

Article

Implications of Microbial Community to the Overall Performance of Tree-Box Filter Treating Parking Lot Runoff

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Abstract: Most of the studies about stormwater low-impact development technologies (LID) used generalized observations without fully understanding the mechanisms affecting the whole performance of the systems from the catchment to the facility itself. At present, these LID technologies have been treated as black box due to fluctuating flow and environmental conditions affecting its operation and treatment performance. As such, the implications of microbial community to the overall performance of the tree-box filter (TBF) were investigated in this study. Based on the results, summer season was found to be the most suitable season for microorganism growth as greater microorganism count was found in TBF during this season compared to other seasons. Least microorganism count was found in spring which might have been affected by the plant growth during this season since plant phenology influences the seasonal dynamics of soil microorganisms. Litterfall during fall season might have affected the microorganism count during winter as, during this season, the compositional variety of soil organic matter changes affecting growth of soil microbial communities. Microbial analyses of soil samples collected in TBF revealed that the most dominant microorganism phylum is Proteobacteria in all the seasons in both inlet and outlet comprising 37% to 47% of the total microorganism count. Proteobacteria is of great importance to carbon, sulfur, and nitrogen cycling in soil. Proteobacteria was followed by Acidobacteria, Actinobacteria, and Chloroflexi which comprises 6% to 20%, 9% to 20%, and 2% to 27%, respectively, of the total microorganism count for each season. Each microorganism phylum was found to have varying correlation to different soil chemical parameters implying the effects of these parameters to microorganism survival in LID technologies. Depending on the target biogeochemical cycle, maintaining a good environment for a specific microbial phylum may be decided. These findings were useful in optimizing the design and performance of tree box filters considering physical, chemical, and biological pollutant removal mechanisms.



Citation: Geronimo, F.K.; Reyes, N.J.; Choi, H.; Kim, L.-H. Implications of Microbial Community to the Overall Performance of Tree-Box Filter Treating Parking Lot Runoff. *Sustainability* **2021**, *13*, 10877. <https://doi.org/10.3390/su131910877>

Academic Editor: Sung Min Cha

Received: 30 August 2021

Accepted: 27 September 2021

Published: 30 September 2021

Keywords: low-impact development; green infrastructure; microorganism; nature-based solution; tree-box filter

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1. Introduction

Land use and land use changes (LULUCs) greatly affected natural landscapes and ecosystem productivity. Over the last millennium, approximately 75% of the World's surface was subjected to change or conversion [1]. Urban expansion was the most remarkable land use change observed in the past decades. Alongside the expansion of urban regions, the percentage of population living in urban areas also increased exponentially. It was previously estimated that the global population residing in urban areas will increase by up to 66% in 2050 [2]. Densely populated urban areas increase the risk of environmental degradation due to greater pollutant generation. The large volume of wastewater from urban areas serves as primary point sources of pollutants in waterways. Moreover, the conversion of natural landscapes into urban spaces greatly affects the pattern of non-point source (NPS) pollutant deposition [3]. Urban catchments usually exhibit high stormwater pollutant concentrations due to the accumulation of pollutants in the impermeable surface

during periods of dry days. Unlike wastewater that undergoes treatment before discharge, stormwater runoff does not usually receive further treatment before being discharged in the natural environment. Generally, diffuse pollution is considered as one of the primary factors affecting natural water quality degradation and aquatic ecosystem damage [4].

Decentralized stormwater management is a common practice utilized to effectively address the problems concerning NPS pollution from urban areas. Nature-based schemes that employ micro-scale facilities applied in a basin-wide framework are widely utilized to control peak flow, runoff volume, and pollutant flux from highly polluted stormwater runoff [5,6]. Nature-based solutions (NBS) primarily includes low impact development (LID), green infrastructures (GI), sustainable urban drainage systems (SUDS), and other technologies that aim to restore the predeveloped condition of an area. These strategies that employ natural processes also provide more ecosystem services as compared to conventional flood control structures. In the study conducted by Sparkman et al. (2017), LID facilities showed higher water quality benefits as compared with conventional drainage designs [7]. Simpson and Roesner (2018) also highlighted the advantages of LID systems in managing excessive stormwater runoff volumes in urban areas [8]. Apart from the ability of LID facilities to restore the predevelopment hydrology, the model also suggested that these systems can serve as cost-effective alternatives to conventional stormwater management strategies on certain conditions.

Bioretention, tree-box filter, constructed wetlands, green roof, and pervious pavements are among the most commonly utilized type of nature-based stormwater treatment technologies. These facilities were proven as an innovative way of controlling nutrients in stormwater runoff, an example of a nature-based solution to address the negative effects of climate change and urbanization on the natural urban water cycle [9]. LID technologies mimic the predeveloped state of an area thereby preventing the water cycle disruption by employing different physical, chemical, and biological mechanisms. Ahiablame et al. (2012) have already summarized and reported the performance of the LID technologies in controlling several pollutants including nutrients in urban stormwater runoff from different studies [10]. TN and TP were removed by 7% to 99% and −3% to 99%, respectively. High variability of nutrient removal in LID technologies was due to the complexities of the chemistry of these pollutants making it difficult to attain relatively similar removal efficiencies, especially when applied to a different site and environmental conditions [11]. Designs of LID differ depending on target pollutants. Pretreatment units were usually employed to LID technologies to reduce the flow of incoming runoff or receive the initial highly polluted runoff commonly known as first flush [12]. Different manuals have been established in different countries to guide designers in applying appropriate stormwater treatment technologies in a catchment. However, manuals only focused on the overall treatment capabilities of these technologies without fully understanding the mechanisms behind these results.

Microorganisms play an important role as decomposers, pathogens, and mutualists as they regulate the mass of ecological processes and biochemical cycling in soil [13]. At present, studies about microorganisms have already revealed their function and roles in soil but it is still lacking in stormwater treatment technologies [14]. The function of soil microorganisms in regulating ecosystem function is still not fully understood which might eventually lead to poor prediction in soil biodiversity affecting ecosystem sustainability [15].

Soil microorganisms are responsible for soil organic matter decomposition and nutrient cycling by producing a variety of soil enzymes and releasing the largest amount of CO₂ from soils to the atmosphere [16]. Most of the studies about stormwater low impact development technologies used generalized observations without fully understanding the mechanisms affecting the whole performance of the systems from catchment to the facility itself. At present, these LID technologies have been treated as black box due to fluctuating flow and environmental conditions affecting its operation and treatment performance. As such, the implications of microbial community to the overall performance of the tree-box fil-

ter were investigated in this study. Specifically, the relationship of microorganism survival to the sediment characteristics in a tree-box filter was investigated.

2. Materials and Methods

2.1. Characteristics and Design of the Tree-Box Filter

The tree-box filter was installed inside the Kongju National University, Cheonan City, South Korea in 2009. From 2009 to 2020, Cheonan City received an average annual rainfall depth of 1180 ± 289 mm and an average annual temperature of 12.32 ± 0.37 °C. Specifically, 39% to 84% of the annual rainfall depth was observed during the summer season (June to August) alongside the highest mean temperature of 23 to 26 °C. The storage volume capacity of the tree-box filter is 0.71 m^3 , which is initially designed to capture approximately 5 mm of rainfall. Sand, woodchip, and gravel were used as filter media as shown in Figure 1. The tree-box filter was planted with a *Metasequoia* tree. The facility aspect ratio (L:W:H) of the tree box filter was 1:1:0.87 and has a storage volume to total volume ratio of 45.4%.

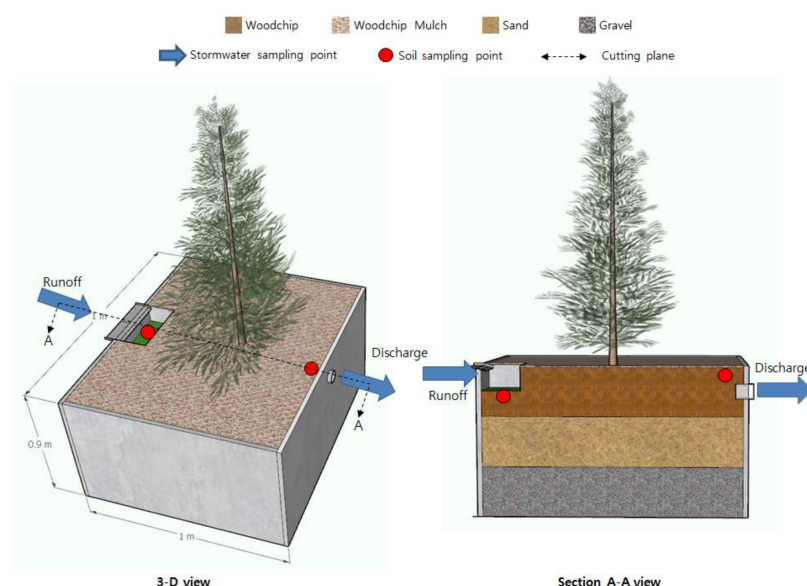


Figure 1. Schematic design of parking lot tree-box filter.

2.2. Soil and Microorganism Sampling Analytical Analysis

A total of four homogenous soil samples were collected each season near the inflow and outflow ports of the tree-box filter for soil chemical and microorganism analysis from 2016. Soil samples were also collected in the nearby landscape and was subjected to microbial analysis which was referred to as original soil (IS) collected at least 1 m away from the tree-box filter to compare the chemical properties to the tree-box filter. The chemical analyses of soil samples were based on the Soil Sampling and Methods of Analysis [17]. Soil samples for microorganism analysis were collected at the initial 10 cm of the media part after the inlet and 10 cm of the media part before the outlet. This was conducted as the biological treatment mechanisms occurred in the media part of the LID technologies [14]. Although the runoff flow rate varies with the rainfall depth, generally it flows horizontally and vertically in the media part from the inlet to the outlet of the tree-box filter. In addition, top and bottom layers of the media part have different properties including water content, temperature, and pollutant concentration. As such, soil sample collections for microorganism analysis were conducted at the top and bottom layers of the sample points near the inlet and outlet of the media part. Similarly, IS samples were also collected and subjected to microorganism analysis. Soil samples were stored at 5 °C to ensure the precision of the results of analyses. 16S rRNA gene sequence obtained by the Roche 454 pyro-sequencing technology was used for the microbial analysis of the samples same

as the method of analyses summarized in the study conducted by D'Argenio and Francesco, 2015 [18]. Among the three DNA/RNA extraction method, 16S rRNA sequencing was chosen due to its advantage of being easy to perform, fast, and relatively inexpensive. PCR was performed to analyze the phylum and the count of the microorganisms in which the resulting count would be unitless.

3. Results and Discussion

3.1. Characteristics of Sediment in the Tree Box Filter

Figure 2 compared the sediment quality from TBF and IS. Apparently, IS contained less pollutants compared to TBF except for phosphorus. TP and Org-P concentrations in the sediment from TBF were 752 and 568 mg/Kg of soil were lower by 2.4 and 2.9 times than IS, respectively. Higher phosphorus concentration in soil may be due to less phosphorus release from IS as most of the phosphorus is soil- or sediment-bound and the source of IS were only planted with small grasses compared to TBF which is planted with *Metasequoia* tree [19]. This was also evident with the comparison of phosphorus uptake by plants wherein shrubs uptaken less phosphorus compared to woody plants [11]. Apart from plants, microorganisms may also be an affecting factor for the difference in pollutant concentration of soil in TBF and IS. The average TN concentration in sediments collected from TBF amounted to 1215 mg/Kg of sediment which was found to be 1.4 times greater than IS. In addition, the average heavy metals concentration in sediments from TBF including Cr, Cu, Zn, Cd, and Pb were 0.13, 3, 75, 0.38, and 11 mg/Kg of sediment were greater by 5, 3.5, 8.66, 10.82, and 128 times than IS, respectively. The difference between pollutant concentrations was attributed to continuous pollutant inflow during storm events as stormwater runoff contains sediments with high pollutant concentration washed off during storm events. Specifically, heavy metals from stormwater have been recognized to be directly associated with traffic volume and were affected by land use characteristics, materials used in the drainage area and hydro-meteorological factors [12].

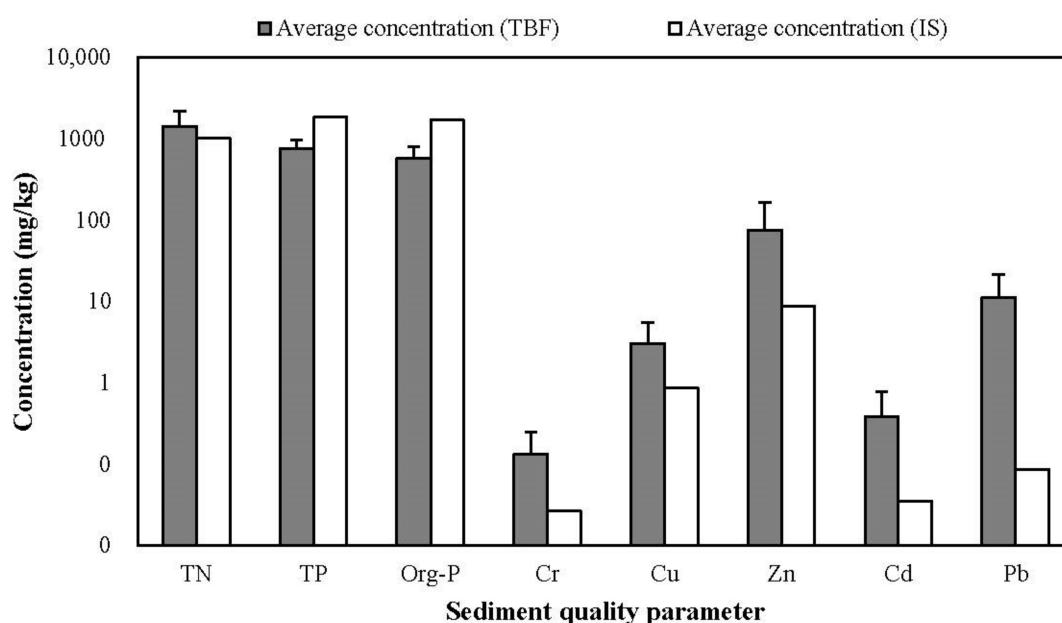


Figure 2. Comparison of soil chemical parameters of original soil (IS) and sediment from tree-box filter.

3.2. Changes and Behavior of Microorganism in the Tree Box Filter

Seasonal changes in soil microorganism in TBF is exhibited in Figure 3. Apparently, the summer season is the most suitable season for microorganism growth since more microorganisms were found during this season. The summer season in Cheonan City, South Korea, is the wettest and hottest season encompassing 39% to 84% of the annual

rainfall which occurred in Cheonan city from 2010 to 2019. In a study conducted by Galić et al. (2020), it was found that temperature and soil moisture are the key drivers of soil respiration wherein the hottest and wettest season tend to have higher observed CO₂ compared to other seasons [20]. On the other hand, the lowest microorganism count was observed in spring and fall. Least microorganism count in spring was found because of the plant growth during this season. In a research conducted by Shigyo et al. (2019), it was found that plant phenology influences the seasonal dynamics of soil microorganisms as it directly affects the C and N availability for soil microorganisms [21]. Litterfall during fall season might have affected the microorganism count during winter since during this season, the compositional variety of soil organic matter changes affecting the growth of soil microbial communities as a result of exudation of labile C through the roots and substrate input by litterfall [22]. It was also observed that higher microorganism count was observed in the outlet compared to the inlet of TBF of about 1.01 to 1.64 times which is attributed to the influent water during stormwater which might have been detrimental to microorganism growth and survival in the inlet compared to the outlet. The most dominant microorganism phylum is *Proteobacteria* in all the seasons both in inlet and outlet comprising 37% to 47% of the total microorganism count similar to the findings of other studies about soil microorganism's dominance [23,24]. *Proteobacteria* is one of the major phyla of Gram-negative bacteria constituting the largest and most diverse prokaryotes which is of great importance to carbon, sulfur, and nitrogen cycling [24–29]. *Proteobacteria* is followed by *Acidobacteria*, *Actinobacteria*, and *Chloroflexi* which comprises 6% to 20%, 9% to 20%, and 2% to 27%, respectively, of the total microorganism count for each season. *Acidobacteria* and *Actinobacteria* are both responsible and important for carbon cycling [30–32] (Ivanova et al., 2020; Lewin et al., 2016, Zhang et al., 2019). On the other hand, phylum *Chloroflexi* acquires energy and fix CO₂ through photosynthesis also known as the process called respiration [33].

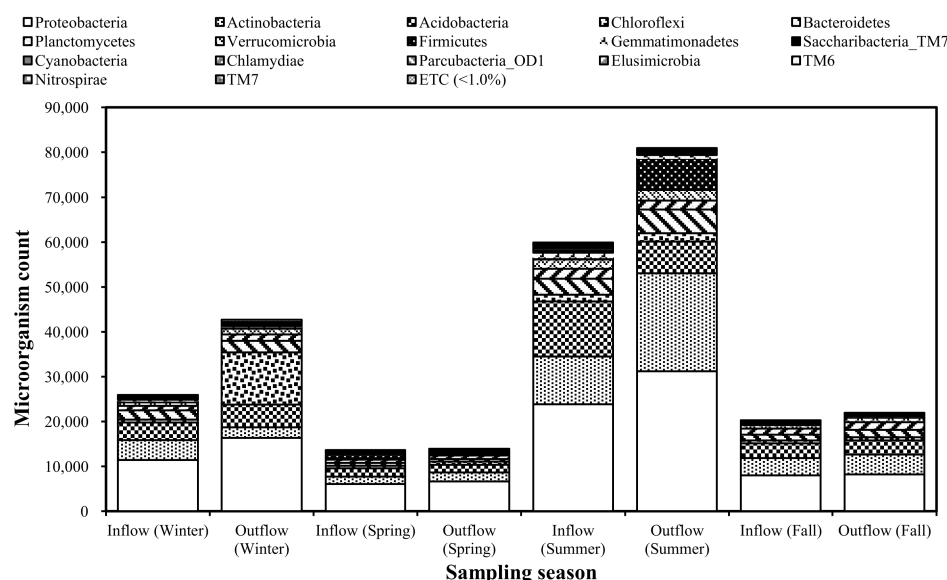


Figure 3. Seasonal changes in microorganisms in tree-box filter.

Table 1 shows the correlation between microorganism phyla greater than 1% of the total microorganisms and soil chemical parameters. Water content was observed to be negatively correlated to most of the microorganism phylum including the dominant phylum *Proteobacteria* and *Actinobacteria* with *Actinobacteria* having negative significant correlation to water content implying that an increase in water content could result to less *Actinobacteria* survival in TBF (r -value: -0.82 to -0.96). Among the microbial phylum, only *Chloroflexi* and *Parcubacteria* showed positive correlation to moisture content (r -value: 0.69 to 0.83). These results may have been affected by moisture from stormwater inflow during storm

events. The water content of sediments collected from TBF ranges from 29% to 79%. pH was identified as one of the factors affecting the presence, survival, and growth of different microbial phylum in soil [34–38]. However, in this study, it was found that only phylum *Chloroflexi* and *Parcubacteria* has positive correlation with pH (r -value: 0.53 to 0.56). High correlation was found between *Chloroflexi* and pH similar to the findings of Chodak et al. (2013) where it was found that higher soil pH favors *Chloroflexi* [35]. The finding of this study that *Planctomycetes* was negatively correlated with pH contradicted the finding of Constancias et al. (2015) which might have been affected by the stormwater input in TBF and difference between environmental conditions of TBF, deciduous oak-hornbeam forests and agricultural croplands [39]. pH measurements in the sediments collected from TBF range from 3.32 to 6.45. Ignition loss is a measure of for estimating organic and carbonate content in sediments. *Chloroflexi* and *Parcubacteria* were found to be positively correlated with ignition loss while *Actinobacteria*, *Cyanobacteria*, and *Nitrospirae* were found to be negatively correlated. This study coincides with the findings that *Chloroflexi* dominates in organic-rich sediments and *Nitrospirae* is negatively correlated to organic matter [40,41]. *Actinobacteria* contribute to the global carbon cycle through the production of extracellular hydrolytic enzymes which can degrade organic compounds (Lewin et al., 2016; Zhang et al., 2019). Similarly, *Cyanobacteria* are associated with carbon utilization and stress response which increases soil fertility and water retention and improves soil structure and stability [29,42]. Among the microorganism phyla only *Chloroflexi* have high negative correlation with TN (r -value = -0.58) which is similar to the findings of Ding et al., 2013, where *Chloroflexi* prevail in nutrient-poor soil [33]. TP was found to be positively correlated to microbial phyla including *Proteobacteria*, *Acidobacteria*, *Chloroflexi* *Parcubacteria*, and TM6 (r -value: 0.50 to 0.64). Similarly, Org P was found to be positively correlated with *Proteobacteria*, *Acidobacteria*, *Chloroflexi* *Bacterioidetes*, *Verrucomicrobia*, *Gemmatimonadetes*, *Chlamydiae*, *Parcubacteria*, TM6, and *Nitrospirae* (r -value: 0.52 to 0.78). This finding was in concurrence with the findings that the bicarbonate Org-P fraction has a strong influence on microbial community composition [43]. Among the microbial phyla, Cr was found to be significantly correlated with *Actinobacteria*, *Planctomycetes*, *Verrucomicrobia*, and *Saccharibacteria* (r -value: 0.83 to 0.91, p value < 0.05) similar to the finding of Sheik et al., 2012 wherein total Cr was found to be significantly correlated with diversity [44].

Among the microorganism phylum, only *Cyanobacteria* was found to be highly correlated with Cu with an r -value of 0.78 which might be due to the generation of protection by *Cyanobacteria* to stresses triggered by Cu [45]. High negative correlation was found between Zn and microbial phylum including *Proteobacteria*, *Acidobacteria*, *Bacterioidetes*, *Gemmatimonadetes*, *Chlamydiae*, TM6, and *Nitrospirae* with r -value ranging from -0.5 to -0.62 . This was supported by the finding that Zn significantly affects microbial community structure in soil wherein excessive concentration caused lower microbial diversity and enzyme activity [46]. On the other hand, Cd showed a high positive correlation with *Proteobacteria*, *Actinobacteria*, *Acidobacteria*, *Planctomycetes*, *Verrucomicrobia*, *Saccharibacteria*, *Cyanobacteria*, *Chlamydiae*, TM6, and *Nitrospirae* with r -value ranging from 0.50 to 0.90. Positive correlation to Cd of microbial phylum contradicted the findings of Sardar et al., 2007 wherein it was found that Cd was negatively correlated with all enzymatic activities [47]. Similarly, Pb was found to have high correlation with microbial phylum including *Proteobacteria*, *Actinobacteria*, *Acidobacteria*, *Bacterioidetes*, *Planctomycetes*, *Verrucomicrobia*, *Firmicutes*, *Gemmatimonadetes*, *Saccharibacteria*, *Cyanobacteria*, *Chlamydiae*, *Elusimicrobia*, TM6, and *Nitrospirae* with r -value ranging from 0.5 to 0.83. This finding might be attributed to the similar finding of Li et al., 2017 where it was found that Cd and Pb were significantly correlated with soil microbial community structure [48].

Table 1. Correlation between soil chemical parameters and microorganism phylum.

Microorganism Phylum	Water Content	Ignition Loss	pH	TN	TP	Org-P	Cr	Cu	Zn	Cd	Pb
<i>Proteobacteria</i>	−0.82	−0.26	−0.26	−0.47	0.56	0.69	0.76	0.16	−0.62	0.51	0.69
<i>Actinobacteria</i>	−0.97	−0.58	−0.50	−0.22	0.19	0.32	0.90	0.10	−0.31	0.50	0.79
<i>Acidobacteria</i>	−0.34	0.01	−0.31	−0.13	0.51	0.67	0.59	0.29	−0.50	0.85	0.70
<i>Chloroflexi</i>	0.69	0.92	0.56	−0.58	0.56	0.55	−0.39	−0.32	−0.45	−0.40	−0.43
<i>Bacteroidetes</i>	−0.87	−0.35	−0.25	−0.46	0.49	0.62	0.76	0.14	−0.60	0.44	0.66
<i>Planctomycetes</i>	−0.56	0.00	−0.69	0.22	0.03	0.27	0.83	−0.26	−0.08	0.88	0.78
<i>Verrucomicrobia</i>	−0.75	−0.18	−0.44	−0.25	0.41	0.59	0.84	0.04	−0.47	0.69	0.78
<i>Firmicutes</i>	−0.85	−0.49	−0.34	−0.37	0.17	0.25	0.74	−0.04	−0.28	0.15	0.56
<i>Gemmatimonadetes</i>	−0.68	−0.42	−0.32	−0.19	0.48	0.61	0.70	0.46	−0.56	0.79	0.76
<i>Saccharibacteria_TM7</i>	−0.71	−0.16	−0.66	0.09	0.10	0.33	0.91	−0.16	−0.18	0.82	0.83
<i>Cyanobacteria</i>	−0.56	−0.67	−0.17	−0.16	0.42	0.46	0.47	0.78	−0.49	0.64	0.62
<i>Chlamydiae</i>	−0.01	0.30	−0.09	−0.24	0.64	0.78	0.36	0.30	−0.60	0.71	0.50
<i>Parcubacteria_OD1</i>	0.83	0.99	0.53	−0.42	0.50	0.49	−0.50	−0.29	−0.33	−0.31	−0.46
<i>Elusimicrobia</i>	−0.30	−0.12	−0.36	0.10	0.32	0.47	0.53	0.36	−0.35	0.90	0.66
TM6	−0.20	0.11	−0.16	−0.21	0.60	0.74	0.47	0.34	−0.60	0.77	0.58
<i>Nitrospirae</i>	−0.60	−0.54	−0.27	−0.12	0.42	0.52	0.59	0.63	−0.50	0.77	0.70

Bold values indicate high correlation. Bold and shaded values indicate significant correlation.

3.3. Considerations for Microorganism Growth and Survival

Designing and maintenance of a good growing environment for microorganisms in LID technologies required controlling its environmental conditions. Table 2 summarizes the optimal growing conditions of different dominant soil microorganisms from different studies and this study. pH is one of the most important factors affecting the growth of microorganisms. Based on different studies, optimal pH for the good growing condition of dominant microorganisms in LID should be between 7.0 to 7.3. This may only be controlled by applying filter media with those pH values. However, as the LID technologies started to receive stormwater runoff, pH will vary depending on the influent water characteristics. While the analysis in this study revealed that soil moisture is mostly negatively correlated with microbial growth, other studies suggested that soil moisture play a key role in microorganism growth. Moisture content in the LID technologies during spring and fall season, which was found to have the least microbial abundance, should be maintained by irrigation, which will be helpful to both plants and microorganism growth. Depending on the target biogeochemical cycle, maintaining a good environment for a specific microbial phylum may be decided. For an enhanced carbon, sulfur, and nitrogen cycle and oxidation of iron and methane, the installation or use of smaller porous media good for *α-proteobacteria* growth should be considered in LID technologies [24]. Applying small porous media will also enhance other biogeochemical cycles including phosphorus and potassium cycle and breaking down of plant biomass performed by *Actinobacteria* [32]. Similarly, it will also provide a good growing environment for *Acidobacteria* responsible for expressing multiple active transporters, degrading gellan gum, and producing exopolysaccharide [49]. The use of smaller porous media will also provide a good environment for the growth of *Chloroflexi* and *Gemmatimonadetes* responsible for acting as organohalide respirer and performing nitrogen fixation, respectively [50,51].

Table 2. Summary of optimum growing environment for dominant microorganisms.

Microorganism Phylum	Growth Temperature	Growth pH	Growth Moisture Condition	Soil Type	Abundance in Large and Small Aggregate Size	References
<i>Proteobacteria</i>	20 to 45 °C	4.5 to 8.5 4.5 (Optimum)	increase significantly with the soil moisture	black (lessive 20.29%; chernozem 18.84%; black 14.01%), dark brown (20.29%), sandy (9.18%), saline (5.31%), alluvium (4.35%), meadow (4.35%), brown (1.93%), and chestnut	Genus: <i>Burkholderia</i> , <i>Afipia</i> L > S Class: <i>α-proteobacteria</i> ; Family: <i>Xanthomonadaceae</i> S > L	[51–54]
<i>Acidobacteria</i>	2 to 32 °C 15 to 22 °C (Optimum)	3.1 to 7.8 3.5 to 4.5 (Optimum), 4.5 to 8.5 4.5 (Optimum)	relatively more abundant in soils with high moisture content	Lessive, Black, Dark Brown, Alluvium, Brown, Sandy, Meadow, Saline, Chernozem, Chestnut (Abundance of Microorganisms in decreasing order)	Order: <i>Gp6</i> and <i>Gp1</i> S > L	[51,53,55,56]
<i>Actinobacteria</i>	25 to 30 °C (Optimum)	6.0 to 9.0 7.0 (Optimum)	abundance is higher in medium moisture	Chestnut, Sandy, Saline, Chernozem, Meadow, Alluvium, Brown, Black, Dark Brown, Lessive, Brown (Abundance of Microorganisms in decreasing order)	Genus: <i>Streptosporangium</i> L > S Family: <i>Streptosporangiaceae</i> , <i>Intrasporangiaceae</i> ; Genus: <i>Catenulispora</i> S > L	[51,52,56,57]
<i>Chloroflexi</i>	37 to 65 °C 60 °C (Optimum)	4.5 to 8.5 8.5 (Optimum), 5.5 to 7.3 6.0 (Optimum), 4.5 to 8.5 6.0 (Optimum)	relatively more abundant in soils with high moisture content	Meadow, Lessive, Black, Chernozem, Alluvium, Saline, Sandy, Dark Brown, Brown, Chestnut (Abundance of Microorganisms in decreasing order)	Genus: <i>Thermosporothrix</i> S > L	[51,52,56,58]
<i>Planctomycetes</i>	20 to 56 °C 47 to 50 °C (Optimum), 30 to 68 °C 55 °C (Optimum)	4.5 to 8.5 7.0 to 7.5 (Optimum), 5.0 to 9.0 7.0 to 8.0 (Optimum)	increased from low to high moisture	marine and freshwater sediments, salt pits and peat bogs, coastal marine sediments, and oceanic and freshwater anoxic zones	ND	[30,56,59]
<i>Bacteroidetes</i>	30 to 85 °C 50 to 80 °C (Optimum)	7.0 to 8.5 (Optimum)	increased from low to high moisture	Saline, dry mineral, Soil majority composed of clay, silt, and sand, with traces of CaCo ₃ , Cd, Cr, Cu, Ni, Pb, Zn, As and Hg, Pasture soil, forest soil, agricultural soil, mature and forest soil, grassland soil	Genus: <i>Niastella</i> L > S	[52,60–62]
<i>Verrucomicrobia</i>	10 to 40 °C 33 to 37 °C (Optimum)	5.0 to 9.0 6.5 to 8.0 (Optimum)	increases with soil moisture	ND	ND	[63,64]

Table 2. Cont.

Microorganism Phylum	Growth Temperature	Growth pH	Growth Moisture Condition	Soil Type	Abundance in Large and Small Aggregate Size	References
<i>Firmicutes</i>	30 to 80 °C	4.7 to 8.8	abundant at low-soil-moisture sites	Saline, dry mineral	Genus: <i>Paenibacillus</i> L > S	[52,60,62,65,66]
<i>Gemmatimonadetes</i>	25 to 35 °C 30 °C (Optimum)	6.5 to 9.5 7.0 (Optimum)	inversely correlated to soil moisture	Soil majority composed of clay, silt, and sand, with traces of CaCo ₃ , Cd, Cr, Cu, Ni, Pb, Zn, As and Hg, Lessive, Brown, Black, Dark Brown, Alluvium, Chestnut, Sandy, Meadow, Chernozem, Saline (Abundance of Microorganisms in decreasing order)	Genus: <i>Gemmatimonas</i> S > L	[36,51,52]
<i>Nitrospirae</i>	4 to 58 °C, 33 to 85 °C 39 to 58 °C (Optimum)	4.5 to 8.5 6.0 (Optimum), 7.6 to 8.0 (Optimum), 6.7 to 9.4	relatively more abundant in soils with high moisture content	Meadow, Black, Chernozem, Lessive (Abundance of Microorganisms in decreasing order)	Genus: <i>Nitrospira</i> L > S	[51,52,56,67,68]

L > S signified abundance in 1 to 2 mm aggregates compared to 0.05 to 0.1 mm aggregates; S > L signified abundance in 0.05 to 0.1 mm aggregates compared to 1 to 2 mm aggregates.

4. Conclusions

Understanding the behavior of microorganisms in low impact development technologies will help in assessing the contribution of each mechanism to the overall treatment performance of this type of technology. It was found that summer season was the most suitable season for microorganism growth since more microorganisms were found during this season. Least microorganism count was found in spring because of the plant growth during this season since plant phenology influences the seasonal dynamics of soil microorganisms. Litterfall during fall season might have affected the microorganism count during winter since during this season, the compositional variety of soil organic matter changes affecting the growth of soil microbial communities. The most dominant microorganism phylum is *Proteobacteria* in all the seasons both in inlet and outlet comprising 37% to 47% of the total microorganism count followed by *Acidobacteria*, *Actinobacteria*, and *Chloroflexi* which comprises 6% to 20%, 9% to 20%, and 2% to 27%, respectively, of the total microorganism count for each season. Moisture content in the LID technologies during spring and fall season which was found to have the least microbial abundance should be maintained by irrigation which will be helpful both to plants and microorganism growth. Depending on the target biogeochemical cycle, maintaining a good environment for a specific microbial phylum may be decided. For an enhanced carbon, sulfur phosphorus, potassium, and nitrogen cycle, oxidation of iron and methane, and breaking down of plant biomass installation or use of smaller porous media should be considered in LID technologies. As pH level in the LID technologies is highly dependent on the influent characteristics of stormwater while temperature depends on the climatic conditions; moisture content and media characteristics should be considered for optimum microbial growth and survival in different LID technologies.

Author Contributions: F.K.G.: Conceptualization; methodology; software; validation; formal analysis; investigation; data curation; writing—original draft preparation; visualization; N.J.R.: Methodology, investigation, writing—review and editing, visualization; H.C.: Methodology; investigation; software; L.-H.K.: Conceptualization; writing—review, and editing; supervision; project administration; funding acquisition. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Acknowledgments: This research was supported by the National University Development Project by the Ministry of Education in 2020.

Conflicts of Interest: The authors declare no conflict of interest.

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