

Exploring the diversity of cellulolytic microorganisms from tea factory waste and evaluating their potential in breaking down tea waste

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Abstract. Sembiring M, Mukhlis, Razali, Hidayat B. 2025. Exploring the diversity of cellulolytic microorganisms from tea factory waste and evaluating their potential in breaking down tea waste. *Biodiversitas* 26: 377-385. The rate at which organic materials decompose is influenced by their cellulose, lignin, and hemicellulose content. To accelerate the decomposition process, cellulolytic microorganisms can be employed, which can be isolated from organic materials. Tea plants, as a significant plantation commodity, produce various types of waste during processing, including solid, liquid, and gas wastes. Solid waste from tea factories is produced in large quantities year-round and has substantial potential as a source of organic material. This research aimed to find cellulolytic microbes that were sourced from tea waste and have superior potential in the decomposition of organic matter, especially tea waste. The research involved several stages: isolating microbes from semi-processed waste from the Bah Butong tea factory, purifying the microbes to obtain pure isolates, testing the semi-qualitative potency of these isolates on CMC (Carboxyl methyl cellulase) media, and assessing the degradation potential of the superior isolates on raw tea factory waste. The research findings revealed the presence of five bacteria and two fungi from tea factory waste that have potential as decomposer microbes: *Enterobacter oligotrophicus* (AS), *Stenotrophomonas maltophilia* H05 (BS), *S. maltophilia* (CS), *Priestia megaterium* (DS), *Methylophilus methylotrophus* (ES) and cellulolytic fungi *Aspergillus fumigatus* (J1) and *Aspergillus corrugatus* (J2). Overall, the use of these cellulolytic bacteria and fungi can accelerate the decomposition of tea factory waste, with compost nitrogen content increasing by 102%. The application of *Aspergillus corrugatus* (J2) and *Methylophilus methylotrophus* (ES) is the best treatment with the lowest C/N ratios and the highest total nitrogen content.

Keywords: Biodiversity, C/N ratio, organic matter, total nitrogen

INTRODUCTION

The tea plant, scientifically known as *Camellia sinensis* (L.) Kuntze, is an evergreen shrub native to subtropical regions. As a longstanding plantation commodity in Indonesia, tea plays a significant role. Tea is the most demanded beverage after mineral drinking water due to the various health benefits of tea and its antioxidant content that provides a refreshing effect on humans (Aboagyie et al. 2021; Shang et al. 2021; Xu et al. 2021a). Tea waste, if disposed of inappropriately, will result in pollution of the soil, water and air (Lin et al. 2015; Guo et al. 2020; Prabhu et al. 2021). Therefore, the potential and sustainable utilization of tea waste has become a priority issue in handling tea factory waste. Tea waste is basically a lignocellulose biomass consisting of cellulose, hemicellulose, lignin, polyphenols, proteins and tannins (Ren et al. 2019; Zhang et al. 2019; Wang et al. 2020). Tea contains biologically active substances such as polyphenols, methylxanthine, alkaloids, vitamins, minerals, amino acids and polysaccharides. Tea waste generally contains the same components as regular tea with almost the same biological activity (Sökmen et al. 2018; Zhao et al. 2018; Xu et al. 2021b).

During tea processing in factories, black tea waste accounts for 2-3% of total tea production. This waste, primarily composed of solid materials (fiber) from the tea-making process, has high availability and great potential as

a source of organic matter. By converting this waste into compost enriched with indigenous tea microbes, it can be utilized to enhance soil fertility. These two active ingredients are expected to work synergistically to provide nutrients and improve soil properties. Solid waste from tea factories is abundantly available throughout the year and has significant potential as a source of organic matter. Tea waste contains 37% cellulose, 14% lignin and hemicellulose, and 25% polyphenols. The composition of tea waste results in a natural decomposition process that can take place slowly so that local cellulolytic microbes are needed to accelerate the decomposition process so that the utilization of decomposed organic matter can be quickly used. During composting, the C/N ratio generally decreases, but a high C/N ratio (>20-25) may indicate immature compost (Liaud et al. 2014; Pereira et al. 2016; Sembiring et al. 2024).

There are several methods to accelerate the composting process, including physical, chemical, and biological approaches. One common biological method involves adding microorganism inoculants such as bacteria, fungi, and actinomycetes, which are highly effective at decomposing compost materials (Frainer et al. 2015; Khatoun et al. 2017; Real et al. 2020). The cellulase enzyme plays a crucial role in this process by hydrolyzing cellulose, breaking the β -1,4 glycosidic bonds in cellulose, cellodextrin, cellobiose, and other cellulose derivatives into glucose. Cellulolytic bacteria are microorganisms capable of producing cellulase, which hydrolyze cellulose into glucose (Behera et al. 2014; Aziz

et al. 2021; Ilahi and Febria 2021). *Lactobacillus acidophilus* and *Enterobacter cloacae* are bacteria that are able to decompose cellulolytic (Puspawati et al. 2018). Microbes decompose cellulose from plant residues and other sources into simple compounds such as glucose, CO₂, and hydrogen, which serve as essential nutrients for plants and other soil organisms. Fungi with the highest cellulolytic activity include *Aspergillus flavus* and *Penicillium* sp. (Zhang et al. 2014; Boondaeng et al. 2024). Filamentous fungi, such as *Trichoderma* sp. and *Aspergillus*, are also known to produce cellulase enzymes (Liu et al. 2021; Sembiring et al. 2024).

The use of superior microbial types and appropriate environmental conditions can affect the acceleration of the decomposition process of organic matter. Cellulose-rich organic matter serves as a substrate for cellulolytic bacteria and fungi, which naturally exist in farmland, forests, compost, decaying plant matter, and leaf litter (Trivana and Pradana 2017; Sembiring et al. 2024). Therefore, cellulolytic microbes tend to be found in tea waste, which has a high cellulose content. The ability of microbes to decompose organic matter depends on the type and source of microbes used. The decomposition of tea waste can be accelerated by using local microbes sourced from tea waste that have been tested for their ability to decompose cellulose. This research aimed to find cellulolytic microbes that were sourced from tea waste and have superior potential in the decomposition of organic matter, especially tea waste.

MATERIALS AND METHODS

This study was conducted at the Soil Biology Laboratory of the Faculty of Agriculture, Universitas Sumatra Utara, Medan, North Sumatra, Indonesia, starting in July 2023. The waste used was from the Bah Butong Tea Processing Factory, PTPN IV Sidamanik, Simalungun District, North Sumatra Province. Carboxyl methyl cellulase (CMC) was used as a medium to isolate cellulolytic bacteria and fungi, containing 10.0 g CMC, KH₂PO₄ 1 g, K₂SO₄ 0,5 g, NaCl 0,5 g, FeSO₄ 0,5 g, NH₄NO₃ 1 g, MnSO₄ 0,1 g, 0,2 g yeast, 0,5% congo red, 20,0 g of agar dissolved in 1 L of physiological water.

Isolation and screening of cellulolytic microorganisms

Soil microbes were isolated through a serial dilution process and the cup pour plate. 10 g of soil were added to 90 mL of sterile distilled water and shaken in a shaking incubator for 1 h at 120 rpm. A series of dilutions from 10⁻¹ to 10⁻⁵ were prepared. From the 10⁻³, 10⁻⁴, and 10⁻⁵ dilutions, 0.1 mL of the suspension was poured and spread onto CMC agar media, then incubated at 25°C for 3-4 days. Cellulolytic activity testing was carried out using the Congo Red method. Congo Red solution (0.1% w/v) was poured into the culture and left for 15 minutes. The solution is then discarded and rinsed with 1 M NaCl for 15 minutes three times. The presence of cellulolytic microbes is indicated by a clear zone around the colony. Clear

zones appear around bacterial and fungal colonies indicating hydrolysis of cellulose. Bacterial and fungal colonies that have the largest clear zones are selected for the identification and production of cellulase.

Identification of bacteria and fungi

To identify bacteria at the molecular level, universal primer 63f (5'CAG GCC TAA THE ATG CAA GTC 3'), Primer 1387r (5' GGG CGG WGT GTA CAA GGC 3') is used to amplify the 16S bacterial rRNA gene sequence through PCR and Fungi were identified using PCR-ITS primers (Manter and Vivanco 2007). DNA amplification is carried out in 29 cycles with denaturation at 94°C for 5 minutes, denaturation at 94°C for 1 minute 30 seconds, primer annealing at 55°C for 45 seconds, and extension at 72°C for 1 minute. Reinforced DNA from colonies of bacteria and fungi undergo sequencing. The similarity search for the resulting sequence is carried out using the BLAST program from the National Center for Biotechnology Information (NCBI) (Lane 1991; Marchesi et al. 1998).

Semi-quantitative test for the degradation of cellulose compounds

The purified isolate was subsequently assessed for semi-quantitative cellulolytic activities on CMC agar media to measure the colony diameter and clear zone the Cellulolytic Index (IS) was calculated using the formula provided by Ferbiyanto et al. (2015).

$$\text{Cellulolytic Index (CI)} = \frac{\text{Clear Zone Diameter} - \text{Colony Diameter}}{\text{Colony Diameter}}$$

Effectiveness test of cellulolytic microbes in breaking down tea waste

A total of 250 g of tea factory waste, previously sterilized using an autoclave, was placed into a sterile cup. The tea waste had an organic carbon content of 48.78%, total nitrogen of 1.76%, a C/N ratio of 27.72%, and a pH of 5.32. This stage of the research employed a non-factorial Completely Randomized Design (CRD). The treatment factors included various cellulolytic microbes, specifically *Enterobacter oligotrophicus* (AS), *Stenotrophomonas maltophilia* H05 (BS), *S.maltophilia* IARI-T-21 (CS), *Prieta megaterium* (DS), *Methylophilus methylotrophus* (ES) and cellulolytic fungi colonies from *Aspergillus fumigatus* (J1) and *A. corrugatus* (J2) each with three replicates. One milliliter of each microbial treatment was applied to the tea waste in the plastic cup, and the samples were incubated for 20 days. The parameters measured were organic carbon content, nitrogen content, C/N ratio, and pH, assessed on days 10 and 20. The objective was to evaluate which microbial treatment most efficiently decomposes the tea factory waste.

Statistical analysis

The treatment that had a significant effect on the ANOVA analysis was followed by Duncan's Multiple Range Test (DMRT) 5%.

RESULTS AND DISCUSSION

Isolation and identification of cellulolytic microorganisms

Based on the results of microbial isolation and selection, which involved evaluating macroscopic and microscopic similarities from tea factory waste, five bacterial strains and two cellulolytic fungi were identified as particularly effective in degrading tea waste. Subsequently, these microbes were characterized using PCR techniques.

The bacterial identification results revealed the following species: *E. oligotrophicus* (AS), *S. maltophilia* (BS), *S. maltophilia* (CS), *P. megaterium* (DS), and *M. methylotrophus* (ES) (Figure 1, Table 1). The identified cellulolytic fungi included *A. fumigatus* (J1) and *A. corrugatus* (J2) (Figure 2, Table 1) The morphological characteristics of bacterial cells (100x Magnification) and fungal colonies (40x Magnification) are depicted in Figure 3. The results of the identification of the bacteria in Figure 1 show that the two isolate codes, BS and CS indicate the same species *Stenotrophomonas maltophilia*. This bacterium plays a significant role in enhancing plant growth through organic acid production and nitrogen fixation (Ullah et al. 2015; Priya et al. 2017).

The fungi identified belong to the genus *Aspergillus* with two different species. *Aspergillus* is a fungus that is able to produce cellulolytic enzymes. Microbial diversity is influenced by environmental conditions and the ability of organisms to adapt (Ferreira et al. 2020; Sembiring et al. 2022a,b). Variations in microbial types are affected by both biotic and abiotic factors (Ashwani et al. 2014; Priya et al. 2017; Real et al. 2020). Biotic factors include competition among microbes for resources, while abiotic factors involve environmental conditions such as humidity, temperature, soil pH, and light intensity. These factors determine the suitability of microbes for growth in organic materials derived from tea waste. Ecological interactions such as symbiosis, competition, and predation can often be analyzed and visualized as ecological networks, which can also include dynamic shifts in abiotic factors that affect biodiversity. The organism's small body size and higher metabolic rate allow bacteria and fungi to spread more easily in the environment (Tylianakis and Morris 2017; Custer et al. 2022; Wu et al. 2024). The presence of organic C and the composition of organic matter greatly affect the growth and activity of microbes (Priya et al. 2017; Zandt et al. 2018).

Table 1. Taxon isolate of bacteria and fungi closest to BLAST yield

Isolate code	The closest taxon to BLAST results on NCBI	Max score	Query (%)	E-value	Similarity (%)
AS	<i>Enterobacter oligotrophicus</i>	1729	100	0.00	99.58
BS	<i>Stenotrophomonas maltophilia</i>	2097	99	0.00	95.11
CS	<i>Stenotrophomonas maltophilia</i>	2211	99	0.00	98.95
DS	<i>Priestia megaterium</i>	1733	100	0.00	98.97
ES	<i>Methylophilus methylotrophus</i>	1652	100	0.00	99.56
J1	<i>Aspergillus fumigatus</i>	1057	100	0.00	100.00
J2	<i>Aspergillus corrugatus</i>	1022	99	0.00	100.00

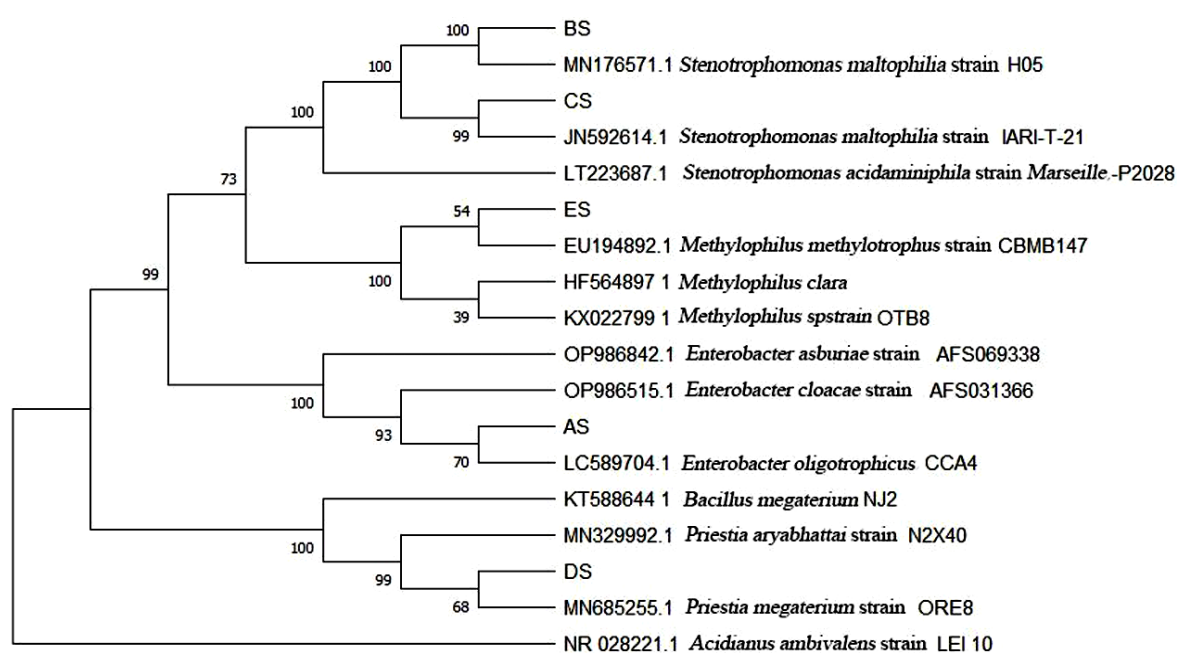


Figure 1. Phylogenetic tree of cellulolytic bacteria isolated from tea factory waste

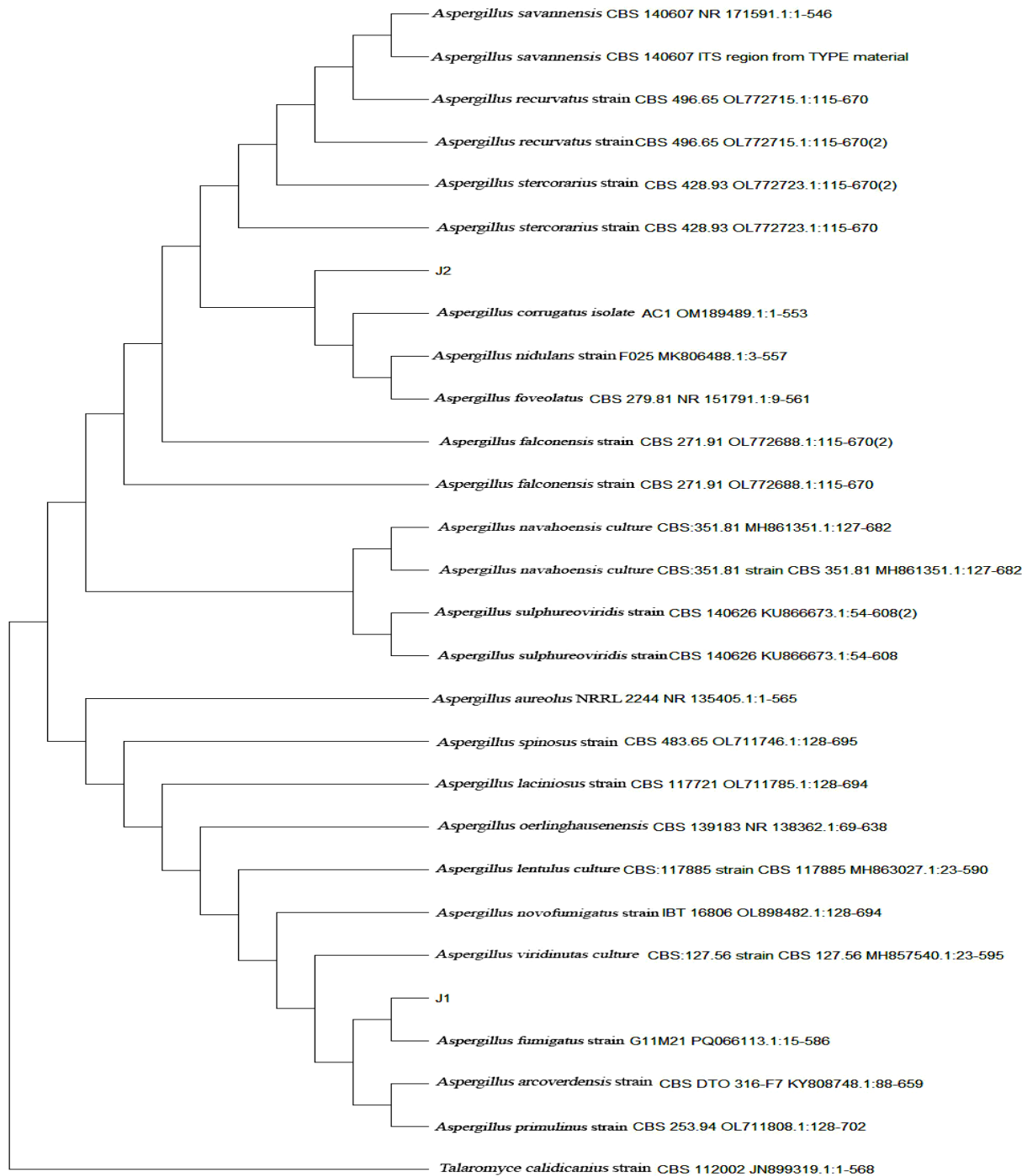


Figure 2. Phylogeny tree of cellulolytic fungi isolated from tea factory waste

Semi-quantitative cellulose compound degradation test

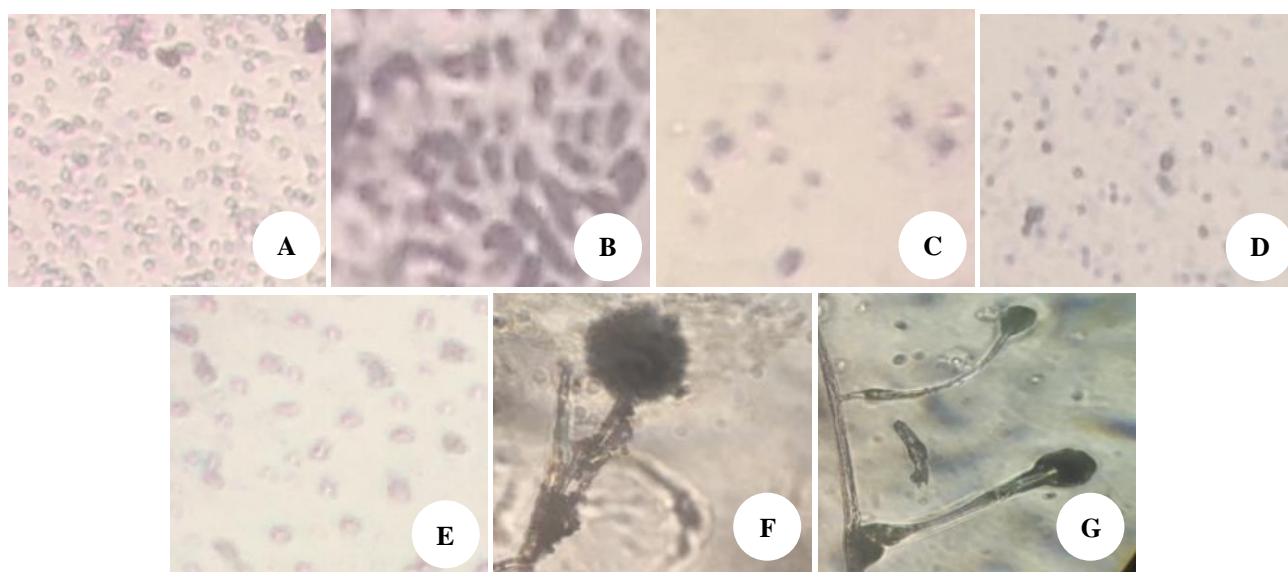
Based on the findings from the research conducted to assess bacterial and fungal isolates in the degradation of cellulose compounds-by measuring colony growth and calculating the cellulolytic index at 72 h post-incubation (Table 2).

All bacterial and fungal isolates tested demonstrated the ability to grow on Carboxymethyl Cellulose (CMC) media. The capability of these microorganisms to degrade cellulose was evidenced by the formation of a clear zone around their colonies on the CMC media. According to Hidayah et

al. (2017), the potential of cellulolytic bacteria can be assessed by their ability to secrete cellulase enzymes, as indicated by the cellulolytic index derived from the clear zone surrounding bacterial colonies on CMC media. Dewi et al. (2020) that the appearance of a clear zone in the cellulolytic activity test confirms the ability of the four isolates to degrade cellulose from CMC. The clear zone formation, attributable to cellulase enzyme activity, highlights the degradation of cellulose (Behera 2014; Nutongkaew et al. 2014; Aziz et al. 2021; Ilahi and Febria 2021).

Table 2. Cellulolytic index of cellulolytic microbes after 72 hours of incubation

Isolate name	Colony diameter (mm)	Clear zone diameter (mm)	Cellulolytic index (%)
<i>Enterobacter oligotrophicus</i> (AS)	13.7	25.2	0.84
<i>Stenotrophomonas maltophilia</i> (BS)	5.7	15.2	1.67
<i>Stenotrophomonas maltophilia</i> (CS)	6.7	14,7	1.19
<i>Priesta megaterium</i> (DS)	6.5	12	0.85
<i>Methylophilus methylotrophus</i> (ES)	9.1	28	2.07
<i>Aspergillus fumigatus</i> (J1)	20.7	41.9	1,02
<i>Aspergillus corrugatus</i> (J2)	17.2	35.4	1.06

**Figure 3.** Cellulolytic bacterial cell form of A. *Enterobacter oligotrophicus* (AS); B. *Stenotrophomonas maltophilia* H05 (BS); C. *Stenotrophomonas maltophilia* IARI-T-21 (CS); D. *Priesta megaterium* (DS); E. *Methylophilus methylotrophus* (ES) and cellulolytic fungal colonies from F. *Aspergillus fumigatus* (J1); G. *Aspergillus corrugatus* (J2)

Among the isolates tested, *M. methylotrophus* (ES) and *A. corrugatus* (J2) exhibited the highest cellulolytic indices, with values of 2.07 (high) and 1.06 (medium), respectively. The cellulolytic index for *M. methylotrophus* (ES) was notably higher than that for *A. corrugatus* (J2), indicating a 95% greater cellulose degradation capability in bacteria compared to fungi. A cellulolytic index value of ≤ 1 is considered low, medium (1-2), and high (≥ 2) (Choi et al 2005). The difference in the value of the cellulolytic index value can be caused by the difference in the type of isolate with the ability to produce different cellulase. The clear zone around the colony indicates the activity of cellulase enzymes. Bacterial isolates capable of decomposing CMC media were identified by the emergence of clear zones around the colonies after testing using Congo red (Shaikh et al. 2013).

All microbial isolates exhibit varying cellulolytic indices, suggesting that those with higher indices produce more cellulase enzymes (Table 1). This observation who noted that microbes with larger clear zones demonstrate greater cellulolytic activity (Mahmood et al. 2020; Ilahi and Febria 2021). The Cellulolytic Index (IS) values obtained

in this study fell predominantly within the medium to high range, with only DS isolates categorized as low. The capacity of microbes to degrade cellulose varies according to the specific type of microbe and its proficiency in producing cellulolytic enzymes. This is evidenced by their ability to form clear zones (Behera 2014; Mahmood et al. 2020; Aziz et al. 2021; Hidayati et al. 2023).

Evaluate the efficacy of cellulolytic microbes in the decomposition of tea waste

Analysis was conducted on the results of compost derived from tea factory waste, with parameters including nitrogen (N), organic carbon (C), pH, and the carbon-to-nitrogen (C/N) ratio of the compost (Table 3). This analysis was performed under sterile conditions with a consistent dose over a 20-day incubation period at room temperature, and included two replicates. The cellulolytic microbes employed for the decomposition of tea processing factory waste were identified as the most effective through semi-quantitative microbial selection. This selection yielded seven microbes in total: five bacterial isolates and two fungal isolates (Figures 1, Table 2).

Table 3. Results of composting tea waste: isolation of cellulolytic bacteria and fungi

Cellulolytic microbial isolate	10 days of composting				20 days of composting			
	C-Organic (%)	N-Total (%)	C/N	pH compost	C-Organic (%)	N-Total (%)	C/N	pH compos
<i>Enterobacter oligotrophicus</i> (AS)	45.26	2.78	16.54	5.78bc	43.19	3.36	12.84	6.02ab
<i>Stenotrophomonas maltophilia</i> (BS)	45.09	2.96	15.19	5.54ab	42.38	3.44	12.32	6.13bc
<i>Stenotrophomonas maltophilia</i> (CS)	43.83	2.87	15.27	5.13a	43.91	3.19	13.76	5.76a
<i>Priestia megaterium</i> (DS)	45.53	3.01	15.13	5.42a	42.99	3.42	12.57	5.88a
<i>Methylophilus methylotrophus</i> (ES)	47.55	2.98	15.96	5.54ab	41.70	3.54	11.77	6.05bc
<i>Aspergillus fumigatus</i> (J1)	47.38	2.85	16.62	6.35d	42.36	3.20	13.23	6.55cd
<i>Aspergillus corrugatus</i> (J2)	46.03	3.03	15.19	6.97e	42.16	3.56	11.84	7.12e

Notes: Values denoted by the same letter are not significantly different (at the 5% level) as determined by the DMRT test

The acidity level of decomposed tea waste compost material, observed over a 10-day composting period, was found to be lowest in the *S. maltophilia* (CS) treatment, with a pH of 5.13, and highest in the *A. corrugatus* (J2) treatment, with a pH of 6.97. The *S. maltophilia* (CS) showed a decrease in pH of 3.7%, whereas other isolates exhibited an increase in pH compared to the initial composting pH. After 20 days of composting, the pH of the compost had risen compared to both the initial and the 10-day observations. Specifically, the pH in the *S. maltophilia* (CS) treatment increased by 8.2% relative to the initial pH, while the *A. corrugatus* (J2) treatment showed a 33.83% increase in pH. For effective field application, a compost pH range of 6-8 is considered optimal. Factors that affect the composting process include the C/N ratio, humidity, oxygen, pH, temperature, The C/N ratio greatly affects the composting process because the ratio that is too wide will prolong the composting process. The composting process as a biological process involves many microorganisms. It is these microorganisms that break down organic substances and organic compounds. In the maturation phase of compost with a low C/N ratio and a moderately alkaline pH value. The optimum pH range for mature pH is pH 6-8. In the ripening phase, the pH reaction is stable at a neutral value, which is closely related to the buffer capacity of the humus. The highest oxygen content is in the thermophilic phase and will decrease in the maturation phase (Awasthi et al. 2016).

The pH of compost that is good for field application is the pH range of 6-8 where the pH is good for the growth of cellulolytic microbes in addition to the temperature invoice also affects (Abu-Gharbia et al. 2018; Islam and Roy 2019). Biodegradation and decomposition of cellulose require components that work simultaneously with three components of the cellulase enzyme, namely endoglucanase, exoglucanase and glucosidase that work synergistically. Many bacteria and fungi can utilize cellulose as a carbon source by synthesizing cellulase enzymes and degrading cellulose into simple sugars that are mostly glucose. Cellulolytic bacteria live freely in the environment and hydrolyze cellulose in the environment such as in piles of dead plants on forest floors and agricultural waste or live in the digestive tract of animals which helps break down food intake in the form of cellulose (Nkohla et al. 2017; Zhang et al. 2018).

Cellulolytic microbial treatment over a 10-day period generally decreased the organic carbon content in tea waste compost. Initially, the organic carbon content was 48.78%. After treatment with *S. maltophilia* (CS), it decreased to 43.83%, reflecting an 11.29% reduction in organic carbon over the 10-day composting period. In a 20-day observation period, compost treated with *M. methylotrophus* (ES) exhibited an organic carbon content of 41.70%, indicating a 16.95% reduction compared to the initial organic carbon content. This reduction in organic carbon levels in the composted material demonstrates that the composting process involves the breakdown of organic compounds and the release of carbon dioxide due to microbial activity, thereby affecting the organic carbon levels of the resulting compost. Carbon and nitrogen content is important in the composting process because microorganisms use carbon as an energy source and nitrogen for protein synthesis (Iqbal et al. 2015; Liu et al. 2021).

The research findings indicate a twofold increase in total nitrogen. Initially, the total nitrogen in composting was 1.76%. After 10 and 20 days of observation, there was a noticeable increase. During the 10-day observation, the *A. corrugatus* (J2) treatment exhibited the highest total nitrogen content at 3.03%, while the *E. oligotrophicus* (AS) treatment had the lowest. By the 20-day mark, the *A. corrugatus* (J2) treatment showed a further increase in total nitrogen, reaching 3.56%. This represents a 102% increase compared to the initial analysis. The rise in total nitrogen during composting can be attributed to the decomposition of compost material by microorganisms, which convert ammonia into nitrite. Generally, the total nitrogen content in compost ranges from 1.0% to 3.0% on a dry weight basis. Additionally, increased nitrogen levels can result from the microbes' ability to fix atmospheric nitrogen (Frainer et al. 2015; Ullah et al. 2015; Sembiring and Sabrina 2022b).

The application of cellulolytic microbes to the decomposition of tea waste material can effectively reduce the carbon-to-nitrogen (C/N) ratio of the compost. Initially, the C/N ratio of the tea waste material was 27.72%. After 10 days of composting, the lowest C/N ratio observed was 15.13 in the Ds treatment, while the highest was 16.62 in the *A. fumigatus* (J1) treatment. By the 20-day observation period, the lowest C/N ratios were found in the *M. methylotrophus* (ES) and *A. corrugatus* (J2) treatments. Specifically, the C/N ratio decreased by 135.51% in the *M.*

methylophilus (ES) treatment and by 134.12% in the *A. corrugatus* (J2) treatment compared to the initial C/N ratio. These reductions indicate significant decomposition of the composted tea waste, leading to a decrease in organic carbon content and an increase in nitrogen content, thus suggesting that the compost is mature or fully decomposed. *Aspergillus*, a fungus known for decomposing organic matter and producing organic acids, played a key role in this process. Bacteria and fungi are microorganisms that can decompose cellulose (Liaud et al. 2014; Liu et al. 2021; Sembiring et al. 2024). The application of fungi can decompose substances that are difficult to decompose such as lignin, cellulose and hemicellulose, fungi can break down compounds that are difficult to decompose such as plastics are also able to be degraded by fungi (Nutongkaew et al. 2014; Lee 2016). *Aspergillus* sp. and *Chaetomium* sp. have a better ability to break down cellulose (Singh and Nain 2014; Sánchez et al. 2017). According to SNI 19-7030-2004, a compost is considered suitable for application when its C/N ratio is approximately 10-20%. Therefore, composting tea waste for 10 days yields a C/N ratio of 15.13-16.62%, making it suitable for practical application. The findings of this research indicate that the bacteria and fungi applied are effective in decomposing organic matter, contributing added value by increasing nitrogen levels. In addition to their role in decomposition, certain microbes can enhance nutrient availability. The rate of decomposition of organic materials is influenced by factors related to the raw materials, environmental conditions, and the activity of decomposing organisms (Ferreira and Canhoto 2015; Pereira et al. 2016; Priya et al. 2017; Real et al. 2020). Furthermore, composting temperature also affects microbial activity (Ferreira et al. 2020; Mahmood et al. 2020). Microbes play an important role in the composting process, especially through the activity of microbes and enzymes secreted. Bacteria have had rapid growth and the ability to use organic matter such as starch and protein, which is the basis for the transformation of materials in compost. Fungi have a better adaptability to environmental changes. Both bacteria and fungi are essential for promoting humification and ensuring the stability of compost products (Wei et al. 2019; Gao et al. 2020; Awasthi et al. 2020).

In conclusion, five bacterial and two fungal strains isolated from tea factory waste exhibit potential as decomposer microbes. Overall, the application of these microorganisms accelerates the decomposition of tea factory waste. After 10 days of composting, the carbon-to-nitrogen (C/N) ratio ranges from 15.13% to 16.62%, and after 20 days, it ranges from 11.77% to 13.76%, meeting the criteria for mature compost. Nitrogen content in the compost increased by 102%. Among the treatments, *A. corrugatus* (J2) and *M. methylophilus* (ES) achieved the lowest C/N ratios and the highest total nitrogen levels.

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