



## Original Research Article

# Bacterial Diversity in Compost and Vermicompost of Cotton Waste at Courtallam, Nellai District in Tamilnadu, India

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## ABSTRACT

### Keywords

Cotton waste, Compost, Vermicompost, Bacteria

The compost and vermicompost samples of cotton waste (CW) were serially diluted up to  $10^4 \text{g}^{-1}$  and 1 ml of diluted sample poured on Petri plates containing potato dextrose agar (PDA) medium in aseptic condition for the culture bacteria. Bacterial isolates comprise under 5 genera namely *Enterobacter*, *Klebsiella*, *Pseudomonas*, *Bacillus* and *Proteus*. Colony forming units (CFU) of bacteria were found more in vermicompost of cotton waste samples composted by three local indigenous earthworm species *Lampito mauritii*, *Perionyx excavatus* and *Eudrilus eugeniae* compared with compost samples of cotton waste.

## Introduction

Vermicomposting is a widely acceptable alternative for converting waste into a more useful eco-friendly organic fertilizer to improve soil fertility (Fang *et al* 1999; Maleena-Imbeah 1998; Venkatesh & Eevera 2008). The amicable role of microbes in vermicomposting process has been realized by scientist all over the world in the past few decades. Along with enzymes of earthworm origin, microbes which inhabit in the gut contribute enzymes to enhance degradation process of waste while the wastes pass through the gut as nutrients (Idowu *et al* 2006). Vermicomposting process actually started with the entry of microbes along with eating wastes and harbor in the gut region of earthworms (Vinothaet *al* 2000).

Earthworms ingest soil microorganisms along with organic residues from the soil and during passage through the earthworm's intestinal tract, their population may increase and the defecated vermicasts have been reported to be much more microbiologically active and richer in microflora than their surrounding un-ingested soils (Scheu 1987; Daniel & Anderson 1992). The ingested microbial populations along with wastes enter the gut and play a prudential role in earthworm nutrition by donating microbial enzymes in the breakdown of organic matter, particularly the components that the earthworms cannot utilize in their natural state (Honor & Mitchell 1981). Composting of manure and

other organic wastes is a microbiologically mediated process with which the readily degradable organic matter in organic wastes is degraded and stabilized. During this process, part of organic C is released as CO<sub>2</sub>, part incorporated into microbial cells and part humified. Composting has a long tradition and has been practiced for centuries by farmers and gardeners. It is found that the microbial population in the compost and vermicompost varying due to the thermophilic action which kill most of the mesophilic microbes in the compost. In contrast, microbial population in earthworm gut and vermicasts consistently increased due to symbiotic relationship between earthworm and gut associated microbes (Hornor & Mitchell 1981). This paper is aimed to compare bacterial population in the compost and vermicompost of the cotton waste (CW) composted by local earthworm species *Lampito mauritii* and *Perionyx excavates* and an exotic species *Eudrilus eugeniae*.

## Materials and Methods

### Collection of compost and vermicompost of cotton waste

From the compost and vermicompost samples of cotton waste samples, one gram was taken separately in sterilized conical flask containing 100 ml of sterile distilled water and mixed well. One ml of diluted sample was taken and poured into 9 ml of sterile distilled water and the samples were serially diluted up to 10<sup>-4</sup> dilutions.

### Culture of bacteria

One ml of diluted sample was poured on Petri plates containing potato dextrose agar (PDA) medium in aseptic condition for the culture of bacteria. Six replicates were prepared for each sample for further statistical analysis. The prepared plates were

incubated at 37<sup>0</sup> C for 72 hours in sterile condition. The bacterial colonies in each plate were identified by cellular morphology and biochemical characteristics (Sneath 1986; Jones and Collins 1986). Data were subjected to students "t" test was also used to compare fungal species at various zones in the septic tank samples.

## Results and Discussion

The kinds of microorganisms in the gut and casts of earthworms depend on the microorganisms of their habitat in which they live and feed (Matthies *et al* 1999; Aira & Domínguez 2007). The amicable role of microbes in vermicomposting process has been realized by scientist all over the world in the past few decades. It is believed that microorganisms constitute an important nutritional component of the earthworm's diet (Edwards & Bohlen 1996). A total of 5 genera of bacteria namely *Enterobacter*, *Klebsiella*, *Pseudomonas*, *Bacillus* and *Proteus* were isolated from compost and vermicompost samples of cotton waste (CW) samples (Table 1). The vermicomposts which are derived from CW composted by *Lampito mauritii*, *Perionyx excavates* and *Eudrilus eugeniae*. All five species of bacteria were isolated from 10<sup>-4</sup> g<sup>-1</sup> dilutions of composts of CW vermicomposts respectively. Colony forming units (CFU) of bacteria were found statistically more in vermicompost samples compared with compost samples of respective wastes.

### Bacterial isolates in compost and vermicompost samples

Among 5 bacterial species isolated, three species such as *Enterobacter aerogenes*, *Klebsiella* sp., and *Pseudomonas* sp. belong to gram negative and the remaining two species *Bacillus* sp. and *Proteus mirabilis* belong to gram positive bacteria.

**Table.1** Diversity and density of bacteria in composts of cotton waste (CW) and vermicomposts of cotton waste composted by *L. mauritii*, *P.excavatus* and *E. eugeniae* (CWC- Cotton waste compost; CWVC- Cotton waste vermicompost)

Sl.No	Bacteria	Compost of cotton waste (CFUx10 <sup>4</sup> g <sup>-1</sup> )	Vermicompost of <i>Lampitoma</i> (CFUx10 <sup>4</sup> g <sup>-1</sup> )	Vermicompost of <i>Perionyx</i> (CFUx10 <sup>4</sup> g <sup>-1</sup> )	Vermicompost of <i>Eudrilus</i> (CFUx10 <sup>4</sup> g <sup>-1</sup> )
	<b>Gram -ve</b>	<b>CWC</b>	<b>CWVC</b>	<b>CWVC</b>	<b>CWVC</b>
1	<i>Enterobacter aerogenes</i>	97	146	116	163
2	<i>Klebsiella sp.</i>	78.5	98.5	102.7	95.2
3	<i>Pseudomonas sp.</i>	45.7	76.5	56.56	76.8
	<b>Gram +ve</b>				
1	<i>Bacillus sp.</i>	56.67	78.34	87.8	78.55
2	<i>Proteus mirabilis</i>	54.3	76.8	102.6	97.4
	<b>No. of species</b>	<b>05</b>	<b>05</b>	<b>05</b>	<b>05</b>
	<b>Average CFU±std</b>	<b>66.43 ±20.93</b>	<b>95.23** ± 29.85</b>	<b>93.13* ± 22.75</b>	<b>102.19* ± 35.26</b>

The number of bacterial isolates in composts and vermicomposts of cotton waste composted *L. mauritii*, *P.excavatus* and *E. eugeniae* were similar. However, vermicompost samples accommodated with rich density of each bacterial isolates compared with compost samples. Statistical investigation denotes that the average CFU in the compost (66.43 ± 20.93) of CW was found less significant when compared with the CFU of bacterial isolates in the CW vermicomposts composted by *L.mauritii* (95.23±29.85; t=4.12, p=0.0059\*\*), *P. excavatus* (93.13±22.75; t=4.21, p=0.0135\*) and *E. eugeniae* (102.19±35.26; t=4.07, p=0.0153\*). The microbial populations isolated in 10<sup>-4</sup> dilutions from pressmud and agriculture weed wastes composts and vermicomposts (Perungkottur Selvi et al 2012), cow dung and goat dung composts and vermicomposts (Perungkotturselvi et al 2012a) composted by earthworm species *L. mauritii*, *P. excavatus* and *E. eugeniae* at Courtallam already were documented. It is widely believed that vermicompost greatly exceeds conventional compost with respect to levels of beneficial microbial activity. Much of the work on this subject has been

done at Ohio State University, led by Dr. Clive Edwards (Subler et al 1998). Edwards (1999), has stated that vermicompost had more microbial species than conventional compost and these microbes can able to transform nutrients into simple forms that can be readily taken up by plants than in compost.

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