

**Effect of pine bark and compost on the biological denitrification process of non-hazardous landfill leachate: focus on the microbiology**

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**Abstract:** In an attempt to optimize the cost-efficiency of landfill leachate treatment by biological denitrification process, our study focused on finding low-cost alternatives to traditional expensive chemicals such as composted garden refuse and pine bark, which are both available in large amount in South African landfill sites. The overall objective was to assess the behaviour of the bacterial community in relation to each substrate while treating high strength landfill leachates. Denitrification processes in fixed bed reactors were simulated at laboratory scale using anaerobic batch tests with immature compost and pine bark. High strength leachate was simulated using a solution of water and nitrate at a concentration of 500 mg l<sup>-1</sup>. Results suggest that pine bark released large amounts of phenolic compounds and hydroxylated benzene rings, which both can delay the acclimatization time and inhibit the biological denitrification (only 30% efficiency). Furthermore, presence of potential pathogens like *Enterobacter* and *Pantoea* agglomerans prevents the applicability of the pine bark in full-scale operations. On the other hand, lightly composted garden refuse (CGR) offered an adequate substrate for the formation of a biofilm necessary to complete the denitrification process (total nitrate removal observed within 7 days). CGR further contributed to a rapid establishment of an active consortium of denitrifiers including *Acinetobacter*, *Rhizobium*, *Thermomonas*, *Rheinheimera*, *Phaeospirillum* and *Flavobacterium*. Clearly the original composition, nature, carbon to nitrogen ratio (C/N) and degree of maturity and stability of the substrates play a key role in the denitrification process, impacting directly on the development of the bacterial population and, therefore, on the long term removal efficiency.

**Keywords:** denitrification; landfill leachate; compost; pine bark; microbial diversity

## **Introduction**

The majority of municipal solid waste landfills, including those that previously co-disposed hazardous materials continue to receive a significant proportion of bioreactive wastes which produce mainly greenhouse gases and wastewater known as leachate [1]. Landfill leachate contains organic and inorganic pollutants including humic acids, ammonia, heavy metals, persistent organic pollutants and inorganic salts at high concentrations (e.g. Chemical Oxygen Demand (COD) between 2000 - 6000 mg l<sup>-1</sup>, ammonia between 1000-1600 mg l<sup>-1</sup> and chloride between 1500-2600 mg l<sup>-1</sup>) [2]. If they are not collected carefully and not discharged safely, they may become a potential pollution source which threatens soil, surface water and groundwater [3]. Therefore, landfill leachate is recognized as an important environmental problem by modern societies. In the treatment of landfill leachate, biological systems such as nitrification-denitrification processes are frequently used [4-6]. Even though, these systems ensure a high Biological Oxygen Demand (BOD) removal efficiency, they are usually insufficient in degrading high-molecular-weight fractions and decolouring, and their efficiency is often susceptible to the presence of toxic substances and presence of refractory organics such as humic acids and surfactants [7]. In old sanitary landfills, the amount of organic materials having high molecular weight in leachate is high [7]. In the treatment of these wastewaters, therefore, combined systems including many processes such as aerobic–anaerobic decomposition, chemical oxidation, coagulation–flocculation and adsorption are preferred to single-process solutions [1]. However these combined treatment processes are often costly in terms of capital investment, energy requirements and frequent use of additional chemicals [1,7]. Other methods such as reverse osmosis, active carbon adsorption and advanced oxidation processes have been recently

pointed out as more versatile methods, however they only transfer the pollutants without solving the environmental problem and their full-scale application is not often economically feasible [1,8]. Clearly there is a need to re-evaluate the methods to remove contaminants from landfill leachate in order to shift from “waste treatment” to exploitation of landfill leachate as a resource that can be processed for recovery of energy, nutrients and other constituents.

Biological denitrification is one of the most promising and versatile approaches in the treatment of landfill leachate [7, 8]. In this process, an external organic substrate (i.e. methanol, ethanol, acetic acid) or electron donor is needed [9, 10]. While these compounds are expensive and potentially dangerous, some complex substrates such as tree barks, wood chips, corncobs, sawdust, compost [11] and newspapers [12] have proved to be efficient carbon sources for denitrification and generally more suited to treat high strength effluents [7, 11]. These natural substrates are normally cheaper than the synthetic ones and can be derived from a typical waste stream [13, 14].

Biological denitrification of landfill leachate is often undertaken in sequencing batch reactors (SBR) [7] or in constructed wetlands (CW) [15]. Both treatments are known for their flexibility in terms of adaptation to leachate nature and collection strategies [16, 17]. However, the influence that specific substrates have on the development and nature of active microbial populations is not yet widely understood [15]. Indeed, performance and stability of a bio-denitrification process, as of any biological process, depend on the concentration of the active species and on their metabolic activity. Little is known about their diversity, distribution, metabolic potential and functional roles. The nitrate-based

microbial communities of which they are members remain uncertain as well as the identity of their major and minor players and the ecological parameters that influence denitrification. This information is crucial to better understand the bio-denitrification process particularly in high strength landfill leachate and for the development of knowledge-based technologies to accelerate and optimize this treatment.

The objective of this study was to investigate the influence of garden refuse compost and pine bark on the microbial diversity and denitrification activity in the treatment of high strength nitrified landfill leachates (nitrate concentrations ranging between 500 up to 2000 mg l<sup>-1</sup>). The growth of the microbial community was followed using a spread plate enumeration technique; the colonization of the substrates was assessed through Environmental Scanning Electronic Microscopy (ESEM), and insight into the composition of the bacterial community was obtained by phylogenetic analysis.

## **1. Materials and methods**

### **1.1. Leachate selection**

To avoid analytical interferences, treated leachate from an SBR was simulated in the laboratory with a synthetic solution of potassium nitrate and distilled water with a concentration of 500 mg l<sup>-1</sup> of NO<sub>3</sub><sup>-</sup>.

### **1.2. Carbon sources selection**

Commercial (CGR) and domestic (DGR) garden refuse and pine bark (PB) were collected at the Mariannhill landfill site, Durban, South Africa. The garden refuse was composted for 10 weeks in pilot-scale forced aerated vessels at the University of KwaZulu-Natal, Durban,

South Africa. The properties of the solid substrates were characterized according to standard analytical methods as published by the American Public Health Association [18]: moisture content, total solids, volatile solids, C/N, Dynamic Respiration Index at 7 days (DRI<sub>7</sub>), determined with an OxiTop® respirometric system. Eluate tests were conducted to assess amount and nature of the compounds leached-out from the substrates in distilled water during 24 hours, using a 10/1 Liquid to Solid ratio (L/S) [11]. The following parameters were measured: total solids, volatile solids, pH, conductivity ( $\rho$ ), COD, BOD<sub>5</sub>, NH<sub>3</sub>, NO<sub>x</sub> and C/N ratio [18]. All analyses were carried out in triplicate.

### **1.3. Batch tests**

Batch experiments were designed to study the denitrification patterns of the synthetic leachate using the three substrates as carbon sources. Duplicate tests were conducted in 1.5 L anaerobic bottles equipped with two airtight silicone septa that allow for continuous sampling avoiding air ingress. Each substrate (S) was mixed with the synthetic leachate (L) at L/S=10/1 to ensure full saturation in the batch reactors (Table 1). As the size distribution and consistency of the three substrates were different, and the pine bark chips were reduced to 2-3 cm, varying amounts of materials (masses) were used in setting up the reactors, as reported in Table 1. A control test with distilled water was also carried out for each substrate. Optimal environmental conditions and full liquid to solid transfer were obtained by performing the experiments at a controlled temperature of 25 °C and by shaking at 150 rpm. The batches were flushed with N<sub>2</sub> to set anaerobic conditions.

For nitrate and pH testing, 2 mL samples were collected with a precision syringe connected

to a 0.45  $\mu\text{m}$  filter after 5, 10, 15, 30 and 60 min and then every hour during the first day. Afterwards, samples were collected four times a day. Nitrate and nitrite concentrations were analyzed using Nitrate Test Sticks type Merckoquant (MERCK). This method was selected to avoid large variations of the L/S ratio with time maintaining a reasonable accuracy (error within 10-15%). 1.5 mL samples were taken three times a day with a sterile syringe for microbiological analyses from Batch 1 for each substrate (Fig. 1, 2, and 3). The experiment was stopped when total denitrification was achieved, except for the pine bark for which the final concentration never fell within the discharge limits during the experimental time. The output COD, ammonia and pH were then analyzed on the filtered eluates.

#### **1.4. Batch inoculation**

In order to investigate the effect of inoculation on the reaction rate and the acclimatization time, 5 ml of solution of the first CGR test, were used to inoculate a second CGR batch prepared in the same conditions.

#### **1.5. Semi-quantitative analysis of the bacterial community**

The effect of the substrates on the growth of the bacterial populations was assessed during the batch tests. The 9215-C spread plate method [18] was applied to enumerate the aerobic cultivable microflora. A laminar flow cabinet was used to work in a sterile atmosphere. Samples were diluted in sodium chloride solution at 9 g l<sup>-1</sup> and 100  $\mu\text{l}$  of each dilution ( $10^{-3}$  to  $10^{-7}$ ) were spread on 90 mm agar plates using the Luria-Bertani Broth. The glass rods

were replaced by 4 mm glass beads spread on the plate. Plates were incubated at room temperature (25 °C) in the dark and enumeration was carried out visually after 3 days [19].

### **1.6. Microscopic analysis of the bacterial community**

Colonization of the different solid substrates was assessed using an Environmental Scanning Electronic Microscope (ESEM Philips, FEI XL 30). Samples were fixed in 3% (v/v) glutaraldehyde, washed twice in 0.05 M cacodylate buffer (pH 7.1) for 10 min and dehydrated in an alcohol series (10 min each in 30, 50, 70, 80, 90%, and 3×10 min in 100%) in a fume cupboard. The specimens were then transferred into critical point drier baskets under 100% alcohol and dried in a pre-cooled Hitachi HCP-2 critical point drier. After gold palladium sputter coating (Polaron Equipment Limited SEM, coating unit E5100), the samples were examined in the ESEM at 10 keV.

### **1.7. Genetic analysis of the bacterial community**

DNA extraction from the PB (at 2.5 h, 96 h and 263 h) and the CGR (at 3 h, 74 h and 162 h) liquid samples was carried out using the Zymo Research Fungal/Bacterial DNA extraction kit as described by Lejon et al. [20]. Purified DNA was suspended in 50 µL of sterile water and examined by agarose gel electrophoresis. All extracted genomic DNA samples were stored at –20 °C until further processing. The 16S rRNA gene was amplified by PCR using universal bacterial 16S primers 27-F and 1492-R [21]. PCR amplification was performed using Lucigen EconoTaq plus Green master mix. PCR products (approximately 1400 bp) were analyzed on a 1% agarose gel and cleaned with PCR purification kit (Qiagen). PCR products were then cloned using the CloneJet kit



(Fermentas) according to the manufacture's specifications. The screening of inserts from the transformants was performed by direct PCR amplification from colonies using primers for the pJET1.2F and pJET1.2R sites on the plasmid. Amplified inserts were identified on gel electrophoresis and cleaned by using the ZR-DNA Sequencing Clean-up kit™ (Zymo Research Corp). DNA sequences were determined by using an ABI 3130XL genetic analyzer and the BigDye terminator v3.1 cycle sequencing kit (PE Applied Biosystems). Sequences were compared to the GenBank nucleotide database library by BLAST on-line searches [22].

## **2. Results and discussion**

### **2.1. Substrates characterization**

Characterization of the solid matter showed that different origins and composition of the domestic garden refuse in relation to the commercial sample are evident (Table 2). Primarily large palm leaves, grass and twigs constituted the former, while the latter contained largely woody waste, tree bark and branches that made it more similar to the pine bark. These differences in composition, associated with the substrates' origins and collection methods, reflect also the amount and nature of the available carbon for denitrification which was two times higher in CGR than in DGR (Table 2). The high C/N ratio for the pine bark fell within the expected range as in literature, while the low value for the compost suggested an IV and V degree of maturity for the CGR and DGR, respectively (DIN 4187), with levels slightly higher than the optimum range of 13-16 for stabilised garden refuse compost [11]. Overall, CGR and PB displayed similar characteristics with respect to their composition, origin and C/N before composting suggesting a similarity in

the way carbon is released during denitrification. It is also worthy to note that high amounts of nitrogen, COD and TS are released from the DGR after 24 hours contact time with water (eluate tests) as well as during the batch tests (Table 3) through mechanisms of bio-leaching as observed also by other authors [6, 13, 33]. During this initial period ammonia is promptly converted into nitrites by nitrifiers as oxygen is still trapped in the water, while denitrification is limited by the availability of electron donors with a consequent increase in nitrate concentrations [6].

## **2.2. Batch tests**

Although no significant differences were observed for the DGR, CGR and PB Batch tests in term of nitrate removal, each substrate showed a distinct biotransformation rate. In the test with the CGR, complete removal of nitrates in solution was achieved within 8 days (Fig. 1). The DGR tests showed a large initial release of nitrate ( $500 \text{ mg l}^{-1}$ ) in solution by the substrate, independently of the input nitrate concentration (Fig. 1). However, the nitrate consumption rate remained close to that of the CGR tests and the complete denitrification was achieved within 8 days. The onset of denitrification was generally slower in the tests with PB and complete nitrate removal was not achieved, as the final concentration plateaued around  $150 \text{ mg l}^{-1}$  after 11 days (data not shown). This finding suggests the occurrence of a strong inhibitory effect on the active denitrifier population. Further this could be explained by the low pH observed during the batch tests with PB (Table 4), as suggested by other studies [6, 13, 33]. Although a neutral pH in the batch tests with compost could suggest a more favourable condition for microbial activity, the high release of COD and nitrate in the DGR is of concern and would require further investigation (Table 4).

### **2.3. Initial inoculation effect**

No direct effects were observed on nitrate removal in the inoculated batch test (data not shown). In a denitrification study using newspapers as a carbon source, Volokita et al. [12] found that an initial inoculation with a solid matrix was far more efficient than with a liquid inoculum. On the contrary, Ovez et al. [9] reported an inhibitory effect when inoculating their batches with bacteria from previous experiments. These contrasting effects might be explained by the extreme complexity of the microbial community established during the denitrification process, which is strongly dependent on the nature of the substrate and the experimental conditions. In general, inoculation using a solid substrate containing a well-established microflora should be preferred to an inoculum derived from the liquid phase.

### **2.4. Effect of the solid substrates on the size of the aerobic bacterial community**

The number of colony forming units (CFU) for both the CGR and DGR (Fig. 2) was estimated to be  $5 \cdot 10^7$  CFU ml<sup>-1</sup> at the beginning of the experiment and decreased by five orders of magnitude during the first two days. The viable bacterial community present in the PB test at the beginning of the experiment was accounted to  $3 \cdot 10^8$  CFU ml<sup>-1</sup>, which is ten times higher than in the compost tests (Fig. 2). A logarithmic decrease ( $R^2=0.94$ ) was observed during the first 7 days, leading to a constant bacteria concentration of  $1 \cdot 10^7$  CFU ml<sup>-1</sup> until the test was stopped. Assuming CFU were mainly using carbon and nitrate for their development, it should be possible to establish a relationship between CFU numbers and denitrification rate. The correlation between these two parameters for the liquid phase of the PB batch tests was good ( $r^2 > 0.80$ ) and confirmed that carbon and nitrate depletions

were mainly related to the microbial activity. Whilst this finding is in agreement with previous studies [6, 7, 8], it should be interpreted with much care. Indeed, the enumeration of the bacteria in the liquid phase does not account for those proliferating on the surface of the substrates (biofilms), and as such, it may not constitute a reliable indicator [7].

## **2.5. Effect of the solid substrates on the bacterial community**

Phylogenetic analysis was performed on 16S ribosomal DNA for each treatment in order to obtain further insight into the bacterial community structure and dynamics (Table 2). Even if the same tendencies were observed for the three treatments (dominance of *Gammaproteobacteria*, *Firmicutes* and *Bacteroidetes* in all libraries) differences were observed between composts and PB applications. During the acclimatization period, the bacterial community observed in the CGR and DGR tests was essentially composed of *Gammaproteobacteria* commonly found in natural environments, e.g. *Pseudomonas putida*, *Pseudoxanthomonas*, *Rheinheimera* sp. [23]. In contrast, the PB test was dominated by Enterobacteria including *Rahnella*, *Pantoea*, *Kluyvera* and *Enterobacter* which are typical of pine bark [24]. The population of *Rahnella* sp. largely dominated during the experiment while *Pantoea* agglomerans disappeared halfway through the experiment as being outcompeted by *Lactobacillus* and *Erwinia* sp. which both are known to be unable to reduce nitrate [25]. *Enterobacter* sp. and *Pantoea* agglomerans are potential human pathogens [24] and as such could prevent the applicability of the pine bark in full-scale operations. .

Bacteria capable of reducing nitrate into ammonia such as *Acinetobacter* sp. for *Gammaproteobacteria* [26] and *Clostridium* sp. for *Firmicutes* [27] as well as bacteria

capable of dissimilatory nitrate reduction such as *Rhizobium sp.* and *Thermomonas sp.* [28]) were identified after 74 hours treatment in the CGR eluates. In contrast, dominance of *Thermoactinomyces* in the DGR eluate after 74 hours suggests that these bacteria can first produce nitrous acid from nitrate followed by the generation of ammonium as they have both nitrate-reducing and ammonium-forming ability [29]. Over time, the bacterial community in the CGR eluate evolved towards a consortium of denitrifiers mainly composed of *Rheinheimera sp.*, *Phaeospirillum sp.* and *Flavobacterium sp.* [23, 30, 31]. *Phaeospirillum sp.* has been described as being able to use ammonia as a nitrogen source [31]. This suggests that it could counterbalance the presence of the ammonia-producing bacteria present in the second step of the experiment. This hypothesis is further supported by the low concentration of ammonia found at the end of the experiment ( $\text{NH}_3\text{-N} = 3 \text{ mg L}^{-1}$ )

## 2.6. Bacterial colonization of the solid substrates

The interpretation of ESEM micrographs could be challenging as the preparation of the samples may significantly change the matrix structure through shrinking and deformation [32]. To overcome this limitation, solid substrates before and after treatment were compared. Before treatment, cocci and fungal spores were the two most abundant organisms colonizing the surfaces of CGR while numerous cocci and rod-shaped bacteria were observed on the surfaces of DGR (Fig. 3 and 4). After treatment, rod-shaped bacteria dominantly colonized CGR surfaces (Fig. 5) whilst no changes were observed in DGR tests (data not shown). This finding suggests that the composted domestic garden refuse (DGR) offers a favourable surface for the rapid development of a biofilm of denitrifiers and that

$\text{NO}_3^-$  exerts a selective pressure on promoting the growth of rod-shaped bacteria leading to the formation of a superficial biofilm.

Numerous cocci were visible on the surface of the PB before incubation (Fig. 6). After treatment, very few bacterial cells were observed in the control and nitrate-rich tests (data not shown) due to possible inhibitory effects or desorption of most of the bacteria from the surface of the pine bark into the liquid phase. Previous studies demonstrated that pine barks could release large amounts of phenolic compounds and hydroxylated benzene rings, which both can inhibit the activity of various bacterial enzymes [32, 33]. Added to this, a constantly low pH during the process did not contribute in creating favourable conditions to bacterial growth.

### **3. Conclusion**

The composts (CGR and DGR) proved to be efficient substrates for denitrification, promoting the sustained development of a complex biofilm as a niche for the denitrifying communities. The phylogenetic analysis carried out on CGR and DGR samples showed that the bacterial community evolved from a diverse community towards a limited consortium of active denitrifiers. Pine bark was found to be far less efficient in promoting favourable conditions for microbial growth because of the combined effect of a low pH and the release of potentially inhibitory compounds leading to the irreversible release of biofilm forming cells into the leachate. Furthermore, potential pathogens have been detected in association with the pine bark, rendering unsuitable its use as a carbon source for the treatment of nitrate-rich leachates at a large scale. Overall, this study contributes in pointing out the different behaviour displayed by the microorganisms from different substrates in the solid

and liquid phases and highlights the important role of biofilms in the denitrification process and their sensitivity to prevailing environmental conditions.

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Table 1 Batch experiment set-up

	Mass of substrate (g)	Volume of the solution (ml)	Concentration of the solution (g.l <sup>-1</sup> of KNO <sub>3</sub> ·)
CGR	313	787	1.4
DGR	295	805	1.0
PB	196	905	0.9

Commercial (CGR) and (DGR) domestic garden refuse; Pine bark (PB)

Table 2 Solid matter characterisation for each substrate

	Moisture Content (%)	Total Solids (%)	Volatile Solids (%)	RI <sub>7</sub> (mgO <sub>2</sub> /g DM)	C/N (before composting)	C/N
CGR	67 ± 1	33 ± 1	47 ± 2	8.5 ± 0.6	40	24
DGR	66 ± 6	34 ± 6	62 ± 12	14.1 ± 0.4	22	13
PB	49 ± 3	51 ± 3	97.1 ± 0.1	17.8 ± 0.4	n.a.	62

Table 3 Physicochemical characteristics of the eluates after 24 hrs

	Total Solids (g l <sup>-1</sup> )	Volatile Solids (g l <sup>-1</sup> )	pH at 20°C	ρ (mS/cm) at 20°C	COD (mg l <sup>-1</sup> )	BOD <sub>5</sub> (mg l <sup>-1</sup> )	NH <sub>3</sub> -N (mg l <sup>-1</sup> )	NO <sub>x</sub> -N (mg l <sup>-1</sup> )	C/N
CGR	2.4 ± 0.1	1.6 ± 0.1	6.9	0.81	2800 ±400	155	9.8 ± 1.2	0.19 ± 0.05	1.8
DGR	17 ±3	12 ±0.2	7.5	5.1	17600 ±1300	350	82.0 ± 0.4	8 ± 2	8.3
PB	3.6 ± 0.01	3.3 ±0.3	4.2	0.85	4500 ±450	297	8.5 ± 0.1	0.03 ± 0.01	3.6

Table 4 Evolution of COD, pH and NH<sub>3</sub> in the liquid phase during the batch tests

	COD (mg l <sup>-1</sup> )	pH at 20°C	NH <sub>3</sub> -N (mg l <sup>-1</sup> )
CGR 24h	2800 ± 400	6.9	9.8 ± 1.2
CGR final	3200 ± 100	7.5	3.0 ± 0.1
DGR 24h	17600 ± 1300	7.5	82.0 ± 0.4
DGR final	17800 ± 1100	7.6	87.2 ± 0.4
PB 24h	4410 ± 20	4.2	8.5 ± 0.1
PB final	14200 ± 1200	4.3	22.5 ± 10

Table 5: Summary of bacterial sequence identification (expressed as %) according to the closest matches to sequences in the Genbank database found by BLAST

Phylogenetic group / genus level	PB eluate			CGR eluate			DGR eluate		
	2.5 h	96 h	263 h	3 hr	74 h	162 h	3 hr	74 hr	162 hr
<b>α-proteobacteria</b>									
<i>Phaeospirillum</i>						26	-	-	-
<i>Rhizobium</i>				-	20	8	-	-	-
Alpha proteobacterium INAWF007							-	7	3
<i>Aquicella siphonis</i>				-	-	-	21	12	8
<b>γ - proteobacteria</b>									
<i>Pseudoxanthomonas</i>	-	-	-	30	4	-	4	-	-
<i>Rheinheimera</i>	-	-	-	25	9	14	11	-	-
<i>Acinetobacter</i>	-	-	-	-	12	2	4	-	-
<i>Pseudomonas</i>	-	-	-	-	-	17	12	8	5
<i>Thermomonas</i>	-	-	-	-	20	5	-	-	-
<i>Rahnella</i> *	24	22	34	-	-	-	-	-	-
<i>Pantoea</i> *	12	-	-	-	-	-	-	-	-
<i>Kluyvera</i> *	6	6	4	-	-	-	-	-	-
<i>Enterobacter</i> *	14	11	8	-	-	-	-	-	-
Uncultured gamma proteobacterium clone 16S5	11	-	-	-	-	-	-	-	-
<i>Erwinia</i> *	-	22	10	-	-	-	-	-	-
<b>Firmicutes</b>									
Uncultivated clostridium sp clone 3.28	-	-	-	8	7	-	-	-	-
<i>Geobacillus</i>				23	3	-	-	-	-
<i>Bacillus</i>	-	-	-	-	-	-	13	29	40
<i>Thermoactinomyces</i>	-	-	-	-	-	-	2	24	27
<i>Lactobacillus</i>	-	33	29	-	-	-	-	-	-
<b>Bacteroidetes</b>									
<i>Flavobacterium</i>	-	-	-	-	-	17	-	-	-
<i>Pedobacter</i>	-	-	-	-	18	3	-	-	-
Unknown	33	6	15	14	7	8	33	20	17

Phylogenetic grouping based on the highest identity score obtained after submitting the sequence to BLAST (sequence identity with > 97% homology). Data are expressed as % of 16S rRNA clones.

“-“ : not detected; \* Enterobacteria

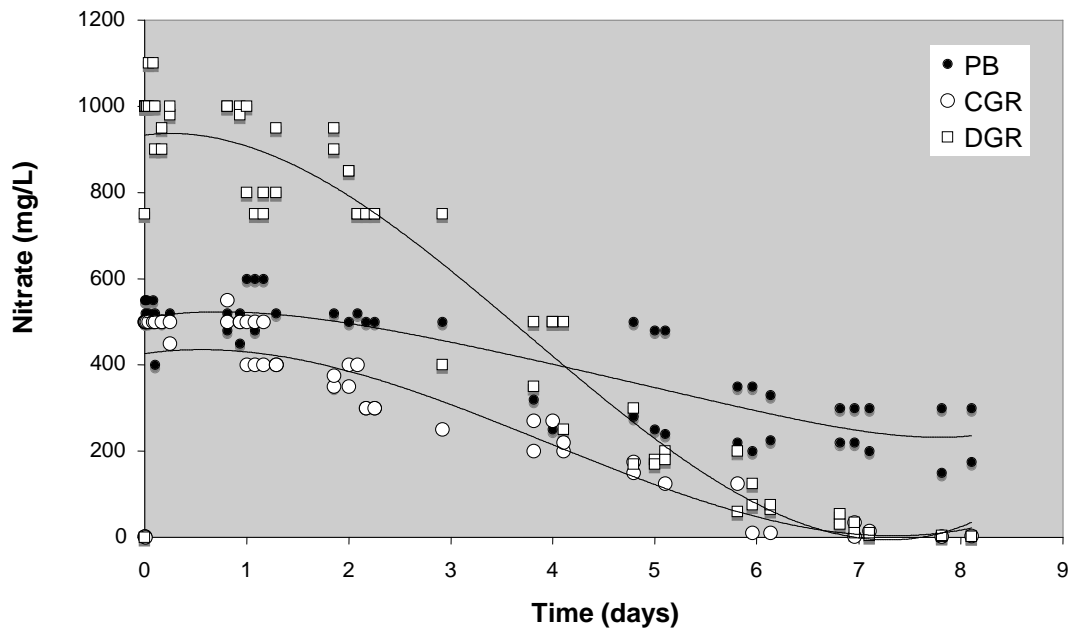


Fig. 1: Influence of Pine Bark (PB), Commercial Garden Refuse (CGR) and Domestic Garden Refuse (DGR) amendment on the nitrate removal in batch tests.

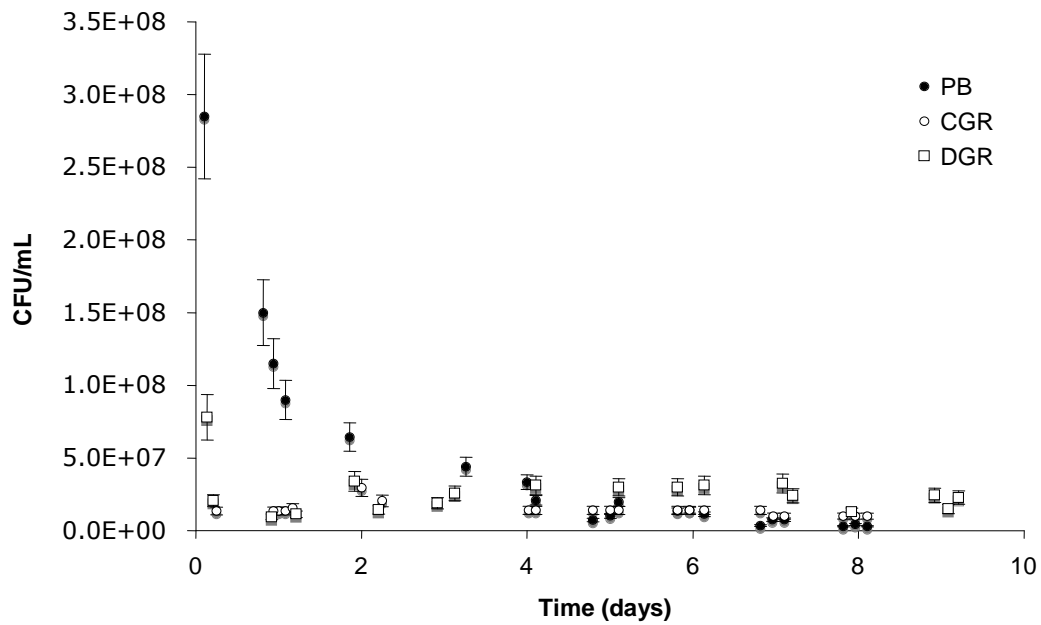


Fig. 2: Change in the abundance of the microbial population according to the carbon sources used in batch tests.



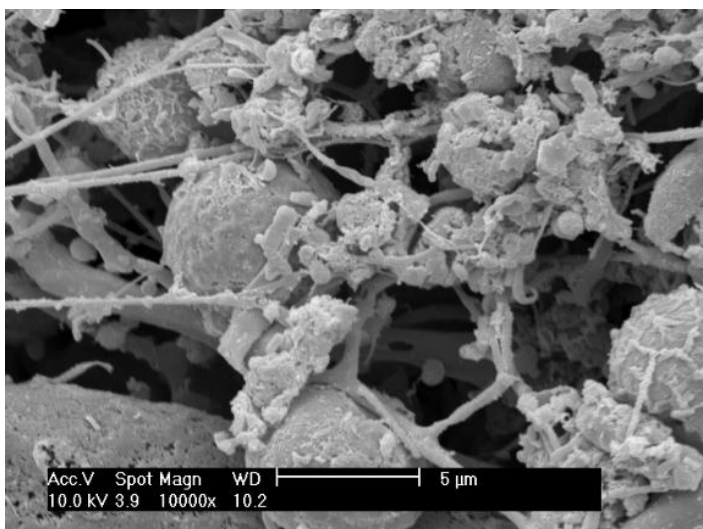


Fig. 3: ESEM micrograph of the surface of CGR before incubation

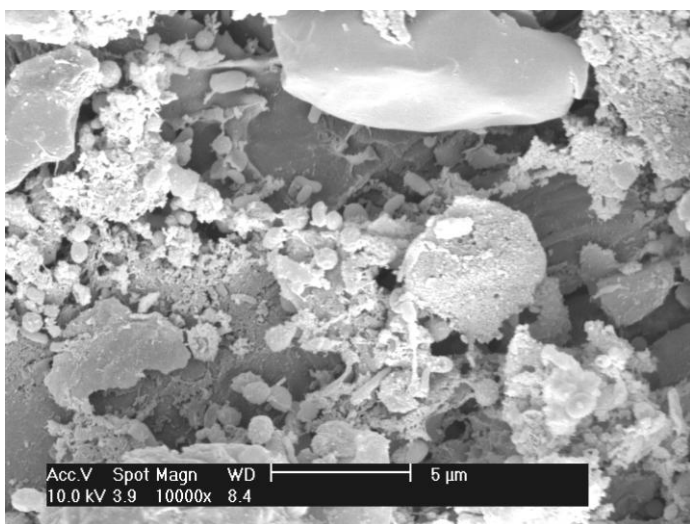


Fig. 4: ESEM micrograph of the surface of DGR before incubation

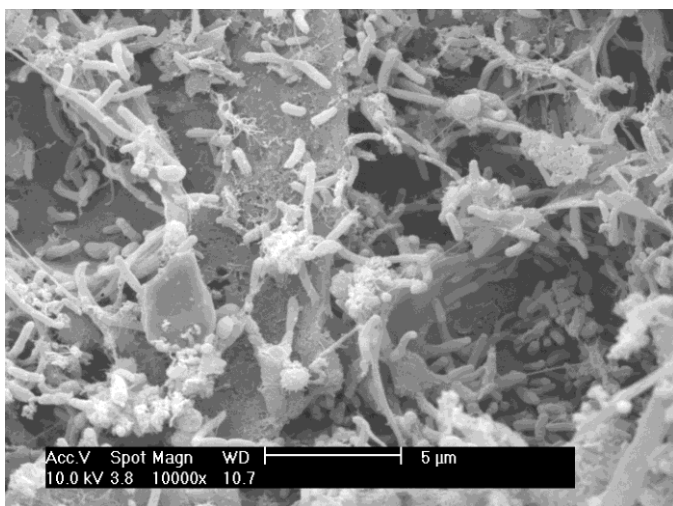


Fig. 5: ESEM micrograph of the surface of CGR 500 after 8 days

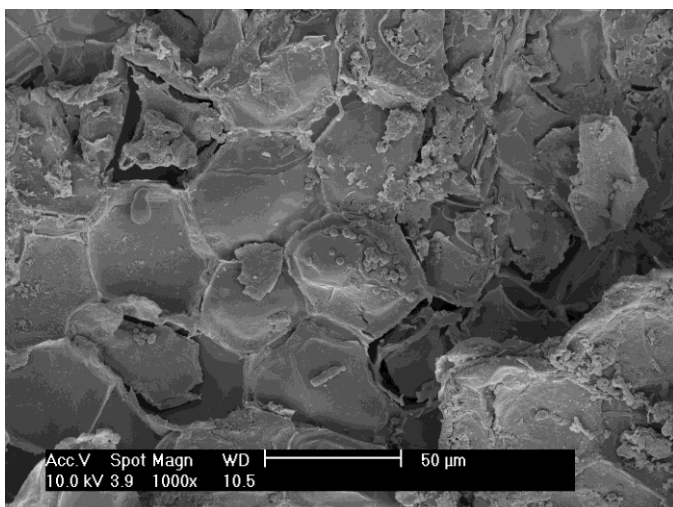


Fig. 6: ESEM micrograph (magn. x 10000) of the surface of pine bark (PB) before incubation

# Effect of pine bark and compost on the biological denitrification process of non-hazardous landfill leachate: Focus on the microbiology

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2010-09-15

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Cristina Troisa, Frédéric Coulon, Cécile Polge de Combret, Jean M.F. Martins and Laurent Oxarango, Effect of pine bark and compost on the biological denitrification process of non-hazardous landfill leachate: Focus on the microbiology, Journal of Hazardous Materials, Volume 181, Issues 1-3, 15 September 2010, Pages 1163-1169

<http://dx.doi.org/10.1016/j.jhazmat.2010.05.077>

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