The Micro-food Web: Communities in Various Compositions of Composted Organic Matter

Ardhini R Maharning[1*], *Dini* Ryandini[1], *Erwin R* Ardli[1], and *Wilda* Khafida[1]

[1]Faculty of Biology, Universitas Jenderal Soedirman, Purwokerto 53122, Indonesia

Abstract. The micro-food web decomposer is the primary community of the soil food web responsible for organic matter transformation in terrestrial ecosystems, providing minerals for plant growth. Their composition, however, depends on the quality of organic matter as their basal resource, which, in turn, determines the available nutrients in the soil. Our study examined the micro-food web community over three different organic matter compositions, differentiated by their organic carbon and total nitrogen contents. We compared the communities of composted organic matter that differed in their C to N proportion. Given in percent, they were 40:40:20, 50:40:10, and 60:30:10 of high C to N, medium C to N, and low C to N, respectively. After four weeks of finished composting, samples were obtained and enumerated for bacterial number, fungal biovolume, protozoan (amoebae, testate-amoebae, ciliate, flagellate), and nematode abundances. Our data show that a 20% change in low quality organic matter (high C to N ratio) suggests an 82.47% decline in bacterial abundance but a 22.15% increase in fungal abundance. These findings emphasize the importance of the organic matter Carbon and Nitrogen content in determining the composition of the micro-food web communities and the potential to manage the intended micro-food web community during the composting process for soil health improvement.

1. Introduction

The decomposer micro-food web is a fundamental community of an intricate and complex soil food web. It covers primary decomposers and soil micro-fauna communities responsible for organic matter transformation in terrestrial ecosystems. This transformation process is vital as it provides minerals for plant growth. Bacteria and fungi serve as decomposing agents that break down even the most recalcitrant organic matter with their secreted exoenzymes, thereby mineralizing it (1) (2). The presence of soil micro-fauna, especially nematodes, in the system, increases C sequestration (3), and the availability of nutrients in the soil due to their inefficient assimilation (4).

The community structure of the decomposer micro-food web in a given soil system depends on the available quality of organic matter in the system. As the basal resource, organic matter influences the decomposition pathways. High quality organic matter has been shown to stimulate bacterial channels, whereas low quality organic matter triggers the fungal community and its consumers (5). However, these patterns are general and do not explain how the micro-food web communities might develop when the varied quality of organic matter is combined, and to what extent the quality composition stimulates bacterial or fungal decomposition pathway. Therefore, we intended to examine the possible effects of organic matter quality compositions on the micro-food web community using a comparative experiment. The objective was to understand the micro-food web community over three different organic matter compositions, differentiated by their organic carbon and total nitrogen contents. This study provides data for efficient compost application to soil, which is justified by the micro-food web community and thus increases soil functionality.

2. Methods

2.1 Experimental Arrangement

We set up organic matter mixtures with three different compositions based on their carbon to nitrogen ratios: high C to N ratio (> 60), medium C to N ratio (30-60), and low C to N ratio (<30). The arranged compositions of organic matter given in percent were 40:40:20 (C442), 50:40:10 (C541), and 60:30:10 (C631) of high, medium, and low carbon to nitrogen ratio, respectively. The organic matter with a C to N ratio >60 consisted of wood chips, wood shaves, and dried leaves; a C to N ratio of 30-60 included fresh grass cut, green leaves, groundnut plants, corn stalks, and paddy plants; C to N ratio <30 were manure, and fish hydrolysate. The organic matter was composted using the thermal aerobic composting method, with each combination reaching a volume of approximately 1,000 Liters. Each of C442, C541, and C631 was then separated into four smaller piles after reaching maturity for further incubation. After four weeks of incubation, we enumerated the micro-food web decomposers covering bacteria, fungi,

* Corresponding author: ardhini.maharning@unsoed.ac.id

protozoa, and nematodes over 48 sample units obtained randomly from the composts (3 organic matter composition x 4 piles x 4 samples).

2.2 Micro-food Web Community Enumerations

We applied direct enumeration using a light compound microscope of 400X total magnification. Two subsamples were obtained from each sample. One gram of the sample was diluted five times and homogenized. One drop (0.05 mL) of diluted sample was placed on a microscope slide and observed under a microscope with three slide transects for fungi and protozoans with a total of 96 observations (3 organic matter compositions x 4 piles x 4 samples x 2 subsamples). The fungal fragments were measured for their hyphal diameter and length. Their biovolume was calculated according to cylinder volume (6). The protozoans were grouped into amoebae, test-amoebae, flagellates, and ciliates by identifying and counting their number. For bacterial enumeration, the sample was diluted 10^3 times. Nematode extraction followed the Baermann funnel method by submerging 5-10 grams of compost into the funnels (7). After 48 hours, the nematodes were transferred into the conical tube for fixation with 4% formaldehyde. All collected data were converted to abundance in one gram compost.

2.3 Data Analyses

We employed a one-way permutation multivariate analysis of variance (Permanova) to examine differences in community abundance between composts. The permanova was followed by pairwise analysis to compare the significance of the micro-food web community between compost using PAST4.5 software. We also applied principal components analysis (PCA) to investigate differences in the micro-food web community structure across C442, C541, and C631 composts. For the PCA, we used Canoco version 5 software.

3. Results and Discussion

The abundance of micro-food web communities significantly differed over three compositions of composted organic matter (Permanova p: 0.025). The difference was significant between C442 and C631 communities (p: 0.042) but not the case between C442 and C541 (p: 0.064) or C541 and C631 (p: 0.177) (**Table 1**).

Table 1. Permanova pairwise analysis between three different composts of C442, C541, and C631

Compost	C442	C541
C541	0.064	
C631	0.042*	0.177

Table 2 presents variations in the micro-food web of the composts**.** Bacterial abundance decreased in compost with a high amount of low quality organic matter (C631). Compared to compost with a high amount of high quality organic matter (C442), the bacterial number in C631 declined to 17.53% and 22.04% in C541. In contrast, the fungal abundance increased in C631 compared to C442, but it was similar between C541 and C442.

These findings indicate that changes in nutrient availability, in this case, a 20% replacement of high quality to low quality organic matter, suggest an 82.47% decline in bacterial number but a 22.15% increase in fungal abundance. Low quality organic matter is more recalcitrant to decompose and does not contain available nutrients required by bacteria (8), which led to a decline in bacterial abundance in our study. On the contrary, the replacement of the organic matter allowed fungi to effectively exploit the resource, stimulating an increase in their abundance.

Table 2. The micro-food web abundance (number per gram compost, except fungi in μm^3 per gram compost) of C442, C541, and C631

Parameter	C442	C541	C631
Bacteria	5.63 x 10^9	1.41 x 10^9	9.86 x 10^8
Fungi	1.08 x 10^8	1.08 x 10^8	1.33 x 10^8
Amoebae	2.09 x 10^4	1.35 x 10^4	2.92 x 10^4
Ciliates	1.88 x 10^4	1.26 x 10^4	2.89 x 10^4
Flagellates	1.25 x 10^5	6.79 x 10^4	5.16 x 10^4
Test-amoebae	2.54 x 10^5	2.49 x 10^5	1.59 x 10^5
Free-living Nematodes	1.00 x 10^3	4.25 x 10^2	4.00 x 10^2

All groups of the micro-food web were present in all compost but showed varied abundance and compositions (**Figure 1**). Consistent with permanova pairwise analysis, the PCA also demonstrated the largest differences in community structure between C442 and C631. The analysis revealed an eigenvalue of 0.76 in axis 1, which indicates that 76% of the total variability in our data, determined by the different compositions of organic matter, is explained by the first principal component. This result emphasizes the significant difference in micro-food web community structure between compost created with a larger versus smaller amount of high quality organic matter as indicated by their prior C to N ratio.

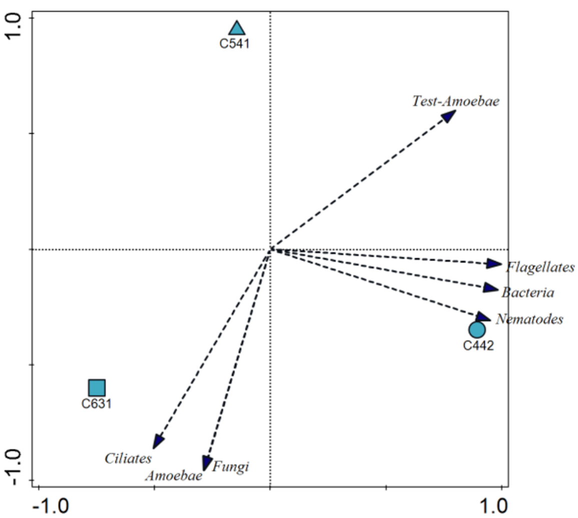

Fig 1. PCA biplot showing the micro-food web communities in C442, C541, and C631 (eigenvalue Axis 1: 0.76, axis 2: 0.24)

The C442 was characterized by high numbers of bacteria, flagellates, and nematodes but a low abundance of fungi, amoebae, and ciliates. This community structure was in contrast to that of C631, whose fungi, amoebae, and ciliates were the highest, and test-amoebae were the lowest in abundance.

C541 showed a unique community structure. It appeared to have transitional communities in which test-amoebae abundance was similar to that in C442, whereas bacteria, flagellate, and nematode numbers were close to C631. It is possible that C541 contained a balanced composition of high and low quality organic matter supporting a community structure that shares features with both C442 and C631.

Our observations suggest that a 10% change in low quality to high quality organic matter stimulates the development of the bacterial community but not the fungi after four weeks of compost maturity. The bacterial communities have been reported to respond more quickly to changes in organic matter quality compared to fungi, which take longer to establish (9). The effect on the fungal community appeared when the change reached 20%, providing fungal growth requirements due to the high C content in the organic matter. These results coincide with the findings reporting that 20% substitution of organic manure significantly improved soil bacterial community but was less pronounced in the fungal community (10).

The micro-fauna demonstrated a less consistent pattern than the primary decomposers in responding to changes in organic matter. The nematodes, flagellates, and test-amoebae were bacterial feeders, which coincided with a high abundance of bacteria in C442. However, the other two groups of bacterial feeders, amoebae and ciliates, were the most abundant in C631, where the bacterial abundance was the lowest. It is unclear what might cause this, but it might be explained as follows.

The availability of more soluble nutrients, indicated by high N, in C442 highly stimulates bacterial growth (11); thus, their abundance was most significant. This was not the case in C631, which contained more recalcitrant organic matter and less soluble nutrients. This condition allowed bacteria to flourish more in C442 than in C631, even though they have been consumed by nematode, flagellate, and test-amoebae. In the case of C631, other than that, perhaps the ciliate and amoebae were more competitive than flagellate, test amoebae, and nematodes. Consequently, they were more abundant in C631 with less bacterial growth. However, further observations on the micro-food web community and how they relate to nutrient characteristics in the compost might allow clear patterns and explanations.

In all compost, the decomposition pathway was the bacterial channels, in which two nematode families of bacterial consumers, Rhabditidae and Cephalobidae, inhabited the compost. Four weeks of finished compost most likely did not allow fungal feeder nematodes, which typically require more time to establish and develop.

Bacteria can rapidly colonize and decompose organic matter, creating an environment where bacterial-feeding nematodes can quickly establish within the first few weeks (12). Rhabditidae are colonizers that reproduce rapidly, allowing them to exploit resources efficiently. Their short life cycle benefits them from unstable and rapidly changing environments (13), as in the composting process. Cephalobidae are general opportunists capable of adapting to a broader range of environmental conditions than Rhabditidae. Their life cycle is longer than Rhabditidae, allowing them to present over extended periods in the compost.

In contrast, fungi require more time to degrade complex organic compounds and establish a stable community. Consequently, fungal feeder nematodes, which rely on these fungal communities for food, also need more time to become abundant, which might take several weeks to a few months. Thus, the four-week period might not be sufficient for the fungal communities to reach a level that can support a population of fungal feeder nematodes.

The abundance of micro-food web communities in all compost was greater (**Table 2**) than those of typical abundance in healthy soil systems, except fungi. In one gram of healthy agricultural soil, the bacterial number reaches 10^8-10^9; fungal hyphae are several meters, protozoa up to 10^3, and nematodes 10-20 individuals (14). The rich community of the decomposer micro-food web in C442, C541, and C631 demonstrates great biological resources that could improve soil health when applied to the soil.

4. Conclusion

Our findings emphasize the importance of the organic matter Carbon and Nitrogen contents in determining the composition of the micro-food web communities. The composition of organic matter influences the structure and function of the micro-food web. Higher carbon in the organic matter stimulates fungal growth, whereas higher nitrogen supports bacteria. Thus, the micro-food web decomposer output in finished compost can be adjusted by organic matter quality composition at the beginning of the composting to further fulfill requirements for soil health.

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