

ISOLATION AND CHARACTERIZATION OF CELLULASE PRODUCING ANOXYGENIC PHOTOSYNTHETIC BACTERIUM FROM PAPER PULP INDUSTRIAL EFFLUENTS

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Abstract– Cellulose constitutes the primary product of photosynthesis and is the most abundant bio resource produced in the biosphere. It is an important structural component of green plants, many forms of algae, the Oomycetes and some bacterial biofilms. Microorganisms are reported to produce the enzyme cellulase which breaks down cellulose into monosaccharide β -glucose and oligosaccharides. Cellulases are used in paper pulp industry, detergent industry, olive oil extraction; textile industry; clarification of fruit juices and extraction of carotenoids. In the present work, a photosynthetic purple non-sulphur bacterium was isolated from effluents of paper pulp industry, Mahabubnagar, Telangana State, India, by enrichment into Biebl and Pfennig's medium, the culture was streaked onto CMC agar and incubated under anaerobic light conditions. The colonies were examined for the production of cellulase after 2 weeks. Cellulase production in terms of glucose liberated was estimated by DNS method by growing the bacterium in CMC broth. The bacterium is a Gram negative motile rod. The colour of the cell suspension was dark pink. It could utilize fructose, glucose, glycerol, mannitol, tartrate, thiosulphate, galactose, CMC and cellulose as carbon sources. Molecular identification of 16S rRNA sequence has shown similarity to *Rhodospseudomonas* sps. The physicochemical parameters of the sample measured were pH- 7.0, temperature- 37 °C, BOD- 95.2, COD- 160.4, chlorides- 263.6, TSS- 210 and TDS- 910 mg/lit.

INTRODUCTION

Bacteria present an attractive potential for the exploitation of cellulases and hemicellulases due to their rapid growth rate, enzyme complexity and extreme habitat variability. The development of rapid and reliable methods for the screening of cellulases from microorganisms within inhospitable environments will allow a greater number of novel bacterial cellulases to be isolated for industrial use (Miranda *et al.*, 2009). Cellulases have been commercially available for more than 30 years, and these enzymes have represented a target for both academic as well as industrial research (Singh, 1999; Singh *et al.*, 2007). The commonly described mode of action for cellulases on polymers is either exo- or

endo-cleavage, and all cellulases target the specific cleavage of β -1, 4-glycosidic bonds (Wood and Crae, 1979). Anaerobic bacteria like clostridia, few anaerobic fungi like *Neocallimastix*, *Piromyces*, and *Orpinomyces* (Fanutti *et al.*, 1995; Li *et al.*, 1997) possess multienzyme complexes called Cellulosomes. Cellulase-producing photosynthetic bacteria are a fascinating group of microorganisms that possess the ability to degrade cellulose, a complex polysaccharide found in plant cell walls. While the literature on this specific topic may be limited, there are studies that have explored the cellulase production potential of photosynthetic bacteria. A number of microorganisms were reported to produce cellulases and few are listed in Table 1.

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Cellulases are used in paper pulp industries for various treatments of the wood such as refining, grinding of woody raw material and defibrillation (Kuhad *et al.*, 2011). They are used in Detergent Industry along with protease (Singh *et al.*, 2007); for olive oil extraction (Fantozzi *et al.*, 1977) and applied to remove the rough protuberances of fabrics for producing a smoother, glossier, and brighter-colored fabric (Karmakar and Ray, 2011). Use of cellulases for production of carotenoids from orange peel, sweet potato and carrots maintains the natural structure of the pigments in contrast to solvent extraction which dissociates the pigments from protein leading to easy oxidation (Cinar, 2005; Fennema, 1985).

Application of exogenous cellulase improves soil fertility and plant growth due to acceleration of straw decomposition (Han and He, 2010). Cellulases also have an important application as a part of macerating enzyme complex (cellulases, xylanases, and pectinases) used for extraction and clarification of fruit and vegetable juices to increase the yield of juices (Minussi *et al.*, 2002; Carvalho *et al.*, 2008). Use of cellulases and hemicellulases improve feed value and performance of animals (Dhiman *et al.*, 2002). Babykin *et al.*, (1988) reported production of cellulase by genetically altered *Rhodobacter sphaeroides*. Apart from this, no literature is available on cellulolytic photosynthetic bacteria. So, we have taken up this work.

MATERIALS AND METHODS

Collection of the sample

Effluent water (Fig. 1) is collected from Paper pulp industry in a flask filled completely to the neck and stoppered. The pH and temperature of the sample was noted to be 7.0 and 37°C respectively. The

physicochemical parameters of the sample Biological Oxygen Demand (BOD), Chemical Oxygen Demand (COD), Chlorides, Total suspended Solids (TSS) and Total Dissolved Solids (TDS) were estimated by the methods of American Public Health Association (APHA), 2005.



Fig. 1. Effluent water collected from paper pulp industry, Mahabubnagar

Isolation of the bacterium

One ml of the sample was inoculated into Biebl and Pfennig's medium (Biebl and Pfennig, 1981) containing carboxy methyl cellulose as organic carbon in screw cap vials filled with the medium. The vials were incubated at room temperature under anaerobic light conditions. After growth, the culture was inoculated onto agar plates and incubated at room temperature under anaerobic light conditions. Pure cultures were obtained by repeated streaking onto agar plates and again sub cultured into liquid medium.

Screening for Cellulase production

The bacterium was inoculated onto CMC agar ($\text{NH}_4\text{H}_2\text{PO}_4$ - 1g; KCl - 0.2g; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ - 1g; Yeast extract - 1g; Carboxymethyl cellulose - 26g; Agar - 3g and Distilled Water - 1000ml) and incubated under anaerobic light conditions. Colonies were developed by 2 weeks. To check for cellulase production, the plate was stained with 1% Congo red in Distilled water for 30 minutes and destained with 1M NaCl solution. The enzyme activity was measured by DNS method after growing the bacterium in CMC broth for one week.

Identification of the bacterium

The culture was studied for its morphological properties, Gram's staining and utilization of carbon

Table 1. Cellulase producing microorganisms

Bacteria	Reference
<i>Cellulomonas flavigena</i>	Amtul, <i>et al.</i> , 1988
<i>Pseudomonas fluorescens</i>	Sonia Sethi <i>et al.</i> , 2013
<i>Clostridium thermocellum</i>	Hirano <i>et al.</i> , 2016
<i>Thermotoga maritima</i>	Zhiwei Chen <i>et al.</i> , 2013
<i>Ruminococcus flavefaciens</i>	Marco <i>et al.</i> , 2001
Fungi	
<i>Trichophyton terrestre</i>	Marques <i>et al.</i> , 2011
<i>Cladosporium cladosporioides</i>	Isaie and Padmavathi, 2013
<i>Aspergillus niger</i>	Namita <i>et al.</i> , 2012
<i>Penicillium funiculosum</i>	Marcelle <i>et al.</i> , 2014
<i>Trichoderma reesei</i>	Bischof <i>et al.</i> , 2016

sources. Molecular identification was carried out at NCIM, Pune using BLAST (NCBI) using the 16S rRNA gene. The genomic DNA was isolated using a Gen Elute DNA extraction kit, as per manufacturer's guidelines (Sigma Aldrich). The PCR reaction was performed in a 20 μ l reaction volume containing 10 μ mol L⁻¹ primers, 40 ng template DNA, and TaqReadyMix (JumpStart, Sigma-Aldrich, India). The PCR was performed onto Applied BioSystem (Thermo Scientific, USA). The obtained PCR product was purified and sequenced at Agile Life science Technology Ind. Pvt. Ltd. Thus obtained nucleotide sequence was performed for BLAST analysis and a Phylogenetic tree was constructed using the Neighbour-Joining method. 27 F and 1492 R primers are used for the identification (Table 2).

Table 2. Primers used for identification of the bacterium

Target Gene	Primer Sequence (5' to 3')	Tm (°C)
27 F	AGAGTTTGATCM(A/C) TGGCTCAG	56
1492 R	TACCTTGTTACGACTT	

Cellulase Activity

The cellulase activity was measured by DNS method involving action of the enzyme on carboxymethylcellulose followed by determination of reducing power of resulting sugars (glucose) with the aid of Di-Nitro Salicylic acid (Miller, 1959).

RESULTS AND DISCUSSION

The physicochemical parameters of the effluent were measured and given in the Table 3.

The growth of the bacterium was indicated by pigment production in the liquid medium (Fig. 2) and production of colonies in the agar plate. The agar plates have shown clear zones of cellulase production by the bacterial colonies when stained with Congo red (Fig. 3).

The bacterium was found to be Gram negative, rod shaped (Fig. 4) and motile.

Out of the various carbon sources tested, the bacterium utilized cellulose, fructose, galactose, glucose, glycerol, maltose, mannitol, tartarate and



Fig. 2. Culture of the Photosynthetic bacterium



Fig. 3. Colonies stained with Congo red showing cellulolytic activity as clear zone around the colonies

thiosulphate (Table 4). Fructose and glycerol supported more pigment production (+++) by the organism followed by cellulose and glucose (++) whereas maltose, mannitol, tartarate and thiosulphate induced less pigment production (+) by the bacterium. The organism could not utilize acetate, benzoate, lactose, malate, methanol and sodium sulphide.

The cellulase activity is expressed in terms of glucose liberated in mg/ml of the substrate. The

Table 3. Physicochemical parameters of the sample

pH	Temperature	BOD (mg/Lit)	COD (mg/Lit)	Chlorides (mg/Lit)	TSS (mg/Lit)	TDS (mg/Lit)
7.0	37°C	95.2	160.4	263.6	210	910

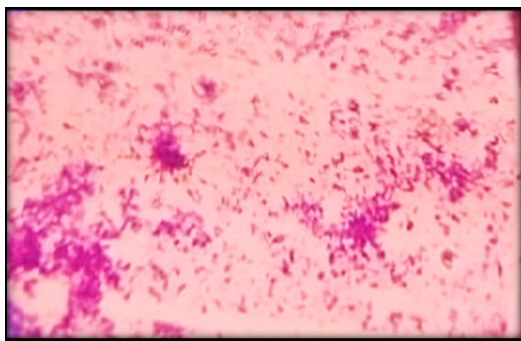


Fig. 4. Gram negative rods as seen under the microscope (oil immersion)

Table 4. Utilization of Carbon sources

Sl. No.	Carbon Source	Utilized/not (Pigment production)
1.	Acetate	-
2.	Benzoate	-
3.	Cellulose	++
4.	Fructose	+++
5.	Galactose	++
6.	Glucose	++
7.	Glycerol	+++
8.	Lactose	-
9.	Malate	-
10.	Maltose	+
11.	Methanol	-
12.	Mannitol	+
13.	Tartarate	+
14.	Sulphide	-
15.	Thiosulphate	+

activity of cellulase produced by the bacterium increased with increasing concentration of carboxy methyl cellulose in the medium (Table 5).

Molecular identification of the bacterium done using BLAST (Basic Local Alignment Search Tool) with 16S rRNA partial sequence is shown in the Table 6 and Taxonomic Tree (Fig.5).

Table 5. Cellulase activity in terms of glucose liberated (mg/ml)

Concentration of CMC (mg/ml)	Glucose liberated (mg/ml)
1.0	0.1
2.0	0.21
4.0	0.45

CONCLUSION

The photosynthetic purple non-sulphur bacterium isolated in the present work was found be Gram negative motile rod and has sequence similarity of 16S rRNA with *Rhodopseudomonas* spp. The bacterium could be utilized for the production of the enzyme cellulase which can be used in various industries. The enzyme may also be applied for bioremediation of cellulosic wastes like paper pulp effluents.

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Conflicts of Interest: Authors express No Conflicts of interest.

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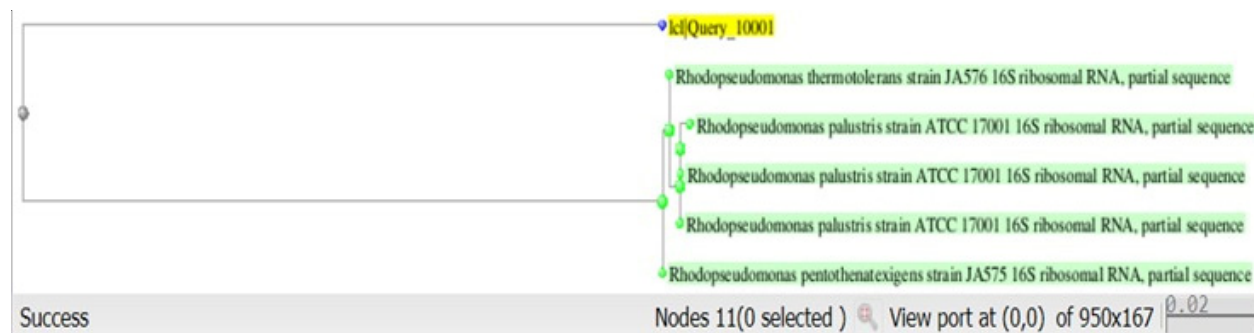


Fig. 5. Taxonomic Tree based on MUSCLE Multiple Alignment computed for Mole BLAST

Table 6. Taxonomy Report

Organism Report Lineage Report			
Taxonomy Report			
Taxonomy	Number of hits	Number of Organisms	Description
Bacteria	100	14	
. Proteobacteria	97	13	
.. Alphaproteobacteria	95	11	
... Rhodopseudomonas	78	10	
.... uncultured <i>Rhodopseudomonas</i> sp.	66	1	uncultured <i>Rhodopseudomonas</i> sp. hits
.... <i>Rhodopseudomonas</i> sp. JA904	1	1	<i>Rhodopseudomonas</i> sp. JA904 hits
.... <i>Rhodopseudomonas</i> sp. EGAT-KU 1/3	1	1	<i>Rhodopseudomonas</i> sp. EGAT-KU 1/3 hits
.... <i>Rhodopseudomonas</i> sp. S8-1	1	1	<i>Rhodopseudomonas</i> sp. S8-1 hits
.... <i>Rhodopseudomonas</i> sp.	3	1	<i>Rhodopseudomonas</i> sp. hits
.... <i>Rhodopseudomonas thermotolerans</i>	2	1	<i>Rhodopseudomonas thermotolerans</i> hits
.... <i>Rhodopseudomonas pentothentaxigens</i>	1	1	<i>Rhodopseudomonas pentothentaxigens</i> hits
.... <i>Rhodopseudomonas</i> sp. S16-VOGS3	1	1	<i>Rhodopseudomonas</i> sp. S16-VOGS3 hits
.... <i>Rhodopseudomonas</i> sp. MV9(ext sed)	1	1	<i>Rhodopseudomonas</i> sp. MV9(ext sed) hits
.... <i>Rhodopseudomonas palustris</i>	1	1	<i>Rhodopseudomonas palustris</i> hits
... uncultured <i>Rhodobacter</i> sp.	17	1	uncultured <i>Rhodobacter</i> sp. hits
.. Betaproteobacteria	2	2	
... uncultured <i>Comamonas</i> sp.	1	1	uncultured <i>Comamonas</i> sp. hits
... uncultured <i>Thauera</i> sp.	1	1	uncultured <i>Thauera</i> sp. hits
. uncultured bacterium	3	1	uncultured bacterium hits

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