (Steger et al. 2007a, 2007b). Although PLFA analyses are generally regarded as a sensitive and reliable method to quantitatively assess the changes in biomass in the major groups of microorganisms (Zeller 1999; Frostegård et al. 2011), the assumed turnover rate of PLFAs and the specificity of markers for any particular group are still subject to intense discussion (e.g. Kaiser et al. 2010; Ruess and Chamberlain 2010). The issue of specificity of biomarkers is especially problematic for fungal markers (Joergensen and Wichern 2008, Ruess and Chamberlain 2010), and our results (Chapter 6) indicate that it is indeed for this group that doubtful PLFA-based quantifications in compost can be expected. The fungal diversity is known to increase with time of composting (Ryckeboer et al. 2003) and it is not impossible that some forms or species of fungi, which are especially important at the end of the process, are not detected with current PLFA techniques. Further screening of the lipid pattern of soil decomposers is necessary to reveal unique fatty acids within food web members. Furthermore, retaining the neutral lipid fatty acids (NLFAs) next to the PLFAs, could be a useful tool to indicate trophic links in the food web, in addition to information on microbial biomass and community structure inferred from the PLFAs. Trophic links may be unraveled through dietary routing, *i.e.* based on the assimilation of marker fatty acids from phospholipids in microbial food sources into neutral lipids of decomposer animals (Ruess 2005, Ruess and Chamberlain 2010).

An alternative possibility to analyze the microbial community using PLFA might be fingerprinting techniques such as denaturing gradient gel electrophoresis (DGGE) and ARISA (Automated Ribosomal Intergenic Spacer Analysis). DGGE of ribosomal genes has for instance successfully been used to identify the main microbial community succession patterns (*i.e.* bacteria and fungi) in compost (Steger et al. 2007a, 2007b; Novinscak et al. 2009). Furthermore, DGGE of functional genes can simultaneously provide information about microbial function and diversity (Tabatabaei et al. 2009). Even so, fingerprinting techniques still cope with problems of over- but mainly underestimation of diversity (Xu 2012). At this moment, several next generation DNA sequencing technologies are becoming widely available and metagenetics and metagenomics approaches of environmental samples are becoming an important tool for understanding taxonomic, functional and ecological biodiversity (Shokralla et al. 2012). Environmental sequencing using the metagenomics approach analyses all genes from all members of the

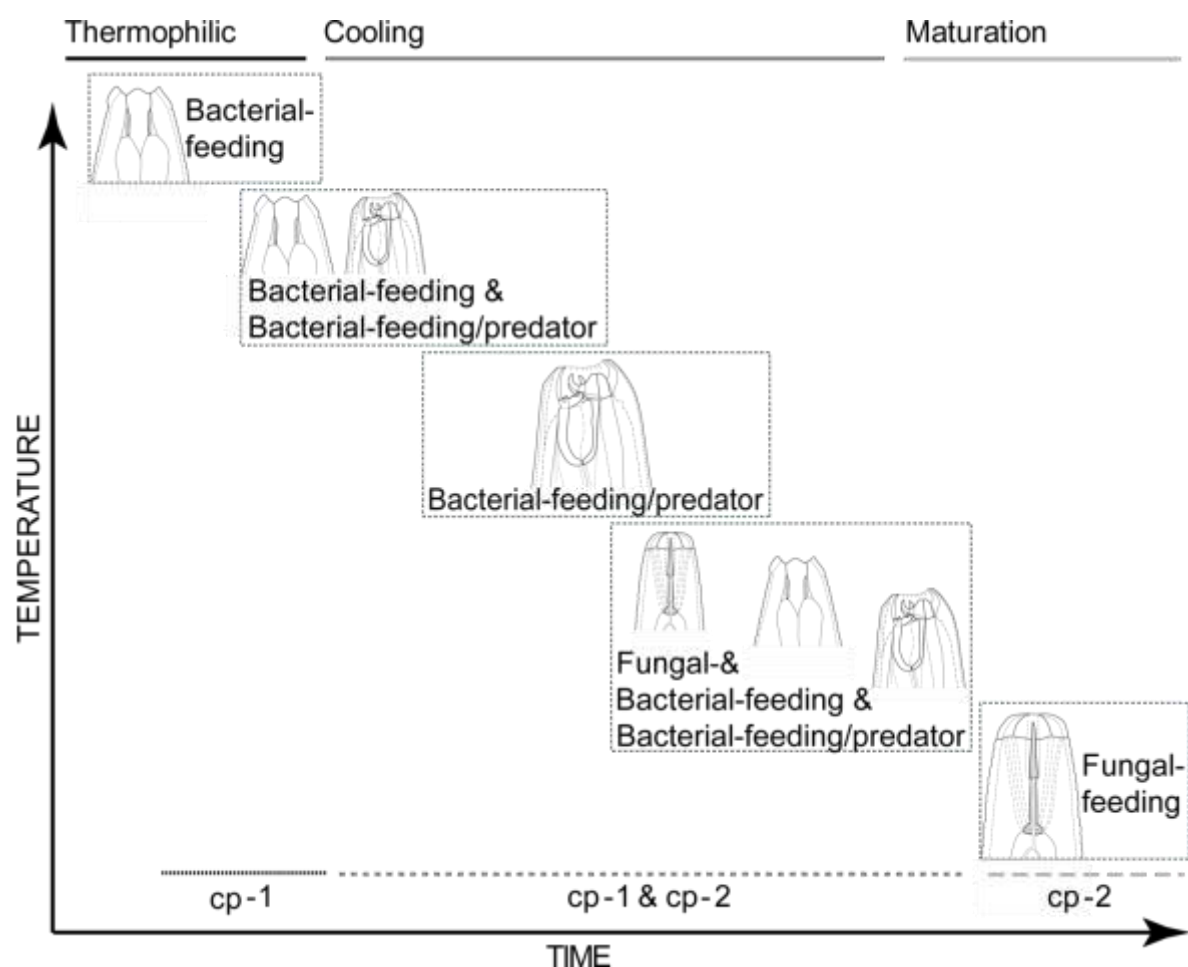
sampled community and thus will probably provide the most complete picture including rare and unknown diversity.

## **8.2 NEMATODE SUCCESSION IN COMPOST, A NEWLY EXPLORED HABITAT**

According to current knowledge, of all mesofauna found in compost (Chapter 1), only nematodes have consistently been found in every compost pile that has hitherto been investigated, and they are effectively omnipresent during all stages of the composting process (Chapter 2, 4, 5, 6, 7), except sometimes during the heat peaks.

Remarkably similar major shifts in nematode assemblage composition occurred in all composting processes in the current study, except in the industrial green waste compost. This succession of nematodes is associated with major shifts in life strategies and feeding behavior (Figure 8.1). At the beginning of the process (thermophilic phase), immediately after the heat peak, the nematode population primarily consisted of bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae and Diplogasteridae), supplemented with fewer bacterial-feeding general opportunists (cp-2) (Cephalobidae) and/or with the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, during the cooling and maturation stages, first the bacterial-feeding/predator enrichment opportunistic nematodes (mainly *Mononchoides composticola*) became dominant and finally, at the most mature stages, the relative importance of the fungal-feeding general opportunists other than Aphelenchoididae, such as Anguinidae (mainly *Ditylenchus filimus*), Neotylenchidae and Tylenchidae increased. Hence, the nematode community actually undergoes a succession of r-strategists, from enrichment opportunists (cp-1) to general opportunists (cp-2), and based on feeding type, from mainly bacterial-feeders via dominance of bacterial-feeding/predators to increased importance of fungal feeders (Figure 8.1). However, regarding the distinct feeding type-related patterns observed here, it is well known that feeding type allocations based on stoma morphology (Yeates et al. 1993) are not always univocal and some species do not restrict to one food source (1.4.4). For instance, bacterial-feeding nematodes might also feed on amoebae or protozoa (Moens et al. 2004) or most diplogasterids are able to feed on other sources next to bacteria (Fürst von Lieven and Sudhaus 2000). Nevertheless, whatever feeding type would be appointed for a given taxon, the same sequence and proportions of specific buccal cavity morphologies recurrently appeared in different compost processes. Determining the exact functional role in the process is important from an ecological point of view, but does not have an essential influence on the observed patterns (Figure 8.1) and the associated possibilities to use nematodes to infer the status of compost.

The replacement of the enrichment opportunists by general opportunists and the increase of fungal-feeding nematodes have also been observed by Ferris and Matute (2003), Wang et al. (2004) and Georgieva et al. (2005) during the decomposition of several plant residues in soil. Nematode succession in compost differs from decomposition processes in soil (Georgieva et al. 2005) mainly in the absence of K-strategists and in the postponed dominance of the Neodiplogasteridae (including *Mononchoides*) in compost compared to soil. This retardation could be explained by the high temperatures during the thermophilic and early cooling phase. The increase in fungivorous nematodes coincides with decreasing C/N ratios during the composting process. It is well known that fungal energy channels predominate when the organic input is characterized by a high C/N ratio, and conversely, bacterial decomposition channels predominate when the organic material has a low C/N ratio (Ruess 2003; Ruess and Ferris 2004). Most likely, when looking at the whole process, during the thermophilic phase the extreme environmental circumstances (i.e. temperature) are the limiting factors for nematode succession, whereas during the maturation phase food resources may be the most selective force driving successional events.



**Figure 8.1:**

General succession of nematodes during composting. Nematodes with cp-1 and cp-2 are enrichment opportunists and general opportunists, respectively. Nematode feeding types are schematically presented by nematode heads of *Panagrolaimus* sp. (bacterial-feeding), *Ditylenchus* sp. (fungal-feeding), and *Mononchoides composticola* (bacterial-feeding/predator).

Based on this succession of nematodes, nematode-based indices were calculated and their changes during the composting process monitored. Both the Maturity Index (MI) (Bongers 1990, 1999) and variations of the fungivores/bacterivores ratio (*i.e.* F/B ratio (Ferris et al. 2001) in Chapter 2 and F/F+B (Yeates et al., 1993 in Chapter 4) increased as the compost matured. The increased fungivores/bacterivores ratios indirectly indicate decomposition of slowly degradable organic materials such as lignin and lignocellulose at the end of the process, which is known to be mainly executed by fungi (Eiland et al. 2001; Vargas-García et al. 2009). The relation with processing time was less unequivocal in the processes of Chapter 6, where the fungivores/bacterivores indices increased after the thermophilic phase, then decreased and increased again at the end of the process. This is likely due to the fact that temperature in these processes did not show a simple decrease with time as in the other studies. This, however, allowed us to better distinguish between the effect of times and temperature. The resulting data of the replicated design in Chapter 6 were modeled and revealed significant relations of changes in the nematode community (*i.e.* nematode abundance, absolute amount of fungal-feeding nematodes and F/F+B ratio) with other parameters of the composting process (*i.e.* time of composting and/or temperature). The nematode abundances were significantly related with temperature. The abundance of fungal-feeding nematodes was significantly related with both time of composting and temperature, and the F/F+B ratio was only significantly related with time of composting. Addition of PLFA based data (*i.e.* fungal PLFA or PLFA based f/b ratio) as a variable in the appropriate models did not significantly add to the explanation of the observed data, which may be due to the lack of sufficient suitable fungal FA markers (see 8.1). As shown, the nematode succession in compost follows a repeatable and predictable pattern which is related with changes during the composting process and thus is a promising tool to evaluate compost maturity (see 8.3).

Since composting is a microbially mediated process, providing the proper environmental conditions for microbes to decompose raw organic materials is crucial for success (Cooperband 2000). The starting materials have an effect on the chemical compost properties (Chapter 7; Francou et al. 2005; Larney et al. 2008; Grigatti et al. 2011) and determine to a large degree the microbial community composition during composting (Ryckeboer et al. 2003). The chief succession patterns in the nematode community (see 8.2), on the other hand, appeared to be much less dependent on feedstock materials. Irrespective of the used feedstock materials or feedstock mixtures, largely the same nematode successions were observed during virtually all composting processes (Chapter 2, 4, 5 and 6), and very similar nematode community compositions in mature farm composts were found (Chapter 7). Next to feedstock proportion,



differential access to the composting process (covered and uncovered treatments) and scale of composting (barrels versus windrow composting) also did not importantly influence overall nematode succession during composting (Chapter 5). Moreover, the nematode succession was unaffected by the season of composting since processes in different chapters of this PhD were started at different moments in time, from spring to summer (chapter 6) or from autumn to winter (Chapter 2 and 4). Also on genus and species level remarkably similar taxa were found in the examined composts, despite the geographic disparity, differential access, different feedstock materials and method and timing of composting (green vs. farm, spring vs autumn) (e.g., the following literature data support the present study: *Eucephalobus*, *Poikilolaimus*, *Diploscapter*, *Aphelenchoides* and *Ditylenchus* were prominent in Gagarin 2000; *Halicephalobus gingivalis* in Nadler et al. 2003; *Panagrolaimus labiatus* in Andrassy 1984). The present study of the compost nematofauna revealed 21 taxa that were new to the Belgian fauna (Chapter 3-Part 1) and included new and numerically very important species, i.e. *Mononchoides composticola* (Chapter 3-Part 2). The genus *Mononchoides* was found in all examined composts and *Mononchoides composticola* was recorded in all farm composts (11). However, in the current study the nematodes were mostly identified only up to genus level. A more thorough and comprehensive taxonomic study might well have revealed several more species new to science and/or to the Belgian fauna.

In contrast to the overall similarity in succession patterns, the nematode successions during industrial green waste composting (Chapter 6) and a finished green waste compost (Chapter 7) were different. The nematode abundances were conspicuously lower and functional group proportions were different because of the virtual absence of fungal feeders. Nevertheless, the limited number of recorded taxa in the green waste composts were also found in the farm processes, except *Procephalobus* sp. which was unique to the industrial green waste compost. The observed difference is most likely mainly based on the composting method. Green waste composting uses standardized procedures for all processes with predetermined time schedules for management practices and duration of the process and depends, compared to the farm composts, on a different waste stream that contains more fresh materials.

### 8.3 NEMATODES AS INDICATORS OF COMPOST MATURITY

Based on the universal shifts in the nematode community during composting and especially on the distinct increase of the amount of fungal-feeding nematodes (see 8.2), the nematode based indices F/F+B and MI were proposed as suitable tools to assess compost maturity (Chapter 2, 4 and 6). However, a well-accepted parameter of compost maturity to validate our nematode data is not available.

#### 8.3.1 Chemical versus biological maturity

During the compost curing phase (*i.e.* maturation) the microbial community continued to change long after the compost organic matter and other biochemical properties had stabilized (Danon et al. 2008). Ryckeboer et al. (2003) confirmed an increase of microbial diversity after cooling during maturation together with a decline in biological activity at the end of the process indicating stability. Therefore, when considering compost maturity, it should be noted that chemical maturity does not necessarily coincide with biological maturity. Often certain chemical parameters indicate compost maturity shortly after cooling while the biological community still undergoes significant changes during maturation. For example, this was the case in the replicated processes of Chapter 6 where measurements after 13 weeks of composting of the  $\text{NO}_3/\text{NH}_4$  (>1, Bernal et al. 1998) ratio and OUR (oxygen uptake ratio, >8, Kalamdhad et al. 2008) already indicated chemically mature composts, whereas the nematode community did undergo some significant changes, including the relative increase of fungal-feeding nematodes, after this period. This chemical stability is also nicely illustrated by other measured process parameters like pH and C/N ratio which prominently increased and decreased, respectively, during the thermophilic and cooling phase and afterwards remained stable or only slightly changed during maturation. Apparently, after a certain chemical equilibrium is reached, the compost biota communities (*i.e.* nematodes and microbes) need time to develop. Hence, a proper identification of true compost maturity requires assessment of one or more biological components. In this respect, it is evident that for the industrial green waste compost addition of a more extensive (low-temperature) maturation period would definitely favor nematode as well as microbial abundance.

The quality of the biological component (*i.e.* both abundance and diversity), though hitherto hardly investigated, may be an explanatory factor for the conflicting findings on the beneficial effects of composts on soil (see also 8.4). The expected benefits of compost application to soil are absent if they lack the correct inoculum of organisms (Ingham and Slaughter 2001). Nematodes possess an important advantage for assessing this component since they are

established environmental indicators (Bongers and Ferris 1999; Neher 2001; Yeates 2003) of underlying ecosystem processes such as organic enrichment (Ferris and Bongers 2006), and changes in the food web are mirrored in shifts in nematode feeding group and taxonomic composition (Yeates et al. 2009).

### 8.3.2 Nematode-based criteria for compost maturity

Based on the nematode patterns observed in this study and on some specific properties of nematodes, the nematode community has potential as a valuable indicator of the biological component in compost and thus of (biological) maturity. Based on all results obtained in this study, four nematode community-based criteria for biological maturity are proposed (Table 8.1). Based on these criteria a putative simple nematode-based index is proposed. For each fulfilled criterion one point is given resulting in an index with a scale from 0 to 4. Since the nematode abundances are strongly negatively influenced by temperature peaks (Chapter 6), near-ambient temperatures of compost are considered a logical prerequisite for maturity and a correct interpretation of the index. Although temperature decline during composting correlated well with a number of commonly used maturity parameters (e.g. C/N ratio, dehydrogenase activity, ATP content) (Tiquia et al. 2002), depending only on compost temperature may give misleading information (Wichuk and McCartney 2010). Heap temperatures are in fact influenced by various other factors such as ambient conditions, winds, pile size, extreme temperatures during the thermophilic phase, lack of free air space, oxygen depletion, drying and high moisture contents (Lasaridi et al. 2000, Khan et al. 2009).

The first nematode-based criterion we propose is nematode density. High numbers of nematodes are potentially beneficial for maintenance of a solid, balanced and healthy soil food web (see 8.4). An abundance of over 500 ind./ 100g DW compost is proposed here because in the experimental controlled and well balanced farm processes nematode abundance was never below 500/ 100g DW at near-ambient temperatures. In contrast, the biologically poor green waste composts contained far fewer nematodes, *i.e.* maximum 300/ 100g DW in sieved<sup>10</sup> samples. The other criteria take into account the functional composition of the nematode community. As repeatedly mentioned above, the nematode based F/F+B ratio reflects the characteristic increase of fungal-feeding nematodes during maturation and therefore is a suitable ratio to assess maturity. Although the MI also increased during the process (chapter 2 and 4), this index was not included, firstly, because only two out of the five original cp-groups (*i.e.* cp-1 and cp-2, Bongers 1990, 1999) occurred during the process, and secondly because the

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<sup>10</sup> It can be expected that densities in sieved compost samples are higher, *i.e.* the observed density of 300 nematodes/100 g is even overestimated relative to the non-sieved samples.

increase in cp-2 nematodes at the end of the process is almost exclusively caused by the increase of fungal-feeding nematodes which is already accounted for in the fungivores/bacterivores ratio. Based on the tremendous difference between the farm composts and the industrial green waste and the lowest levels obtained for this ratio (*i.e.*  $0.003 \pm 0.005$  in the green waste compared to between  $0.37 \pm 0.12$  and  $0.9 \pm 0.06$  in all other composts), an  $F/F+B > 0.02$  is put forward as a second criterion that needs to be fulfilled. Next to the absolute number of fungivorous nematodes, the diversity of fungal-feeding taxa also increased during the examined composting processes. Immediately after the heat peak, usually only one fungal-feeding taxon (mostly Aphelenchoididae) was present, while later, during maturation, other fungal-feeding taxa appeared. Hence, mature compost can be characterized by at least one additional fungal-feeding taxon next to the early appearing Aphelenchoididae, such as species from the Tylenchidae, Neotylenchidae and/or Anguinidae. The fourth and last criterion is also related to an increase in diversity and includes the presence of diplogasterids (Diplogasteridae *sensu lato*). The presence of diplogasterids provides an easy indication of more trophic diversity (*cfr.* morphology of the buccal cavity). Diplogasterids are commonly known as bacterial-feeding nematodes, but often they are also able to feed on other organisms such as nematodes, fungi and algae (especially the Neodiplogasteridae) (*e.g.* Yeates et al. 1993; Fürst von Lieven and Sudhaus 2000; Chapter 3). Hence, diplogasterids may essentially be considered as omnivores *s.l.* to which ecological theory and modeling often attribute a key role in determining food web stability, principally because it increases connectance (Moens et al. 2004) and/or diversity (Gravel et al. 2012). However, according to Dunne et al. (2002), robustness increases with food-web connectance but appears independent of species richness and omnivory.

These four criteria result in a simple index that may also be used by a non-expert after limited training. However, these criteria are still based on a limited dataset of mainly one method of composting (*i.e.* Controlled Microbial farm Composting) in only one geographical region and the index has not yet been tested. In other words, it has not been demonstrated yet that compost with a high index is effectively more beneficial. Hence, the proposed criteria need to be tested, validated and fine-tuned when more data become available.

**Table 8.1:**

Overview of the proposed nematological criteria to assess biological compost maturity. When all criteria are fulfilled, the compost receives a maximal score of 4/4.

Criteria	Required level
Nematode abundance	> 500/ 100 g DW compost
F/F+B ratio	> 0.2
Number of fungal-feeding taxa	> 1
Presence of diplogasterids	X

As an example of how the proposed nematode-based compost index could work, we calculated the index for all composts analyzed in this study (Table 8.2). The closer the index approaches 4, the better the biological maturity of the compost should be. Following this index all farm composts, with a precise monitoring of the process and careful selection of the feedstock materials, have high scores (*i.e.* 3 or 4). The industrial green waste compost is indicated as biologically very poor. Unfortunately, intermediate processes, between fine-tuned farm composts and large industrial processes, are missing. These are necessary for the interpretation of more subtle differences between composts.

**Table 8.2:**

Index score based on the proposed criteria for biological maturity of all examined composts in this study. When values are highlighted in grey the respective criterion was not met.

	abundance	F/F+B	Fungal-feeding taxa	diplogasterids	index score
industrial green waste	177 ± 57	0.003 ± 0.005	1	absence	0
green waste *	300 ± 40	0.4 ± 0.11	2	X	3
poplar bark 1	933 ± 107	0.9 ± 0.06	1	X	3
poplar bark 2	722 ± 158	0.5 ± 0.26	2	X	4
oak bark*	1700 ± 300	0.52 ± 0.05	2	X	4
poplar bark 3*	3100 ± 520	0.67 ± 0.04	2	X	4
Norway spruce*	2000 ± 400	0.56 ± 0.06	2	X	4
75% poplar bark	1662 ± 157	0.77 ± 0.17	3	X	4
50% poplar bark	596 ± 52	0.71 ± 0.09	4	X	4
25% poplar bark	768 ± 113	0.37 ± 0.12	3	X	4
Willow wood chips*	4000 ± 720	0.86 ± 0.02	3	X	4
poplar wood chips*	4400 ± 669	0.73 ± 0.07	2	absence	3
poplar bark 4*	900 ± 190	0.83 ± 0.08	2	X	4

\* only final stage compost available and samples were sieved prior to nematode extraction

## 8.4 THE IMPORTANCE OF NEMATOFAUNA IN COMPOST AND ITS POTENTIAL BENEFITS

Several compost nematode taxa have a phoretic association with insects, likely to enhance their dispersal (Chapter 5). Rarer compost taxa even have a more specific relation, such as Neotylenchidae sp. or *Ektaphelenchoides* sp. Members of the family Neotylenchidae have two types of generations, a free-living fungal-feeding generation and a female parasitic generation in insect or mite haemocoel. *Ektaphelenchoides* species were recorded as associated with insects in xylem of several woods. Given the distinct relations of compost nematodes with insects and given the fact that insect phoresy is considered an important step towards parasitism (Dillman et al. 2012), compost is an under-investigated habitat for nematodes with bio-control potential. In addition, the diplogasterid predators present in mature composts have been proposed as suitable predators for bio-control of pathogenic nematodes (Khan and Kim 2007). However, at first sight they did not appear to survive in high numbers when added to the soil (Chapter 7). Next to the potential specific role of certain species as biological agents, the nematode community in compost might contribute to a more general and important goal: *i.e.* a solid, balanced and healthy soil food web. Nematodes occupy a central role in the food web and contribute substantially to nutrient cycling in the soil (Verhoef and Brussaard 1990). The ecosystem services of nematodes are determined by their metabolic and behavioral activities and include relocations of organisms to new resources and feeding on other organisms (plants, fungi, bacteria, micro-arthropods and other nematodes), taking in more N than is needed for their body structure (Ferris 2010). Excess N is mineralized as ammonia, excreted and available for uptake by plants and bacteria (Ferris et al. 1998). Abundance, activity and (functional) diversity of the nematode community are important for the continuity of their ecosystem services (Ferris 2010). Our results indicated at least short term survival of compost nematodes in soil as total nematode numbers and especially the fungal feeding *Ditylenchus* increased. Hence, when compost nematodes would also have an effect on the longer run in the soil, compost can be considered as much more than an “ordinary” fertilizer because if nematodes effectively contribute to a more balanced soil food web, the ongoing release of nutrients needed for plant growth might be influenced in the longer run. Previous studies on the suppressing effect of compost on plant-parasitic nematodes mostly did not include free-living taxa in their faunal analyses and completely overlooked the nematode population present in mature composts. However, the proportion of beneficial to harmful nematodes might be more important for plant growth than only the decrease of the absolute number of plant-parasites (Ferris 2010). Thoden et al. (2011) already ascribed the positive effect of compost application to the proliferation of non-pathogenic, free-living nematodes and their overall positive effects on soil microbial

populations, organic matter decomposition, nutrient availability, plant morphology and ecosystem stability, making the plant less susceptible for PPN. Admittedly, more experiments with application of biologically rich and poor composts in the field are needed to elucidate the precise contribution of the compost inhabiting nematodes to the beneficial effects of compost or whether the particular characteristics of compost itself stimulate soil food web processes.

Besides nematodes, compost comprises several other organisms that could have similar or additional beneficial functions. Certain micro-organisms that can be found in compost are thought to play a role in plant disease control. Fungal genera, *i.e.* *Trichoderma*, *Penicillium* and *Aspergillus*; bacterial genera, *i.e.* *Bacillus*, *Pseudomonas* and *Pantoea*, and finally actinomycetes are antagonistic to some disease-causing fungi (Hoitink and Boehm 1999). Some of these microbial genera are also known to be suppressive to plant-parasitic nematodes (e.g. Sharon et al. 2001; Kokalis-Burella et al. 2003; Mekete et al. 2009). Also mites are commonly found in compost (own observations and Odegaard and Tommeras 2000) and when acting as a predator might have a structuring effect on the food web.

However, several of these organisms are difficult to detect or require multiple techniques, prohibiting their routine monitoring. As discussed above these beneficial organisms are likely to be only or mostly present in biologically mature compost.

## **8.5 FUTURE PROSPECTS: WHERE TO GO FROM HERE?**

Although important advances have already been made to link features of the nematode succession during composting to compost maturity criteria, some questions remain unanswered. The universality of nematode criteria for composts with different feedstock's, geographical regions and produced by different methods remains to be further investigated. Therefore future endeavors to validate the proposed nematode-based compost maturity index should include and test composts produced with different compost methods from a local to a global scale. Most importantly, the relation of what is here considered as a compost of high quality (compost with a high index) and their effective beneficial aspects needs to be tested. Thoden et al. (2011) hypothesized that the overall positive effect of compost amendments is, inter alia, due to the proliferation of non-pathogenic, free-living nematodes and their overall positive effects on soil microbial populations, mineralization, nutrient supply and plant vitality. This hypothesis can be tested by executing compost application experiments (both short term and long term) with biologically rich and poor composts. Comparison between the effects of nematode poor and rich compost addition will elucidate the precise contribution of compost inhabiting organisms to the

beneficial effects of compost on soil. The validity of this hypothesis is definitely an important consideration for any future research including composts.

Our results indicated that green waste composting resulted in a hyper-sanitized, biologically poor compost. As a guideline to improve the biological quality of this compost we suggest the addition of a low-temperature maturation phase. However, it remains to be investigated whether it is possible for beneficial organisms to colonize these composts after such prolonged periods of high temperatures. In this context we need to know the possibility and the consequences of the colonization of a pathogen. This is certainly not inconceivable in a sterilized and thus nearly antagonist-free compost.

Above the classical use of compost, the investigation of the possibility of enriching compost with specific bio-control agents for specific field problems could be the next important step in compost research. As effective biological regulation requires co-location of predator and prey organisms, or overlaps in their ranges (Ferris 2012), some practical problems frequently preventing successful or sustained biological control might actually be overcome with compost as a carrier. The bio-control agents are readily incorporated into the soil close to their field of action with plenty of resources available for their survival. Experiments on the survival, persistence and reproduction of bio-control organisms are required to further explore this very appealing way of applying bio-control agents. In addition, the effective value (both ecologically as economically) of the compost will enhance tremendously and compost can be more or less designed to tackle specific problems (i.e. pathogens) in the field.

## **8.6 CONCLUSION**

During this project, the nematode community during composting was thoroughly analyzed for the first time. This revealed a repeatable and predictable pattern of nematode succession in all examined processes, except for the industrial green waste compost. This pattern was independent of scale, season of composting, feedstock proportions and also differential access did not importantly influence the nematode succession. In contrast to the microbial community pattern (based on PLFA data), the observed nematode succession was clearly related to changes during the composting process (i.e. composting phases, temperature and duration of composting) and is thus a promising tool to evaluate compost maturity. Four criteria to assess biological compost based on characteristics of the nematode community were proposed maturity: nematode abundances  $>500/100$  g DW compost, a F/F+B ratio  $>0.2$ , the presence of more than one fungal-feeding taxon and the presence of diplogasterids. These criteria need to be validated when more data become available. Important steps were taken to understand how



nematodes colonize a compost process, i.e. by a combination of survival strategies and phoretic transport by insects. It has also been demonstrated that the short term effects of compost application on the soil nematode community might be purely caused by an additional effect of compost nematodes.

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## 9. Summary / Samenvatting

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## 9.1 SUMMARY

Composting is the semi-artificial, aerobic, heat producing and controlled process in which microorganisms convert a mixed organic substrate into carbon dioxide (CO<sub>2</sub>), water, inorganic nutrients and stabilized organic matter. One of the key issues in compost research is to determine when the compost has reached a mature stage. Hitherto numerous tests, based on both physical and chemical parameters, have been proposed to assess compost maturity but unfortunately, none of these have proven rigorous, reliable or consistent enough to be used in standard protocols. Although the biology of compost (i.e. micro-and mesofauna) is considered crucial for its beneficial effects of compost on soil, the compost fauna remains largely unknown. Only the dynamics of the bacterial community has been thoroughly investigated in relation to composting processes. In this study nematodes were used as gateway to examine the composting ecosystem, making use of their excellent qualities as environmental bio-indicators. Our main aims were to (1) acquire fundamental knowledge on the nematode diversity in compost, (2) obtain insight into the succession of the nematode community during composting and link this to relevant biotic and abiotic factors, (3) assess the survival and colonization capacity of compost nematodes and (4) test the effect of compost with its associated nematodes on the existent soil nematode community and the soil chemical properties.

In total 9 complete composting processes (i.e. 5 farm composting processes, 1 industrial green waste process and 3 small-scale processes in compost barrels) and 7 finished composts were examined. Nematodes were consistently found in all investigated composts, and they were effectively omnipresent during virtually all stages of the composting process. Remarkably similar major shifts in nematode assemblage composition occurred in all studied composting processes except the industrial green waste compost. At the beginning of the process (thermophilic phase >45°C), immediately after the heat peak, the nematode population primarily consisted of bacterial-feeding enrichment opportunists (cp-1) (Rhabditidae, Panagrolaimidae and Diplogasteridae), supplemented with fewer bacterial-feeding general opportunists (cp-2) (Cephalobidae) and/or with the fungal-feeding general opportunists (Aphelenchoididae). Thereafter, during the cooling (<45°C) and maturation stages (near ambient temperatures), first the bacterial-feeding/predator enrichment opportunistic nematodes (mainly *Mononchoides composticola*) become dominant and finally, at the most mature stages, the relative importance of the fungal-feeding general opportunists other than Aphelenchoididae, such as Anguinidae (mainly *Ditylenchus filimus*),

Neotylenchidae and Tylenchidae increased. Hence, the nematode community actually undergoes a succession of r-strategists, from enrichment opportunists (cp-1) to general opportunists (cp-2) and based on feeding type, from mainly bacterial-feeders via dominance of bacterial-feeding/predators to increased importance of fungal-feeders.

Next to feedstock proportion, also scale of composting (barrels versus windrow composting) did not importantly influence overall nematode succession during composting. Moreover, the nematode succession was unaffected by the season of composting since processes in different chapters of this PhD were started at different moments in time, from spring to summer or from autumn to winter. Also on genus and species level remarkably similar taxa were found in the examined composts, despite the geographic disparity, differential access, different feedstock materials and method and timing of composting (green vs. farm, spring vs autumn). The present study of the compost nematofauna during composting revealed 21 taxa that were recorded for the first time in Belgium and a new, numerically very important species, *i.e.* *Mononchoides composticola* was described. The genus *Mononchoides* was found in all examined composts and *Mononchoides composticola* was recorded in all farm composts.

Based on the remarkable repeatable succession of nematodes, nematode-based indices were calculated. Both the Maturity Index (MI) the fungivorous/bacterivorous ratio (F/F+B) increased as the compost matured. The relation of these indices with progressing time was less unequivocal for three simultaneously running but independent processes, likely due to the fact that temperature in these processes did not show a simple decrease with time as in the other studies. This, however, allowed us to better distinguish between the effect of times and temperature in a generalized linear mixed model. The nematode abundances were significantly related with temperature; the amount of fungal-feeding nematodes was significantly related with both time of composting and temperature, and the F/F+B ratio was only significantly related with time of composting. As demonstrated by our data, the nematode succession in monitored compost processes follows a repeatable and predictable pattern and especially the nematode based F/F+B holds promise as a reliable indicator of compost maturity since it was not significantly affected by temperature fluctuations but mainly related with time of composting.

Compared to the nematode community succession, the changes in the microbial community as based on our PLFA analyses were mostly concentrated in the first month of composting and were less pronounced and not univocal among examined processes. No distinct changes in the major microbial functional groups (gram-positive, gram-negative, actinomycetes and fungi) related with compost maturity were found. Addition of PLFA-based data (*i.e.* fungal-PLFA or PLFA based f/b ratio) as a variable in the models that describe the changes in the nematode community did not

significantly add to the explanation of the observed data, which may be due to the lack of sufficient suitable fungal PLFA markers.

Due to the heat peak early in the compost process nematodes disappeared completely or to a large extent, but several taxa appear immediately when the temperatures drop. These comprise both taxa present before the heat peak and new taxa. Our results showed that composting processes inaccessible to insects and/or not in contact with soil did not significantly influence the principal nematode succession patterns during composting. However, for some specific taxa differences between treatments were found (i.e. for *Achrostichus* sp., Neodiplogasteridae sp., *Nygolaimoides* sp. and Rhabditidae sp.1) illustrating the importance of insects for the dispersal of nematodes to compost. Experiments in the lab with the blue bottle fly as a possible carrier demonstrated actual transport of nematodes isolated from compost by the fly (i.e. *Halicephalobus* cfr. *gingivalis*, *Diploscapter coronatus*, *Diplogasteritus* sp., *Acrostichus* sp., *Mesorhabditis* sp.). The importance of survival during the compost process was demonstrated for *Aphelenchoides* sp., *Panagrolaimus* sp. and rhabditid juveniles and dauer stages, as they survived an experimentally induced temperature peak (up to 60°C) while Tylenchidae did not. Hence, our results indicate that the rapidly changing nematode community in a composting process is the result of both differential survival and colonization capacities.

Previous studies on the effect of compost on the existing nematode communities in soil never took into account the nematodes that are already present in finished composts. Therefore 11 composts (10 farm composts and one green waste compost), with known nematode populations, were further tested in an incubation experiment to investigate their short-term effect on the existent soil nematode community and on the soil chemical properties. After 12 weeks of incubation all compost amendments resulted in a significant pH increase in the soil (one-way ANOVA,  $p < 0.01$ ) and also the nematode numbers in the soil increased, except in soil amended with the green waste compost. In particular, the abundance of the fungal-feeding *Ditylenchus* increased significantly (one-way ANOVA,  $p < 0.03$ ) in all soils amended with farm compost. This increase may well be purely caused by the addition of nematodes present in the compost and thus results on the effects of compost should be interpreted with caution.



## 9.2 SAMENVATTING

Compostering verwijst naar het semi-artificiële, aerobe, warmte producerende en gecontroleerde proces waarbij micro-organismen een gemengd organisch substraat omzetten in koolstofdioxide (CO<sub>2</sub>), water, anorganische voedingsstoffen en gestabiliseerde organische stof (humus). Een van de belangrijkste vragen in compostgerelateerd onderzoek is: wanneer bevindt compost zich in een rijp stadium? Tot hiertoe werden tal van tests voorgesteld om de rijpheid van compost te bepalen, en deze zijn veelal gebaseerd op fysische en chemische parameters. Helaas is geen enkele van deze tests nauwkeurig, betrouwbaar en consistent genoeg om gebruikt te worden als enige maatstaf voor maturiteit van compost in standaardprocedures. Hoewel de biologie van compost (zowel micro- als mesofauna) beschouwd wordt als cruciaal voor de gunstige effecten van compost op de bodem, blijft de aanwezige fauna in compost grotendeels onbekend. Enkel de dynamiek van de bacteriële gemeenschap in relatie tot compostprocessen werd al grondig bestudeerd. In deze studie werden nematoden gebruikt als middel om inzicht te verkrijgen in het composteringsecosysteem, steunend op hun uitstekende eigenschappen als bio-indicatoren. Onze belangrijkste doelstellingen waren om (1) fundamentele kennis te verwerven over de diversiteit van nematoden in compost, (2) inzicht te krijgen in de successie van de nematodengemeenschap tijdens de compostering en dit te koppelen aan relevante biotische en abiotische factoren, (3) de overleving en kolonisatiecapaciteit van compostnematoden te bepalen en (4) te testen wat het effect is van compost, die reeds nematoden bevat, op de bestaande nematodengemeenschap in de bodem en op de chemische bodemeigenschappen.

In totaal werden negen volledige composteringsprocessen (i.e. vijf boerderij-composteringsprocessen, één industrieel-groenafvalproces en drie kleinschalige processen in compostvaten) en zeven afgewerkte composten onderzocht. Nematoden werden consequent aangetroffen in alle onderzochte composten en waren effectief alomtegenwoordig in vrijwel alle fasen van het composteringsproces. Behalve in de industriële groencompostering deden er zich opvallend vergelijkbare verschuivingen in de samenstelling van de nematodengemeenschap voor in alle onderzochte composteringsprocessen. Aan het begin van het proces (thermofiele fase > 45 °C), onmiddellijk na de temperatuurpiek, bestond de nematodenpopulatie voornamelijk uit bacterie-etende aanrijksopportunisten (cp-1) (Rhabditidae, Panagrolaimidae en Diplogasteridae), aangevuld met minder bacterie-etende (Cephalobidae) en/of schimmel-etende (Aphelenchoididae) algemene opportunisten (cp-2). Daarna tijdens de afkoelings- (<45 °C) en rijpingsfases (bij omgevingstemperatuur), zijn eerst de bacterie-etende/predator

aanrijksopportunisten (voornamelijk *Mononchoides composticola*) dominant. Tenslotte neemt in de meest rijpe stadia het relatieve belang van de schimmeletende algemene opportunisten toe, naast Aphelenchoididae, zoals Anguinidae (voornamelijk *Ditylenchus filimus*), Neotylenchidae en Tylenchidae. De nematodengemeenschap ondergaat dus eigenlijk een transformatie van r-strategen of aanrijksopportunisten (cp-1) naar algemene opportunisten (cp-2) en gebaseerd op voedingstype, van voornamelijk bacterie-etende nematoden via dominantie van bacterie-etende/predators naar een gemeenschap met een belangrijk aandeel schimmeletende nematoden.

Zowel de gebruikte grondstoffen als de omvang van de compostering (vaten versus compostering op grote schaal) hadden geen belangrijke invloed op de algemene nematodensuccessie. De nematodensuccessie werd bovendien ook niet beïnvloed door het seizoen van compostering omdat de processen in de verschillende hoofdstukken van dit doctoraat gestart werden op verschillende momenten in de tijd, van de lente tot de zomer of van de herfst tot de winter. Ondanks de geografische verschillen, de verschillen in toegang, de verschillende grondstoffen, de verschillen in werkwijze (groen vs. boerderij) en timing van de compostering (lente vs. herfst), werden ook op genus- en soortniveau opvallend gelijke taxa gevonden in de onderzochte composten. De huidige studie over de nematofauna tijdens compostering onthulde 21 taxa die voor de eerste keer werden waargenomen in België waarvan één nieuwe, numeriek zeer belangrijke soort, namelijk *Mononchoides composticola*, die werd beschreven. Het geslacht *Mononchoides* werd gevonden in alle onderzochte composten en *Mononchoides composticola* werd aangetroffen in alle boerderij-composten.

Steunend op de steeds terugkerende opeenvolging van nematoden-assemblages tijdens het composteringsproces werden nematodengebaseerde indices berekend. Zowel de Maturity Index (MI) als de fungivorous/bacterivorous ratio ( $F/F + B$ ) stijgen tijdens het composteringsproces als de compost rijpt. De relatie van deze indices met de composteringstijd was minder eenduidig bij drie gelijklopende maar onafhankelijke processen. Waarschijnlijk is dit te wijten aan het feit dat, in tegenstelling tot de andere processen, de temperatuur niet eenvoudig afnam met de tijd. Dit liet ons echter toe een beter onderscheid te maken tussen het effect van tijd en temperatuur in een gegeneraliseerd gemengd lineair model. De nematodenaantallen waren significant gerelateerd met de temperatuur, de hoeveelheid schimmeletende nematoden was significant gecorreleerd met zowel composteringstijd als temperatuur, en de  $F/F+B$  ratio was enkel significant gecorreleerd met de composteringstijd. Zoals blijkt uit onze gegevens, volgt de nematodengemeenschap tijdens compostering een herhaalbaar en voorspelbaar patroon en vooral de nematodengebaseerde  $F/F+B$  ratio is veelbelovend als betrouwbare indicator van

compostmaturiteit, omdat deze niet significant beïnvloed werd door temperatuurschommelingen, maar voornamelijk door composteringstijd.

In vergelijking met de successie van de nematoden, concentreerde de veranderingen in de microbiële gemeenschap (op basis van PLFA analyses) zich vooral in de eerste maand van het composteringsproces en waren ze bovendien minder uitgesproken en niet eenduidig binnen de onderzochte processen. In de belangrijkste microbiële functionele groepen (gram-positieve bacteriën, gram-negatieve bacteriën, actinomyceten en schimmels) werden geen duidelijke rijpheids-gerelateerde veranderingen gevonden. Toevoeging van PLFA-gebaseerde data (d.w.z. schimmel-PLFA of PLFA gebaseerd f/b-verhouding) als variabele in de modellen die de veranderingen van de nematodengemeenschap beschrijven, droegen niet significant bij tot de verklaring van de waargenomen patronen. Dit kan onder andere te wijten zijn aan het ontbreken van voldoende geschikte PLFA merkers voor schimmels.

Als gevolg van de temperatuurpiek vroeg in het composteringsproces verdwenen de nematoden geheel of voor een groot deel, maar zodra de temperatuur zakt, verschijnen er opnieuw verschillende taxa. Hiertoe behoren zowel taxa die al aanwezig waren voor de temperatuurpiek als nieuwe taxa. Onze resultaten demonstreren dat de algemene nematodensuccessie tijdens het composteringsproces niet significant beïnvloed wordt door composteringsprocessen die ontoegankelijk zijn voor insecten en/of niet in contact staan met de bodem. Voor een aantal specifieke taxa werden er wel verschillen gevonden tussen de behandelingen (i.e. voor *Achrostichus* sp., *Neodiplogasteridae* sp., *Nygolaimoides* sp. en *Rhabditidae* sp.1). Deze verschillen illustreren het belang van insecten voor de verspreiding van nematoden in en naar compost. Experimenten in het laboratorium met de blauwe bromvlieg als een mogelijke drager toonde daadwerkelijk transport door vliegen aan van verschillende nematoden (*Halicephalobus* cfr. *gingivalis*, *Diploscapter coronatus*, *Diplogasteritus* sp., *Acrostichus* sp., *Mesorhabditis* sp.), geïsoleerd uit compost. Het belang van overleving tijdens het composteringsproces werd aangetoond voor *Aphelenchoides* sp., *Panagrolaimus* sp. en dauers en juvenielen van rhabditiden omdat ze een experimenteel geïnduceerde temperatuurpiek (tot 60 °C) overleefden, terwijl tylenchiden dit niet konden. Onze resultaten wijzen er dus op dat de snel veranderende nematodengemeenschap in een composteringsproces het gevolg is van zowel differentiële overleving alsook van de kolonisatiecapaciteiten van de aanwezige nematoden.

Eerdere studies naar het effect van compost op de nematodengemeenschap in de bodem hielden nooit rekening met de nematoden die reeds aanwezig waren in de toegevoegde compost. Daarom werden elf composten (tien boerderijcomposten en één groenafvalcompost),

met gekende nematodenpopulaties, verder getest in een incubatie-experiment om hun kortetermijneffect op de bestaande nematodengemeenschap in de bodem en zijn chemische eigenschappen te onderzoeken. Na twaalf weken incubatie resulteerde alle toevoegingen van compost, behalve voor de behandeling met groen compost, in een significante toename van de pH (one-way ANOVA,  $p < 0,01$ ) en een algemene stijging van het aantal nematoden in de bodem. Vooral de hoeveelheden van de schimmel-etende *Ditylenchus* namen aanzienlijk toe in alle bodems verrijkt met boerderijcompost (one-way ANOVA,  $p < 0,03$ ). Deze toename kan echter ook uitsluitend veroorzaakt zijn door de nematoden die werden toegevoegd met compost en de resultaten over de effecten van compost moeten dus met de nodige voorzichtigheid geïnterpreteerd worden.

# List of publications

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**PUBLICATIONS IN SCI-INDEXED JOURNALS**

- Fonderie P., **Steel H.**, Moens T., Bert W. (2012). Experimental induction of intraspecific morphometric variability in a single population of *Halicephalobus* cf. *gingivalis* may surpass total interspecific variability. *Nematology* in press.
- **Steel H.**, Vandecasteele B., Willekens K., Sabbe K., Moens T., Bert W. (2012). Nematode communities and macronutrients in composts and compost-amended soils as affected by feedstock composition. *Applied Soil Ecology* 61: 100-112.
- **Steel H.**, Moens T., Scholaert A., Boshoff M., Houthoofd W., Bert W. (2011). *Mononchoides composticola* n. sp. (Nematoda: Diplogastridae) associated with composting processes: morphological, molecular and autecological characterization. *Nematology* 12(3): 347-363.
- **Steel H.**, de la Peña E., Fonderie P., Willekens K., Borgonie G., Bert W. (2010). Nematode succession during composting and the potential of the nematode community as an indicator of compost maturity. *Pedobiologia* 23(3): 181-190.
- Fonderie P., Willems M., Bert W., Houthoofd W., **Steel H.**, Claeys M., Borgonie G. (2009). Intestine ultrastructure of the facultative parasite *Halicephalobus gingivalis* (Nematode: Panagrolaimidae). *Nematology* 11(6): 859-868.

**OTHER PUBLICATIONS**

- **Steel H.**, Bert W. (2011). Biodiversity of compost mesofauna and its potential as an indicator of the composting process status. Accepted for publication in: Special Issue on Compost III in *Dynamic Soil, Dynamic Plant* 5 (Special Issue 2): 45-50.

**ACTIVE CONTRIBUTIONS TO INTERNATIONAL CONFERENCES**

- 31st International Symposium of the European Society of Nematologists, Adana, Turkey (2012). Oral presentation: "Nematodes in a rapidly changing environment: colonization, microbial links and functional succession in compost." Steel H., Moens T., Buchan D., Fonderie P., De Neve S., and Bert W.
- 2nd International symposium on nematodes as environmental bio-indicators, Ghent, Belgium (2012). Oral presentation: "Nematode community during composting and its potential as indicator of compost maturity." Steel H., Moens T., and Bert W.
- 17th Benelux Congress of Zoology, Ghent, Belgium (2010). Oral presentation: "Nematodes as potential bio-indicator of the composting process." Steel H., Moens T., Buchan D., Houthoofd W., De Neve S., and Bert W.
- 30th International Symposium of the European Society of Nematologists, Vienna, Austria (2010). Oral presentation:

- “Nematode community during composting and its potential as indicator of compost maturity.” Steel H., Moens T., Buchan D., Houthoofd W., De Neve S., and Bert W.
- 5th IOBC meeting on Multitrophic Interactions in Soil, Uppsala, Sweden (2009). Oral presentation:  
“Nematode community as potential indicator of compost maturity and quality.” Steel H., de la Peña E., Scholaert A., Boshoff M., Borgonie G., and Bert W.
  - 61th International Symposium on Crop Protection, Ghent, Belgium (2009). Poster:  
“Nematode community as potential indicator of compost maturity and quality.” Steel H., de la Peña E., Fonderie P., Willekens K., Borgonie G., Bert W.
  - 5th International Congress of Nematology, Brisbane, Australia (2008). Poster: “Nematode succession during Controlled Microbial Composting.” Steel H., Bert W., de la Peña E., Fonderie P., Willekens K., and Borgonie G.