

# Thermophilic lignocellulolytic microorganisms in compost: Characterization

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Anguka J. Effects of antimicrobials in vitro on *Staphylococcus saprophyticus* in planktonic and biofilm forms isolated from patients with urinary tract infections. *J. Environ. Microbiol.* 2022;4(4):1-2.

## ABSTRACT

In order to compost, a microbiota must be chosen that can withstand the high temperatures produced by the process and degrade the lignocellulose. To increase composting efficiency and offer thermostable biomass-degrading enzymes for biorefineries, it is important to have a thorough understanding of the thermophilic microbial population involved in such biotransformation. This study focused on the dynamics, enzymes, and thermotolerance of each member of a lignocellulose-degrading thermophilic microbial community during all stages of composting plant waste. The results showed that 58% of holocellulose (cellulose + hemicellulose) and 7% of lignin had been destroyed at the end of composting. In contrast to 8%-10% of thermophilic bacteria, which only demonstrated this feature for hemicellulose degradation, the entire fungal thermophilic population exhibited lignocellulose-degrading ability (xylan-degrading). Both groups play a significant role in the breakdown of hemicellulose throughout the entire process due to their abundance, enzymatic activity, and wide range of thermotolerance, whereas the degradation of cellulose and lignin is only possible due to the activity of a few

thermophilic fungi that persist at the end of the process. The 159 xylanolytic bacteria isolates were mostly from the Firmicutes (96%) order, with a few Actinobacteria (2%), and Proteobacteria (2%). *Aeribacillus pallidus* and *Bacillus licheniformis* were the two most common species.

Only 4 species- *Thermomyces lanuginosus*, *Talaromyces thermophilus*, *Aspergillus fumigatus*, and *Gibellulopsis nigrescens* of the 27 strains of thermophilic fungi were dominant, with *A. fumigatus* and *T. lanuginosus* the other two species. As a result of the shifting composting environment, several strains of the same species emerged separately at different phases of composting, exhibiting phenotypes with variable thermotolerance and unique enzyme expression that had not been previously recorded for the species. Potential candidates for the synthesis of thermozymes were identified as *Bacillus thermoamylovorans*, *Geobacillus thermodenitrificans*, *T. lanuginosus*, and *A. fumigatus* strains with high enzyme activity. This study establishes the groundwork for future research into how thermophilic lignocellulolytic bacteria adapt and acquire new features during composting, as well as their potential use in biotechnological processing.

**Key Words:** *Geobacillus*; *Thermodenitrificans*; *Lignocellulolytic*; *Thermophilic*; *La nuginosus*; *Thermotolerance*

## INTRODUCTION

A valuable renewable carbon resource is characterised as lignocellulosic materials, including agricultural and forestry waste, in the context of the present biorefineries supported by the circular economy. As a result, its use is seen as a practical and sustainable substitute for conventional refineries that rely on the use of Raw Materials (RMs) obtained from oil. Different enzyme systems with particular catalytic methods have evolved in some microbes to breakdown complex lignocellulose. In fact, lignocellulose depolymerization occurs in natural ecosystems with a high degree of efficiency due to the cooperative activity of several enzymes produced

by microorganisms belonging to different taxonomic groups. For instance, although anaerobic bacteria, such as *Clostridium thermocellum* and *Acetivibrio cellulalyticus*, integrate diverse cellulases, aerobic organisms, such as *Trichoderma* species and several actinomycetes, generate and exude free lignocellulolytic enzymes (Cells).

Composting is one of the most favourable conditions for the recovery of microorganisms that break down lignocellulose. It has undergone comprehensive analysis to ascertain the role played by this particular collection of microbes in the breakdown of this particular resistant polymer. For the past 25 years, composting has been promoted as an effective option for the treatment of organic waste, in which a sophisticated microbial community performs the biotransformation

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Received: 06 July 2022, Manuscript No. puljem-23-6039; Editor assigned: 08 July 2022, Pre-QC No. puljem-23-6039 (PQ); Reviewed: 12 July 2022, QC No. puljem-23-6039 (Q); Revised: 15 July 2022; Manuscript No. puljem-23-6039 (R); Published: 20 July 2022, DOI: 10.37532/puljem.22.4 (4).1-2



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process. Because of the energy provided by exergonic aerobic reactions originating from microbial metabolism, heat is produced during the process.

Because of the energy provided by exergonic aerobic reactions originating from microbial metabolism, heat is produced during the process. This causes several stages of composting to develop, which are mostly determined by the temperature achieved in the materials being converted. The mesophilic, thermophilic, cooling, and maturation thermal stages make up the composting process. The first two stages of the process (the bio-oxidative phase) are when microbial activity is at its peak, but the maturation phase is when the materials are primarily humified. As a result, temperature will affect the composition and dynamics of microbial populations during the composting process. It is also a crucial element frequently used to gauge the efficiency of the process.

According to recent studies, the majority of microorganisms in composting can therefore be classified as thermotolerant since they are able to adapt to the fluctuating temperature of the process. Due to the thermostability of their enzymes, which makes them more competitive in industrial processes than other, more thermolabile microbes, these thermotolerant bacteria are of particular interest. The biotechnological importance of the populations of thermophilic organisms present in the composting process has been stressed by several writers over the past few years. In fact, recent developments in molecular identification, metagenomics, and proteomics have made it possible to comprehend the metabolic diversity and functionality of various bacterial and fungal families involved in the process, specifically in terms of their capacity to degrade lignocellulosic fractions.

From the "secretome" of lignocellulosic materials subjected to various thermal treatments, other authors have characterised the capabilities of microbial consortiums, pointing to a metabolic coordination between various species with a view to the deconstruction of the lignocellulose. In any case, despite the fact that they are novel due to the use of genomic mining and powerful data platforms, the majority of the studies described do not allow knowing the thermal tolerance range of the identified taxa or the actual capacity to deconstruct lignocellulosic fractions.