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Shilpa Lokhande
Shri Shivaji College of Arts,
Commerce and Science, Akola

M Musaddiq
Shri Shivaji College of Arts,
Commerce and Science, Akola

Isolation of cellulolytic bacterial strains for bioconversion of municipal solid waste

Shilpa Lokhande, M Musaddiq

Abstract

Cellulose, a major polysaccharide found in agricultural residues and industrial and municipal wastes. In the present study cellulolytic microorganisms were isolated. Eight isolates of cellulose degrading bacteria were isolated from soil, municipal solid waste, plant residues in 10 different villages of saline belt of Akola District, Maharashtra by enriching the basal culture medium with 1% cellulose as substrate for cellulose degradation. To indicate the cellulose activity of the organisms, diameter of clear zone around the colony were measured. Enzyme activity was determined by DNS method. The most potent cellulolytic isolates were identified as *Bacillus subtilis*.

Keywords: Cellulose degrading bacteria, Municipal Solid waste, Saline belt

1. Introduction

Cellulose is biologically renewable resource abundantly found in agriculture waste. The cellulosic waste material can be hydrolysed to glucose and other soluble sugars by using cellulase enzymes of bacteria and fungi. The reducing sugars obtained can be further used for the production of ethanol as biofuel (Acharya *et al.*, 2012) [1]. The potential cellulose producing bacteria are *Cellulomonas*, *Pseudomonas*, *Thermoactinomyces* and *Bacillus spp.* (Godana, 2007) [11]. Sustainable resources, which are in need of human being, are derived from plant biomass. Cellulose is the major component of plant biomass (Camassola and Dillon 2007) [5]. Plants produce 4×10⁹ tons of cellulose annually (Coughlan 1990) [6]. Cellulolysis is basically the biological process controlled and processed by the enzymes of cellulase system. Cellulase enzyme system comprises three classes of soluble extracellular enzymes: 1, 4-β-endoglucanase, 1, 4-β-exoglucanase, and β-glucosidase (β-D-glucoside glucohydrolase or cellobiase). Endoglucanase is responsible for random cleavage of β-1, 4-glycosidic bonds along a cellulose chain. Exoglucanase is necessary for cleavage of the non reducing end of a cellulose chain and splitting of the elementary fibrils from the crystalline cellulose, and β-1, 4-glucosidase hydrolyses cellobiose and water-soluble cellodextrin to glucose (Shewale 1982)²¹, Woodward and Wiseman 1983) [26]. Only the synergy of the above three enzymes makes the complete cellulose hydrolysis to glucose (Ryu and Mandels, 1982, Wood 1989) [20, 25] or a thorough mineralization to H₂O and CO₂ possible.

Its crystalline structure and insoluble nature represents a big challenge for enzymatic hydrolysis. Microorganisms are important in conversion of lignocellulose wastes into valuable products like biofuels produced by fermentation (Lynd *et al.*, 2002) [15]. Successful bioconversion of cellulosic materials mainly depends on the nature of cellulose, sources of cellulolytic enzyme and optimal conditions for catalytic activity and production of enzymes (Alam *et al.*, 2004) [2]. Cellulose quality, temperature, aeration, carbon sources, incubation period, medium additives, pH of the medium and presence of inducers are important parameters for the optimized production of cellulase enzymes (Immanuel *et al.*, 2006) [13]. Present study is aimed to isolate and screen potential cellulolytic bacteria from saline belt of Akola District, Maharashtra.

2. Materials and Methods

Isolation of cellulolytic bacterial strains were isolated from soil by using serial dilutions and pour plate technique. The medium used for isolation of cellulolytic

Correspondence
Shilpa Lokhande
Shri Shivaji College of Arts,
Commerce and Science, Akola.

bacteria contains 1.0% peptone, 1.0% carboxymethylcellulose (CMC), 0.2% K₂HPO₄, 1% agar, 0.03% MgSO₄·7H₂O, 0.25% (NH₄)₂SO₄ and 0.2% gelatin at pH 7 for 48 hours of incubation at 30 °C (Yin *et al.*, 2010) [27]. Bacterial colonies were purified by repeated streaking. The purified colonies were preserved at 4 °C for further identification and screening for cellulase production.

Screening of Cellulolytic Bacteria

Pure cultures of bacterial isolates were individually transferred in CMC agar plates. After incubation for 48 hours, CMC agar plates were flooded with 1% congo red and allowed to stand for 15 min at room temperature. One molar NaCl was thoroughly used for counterstaining the plates. Clear zones were appeared around growing bacterial colonies indicating cellulose hydrolysis (Andro *et al.*, 1984) [3]. The bacterial colonies having the largest clear zone were selected for identification and cellulase production in submerged system.

Identification of Cellulolytic Bacteria

Identification of cellulolytic bacteria was carried out by method as described by Cowen and Steel (Cowan and Steel 1993) [7] and Cullimore (Cullimore 2000) [8], which was based on morphological and biochemical tests.

Inoculum development

Pure cultures of selected bacterial isolates were individually maintained on CMC supplemented minimal agar slants at 4 °C, until used. Pure cultures of selected bacterial isolates were inoculated in broth medium containing 0.03 % MgSO₄, 0.2% K₂HPO₄, 1% glucose, 0.25% (NH₄)₂SO₄ and 1% peptone at pH 7 for 24h of fermentation period. After 24h of fermentation period these vegetative cells were used as inoculum source.

Estimation of Cellulase activity

Cellulase activity was assayed using dinitrosalicylic acid (DNS) reagent (Miller 1959) [17] by estimation of reducing sugars released from CMC solubilized in 0.05 M phosphate buffer at pH 8 (Bailey *et al.*, 1992) [4]. The culture broth was centrifuged at 14000×g for 10 min at 4 °C and the clear supernatant served as crude enzyme source. Crude enzyme was added to 0.5 ml of 1% CMC in 0.05 M phosphate buffer and incubated at 50 °C for 30 min. After incubation, reaction was stopped by the addition of 1.5ml of DNS reagent and boiled at 100 °C in water bath for 10 min. Sugars liberated were determined by measuring absorbance at 540 nm. Cellulase production was estimated by using glucose calibration curve (Shoham *et al.*, 1999) [22]. One unit (U) of

enzyme activity is expressed as the quantity of enzyme, which is required to release 1µmol of glucose per minute under standard assay conditions.

3. Results and Discussion

The numbers of microbes isolated and details of sample collection from the various locations are shown in Table 1 which indicate that the number of microbes were isolated from 10 different village of Akola District.

Results presented in Table 2 clearly indicate that screening and cellulolytic microbes were isolated and were measured as zone of clearance in mm. highest cellulolytic activity detected in *Bacillus subtilis* (4.2) followed by *Bacillus spp.* (3.9), *Clostridium thermocellum* (0.5), *Pseudomonas aeruginosa* (0.8), *Staphylococcus aureus* (0.7). The present study indicate that number of microbial forms inhabiting various cellulolytic wastes produce extracellular cellulases. The screened bacterial strains will be used for further studies. Cellulose is the most abundant of all naturally occurring organic compounds, probably comprising at least a third of all the vegetable matter on the earth (Han and Shrinivasan 1968) [12]. Cellulose is the main building block of plants and have major fraction of organic carbon in soil. Microorganisms, which live in soil, are accountable for recycling of this organic carbon to the environment (Wang *et al.*, 2008) [24].

Degradation of cellulosic materials is a complex process and requires participation of microbial cellulolytic enzymes. Habitats where these substrates are present are the best sources for isolation of cellulolytic microorganisms (Das *et al.*, 2010) [9]. About one fifth of fresh water and soil samples yield cellulose degrading bacteria after enrichment but some samples did not bear such kind of bacteria (Ivanen *et al.*, 2009) [14]. This is due to existence of microenvironments where different growth conditions for cellulose degrading bacteria are present. These bacteria are generally found in well manure soils (Morris *et al.*, 2008) [17]. Several microorganisms have been discovered for decades which have capacity to convert cellulose into simple sugars (Perez *et al.*, 2002) [19] but the need for newly isolated cellulose degrading microorganism still continues (Niranjane *et al.*, 2007) [18].

Gautam, *et al.*, 2012 [10] isolate total of 250 isolates of these, 165 belonged to 37 fungal species, and 85 to 21 bacterial species. The most frequent fungi were *Aspergillus niger*, *Curvularia lunata*, *A. nidulans*, *A. fumigatus*, *Penicillium sp.*, *Fusarium roseum*, and *Trichoderma viride*, and bacteria were MRLB #39, MRLB #42, and MRLB #44. Strom, 1985²³ reported that a large majority of the total number of bacterial isolates were members of the genus *Bacillus*.

Table 1: Details of sample collection

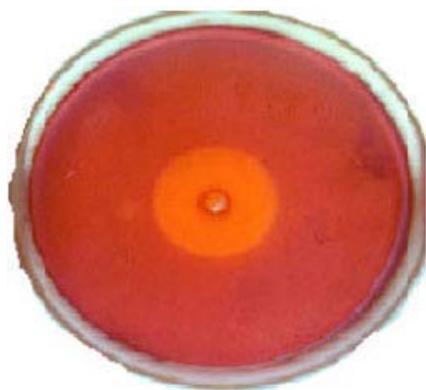
Sr. No	Taluka	Name of Village	No. of sample	Types of material and no. of sample			
				soil	Plant residue	compost	Mixed MSW
1	Akola	Rohana	01	01	-	-	-
2	Akola	Ganori	01	-	-	01	-
3	Akola	Dahihanda	01	01	-	-	-
4	Akot	Dhaga	01	-	01	-	-
5	Akot	Karatwadi	01	-	-	01	-
6	Akot	Sawarkhed	01	-	-	-	01
7	Balapur	Manjari	01	01	-	-	-
8	Balapur	Hatron	01	-	01	-	-
9	Balapur	Singoli	01	-	-	01	-
10	Balapur	Hingana Adsul	01	-	-	-	01

Table 2: Screening and measurement zone of cellulose degradation by different microbes

Sr. No.	Name of Bacteria	Zone of clearance in mm
1	<i>Bacillus subtilis</i>	4.2
2	<i>Bacillus spp.</i>	3.9
3	<i>Clostridium thermocellum</i>	0.5
4	<i>Pseudomonas aeruginosa</i>	0.8
5	<i>Staphylococcus aureus</i>	0.7

Table 3: Measurement of enzyme activity of bacterial isolates

Sr. No.	Microorganisms	Optical density (540nm)	Enzyme activity IU/ml
1	<i>Bacillus subtilis</i>	0.14	2.2
2	<i>Bacillus spp.</i>	0.11	1.9
3	<i>Clostridium thermocellum</i>	0.01	0.2
4	<i>Pseudomonas aeruginosa</i>	0.9	1.7
5	<i>Staphylococcus aureus</i>	0.5	1.5

**Plate 1:** *Bacillus subtilis* showing highest zone of cellulose degradation

From the above findings it is clear that a large no. microorganisms were found in Municipal Solid Waste, compost and soil of saline belt of Akola District. *Bacillus subtilis* had highest cellulose enzyme activity which can be further use for biodegradation of Municipal solid waste.

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