

# Screening of Pectinase producing bacteria from Orange waste

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Abstract – Pectin is one among the nonstarch polysaccharides, which constitutes the main fraction of the plant cell membrane in association and substitutes with other polysaccharides, and they cover an excellent sort of biological functions and chemical structures. occurring polysaccharide Naturally pectin. the methylated ester of polygalacturonic acid, is extremely importance in both scientific and commercial world thanks to its biodegradability. An outsized group of pectinase enzymes causing breakdown of pectin polysaccharides of plants and fruit are utilized in industrial sector to extend the yield and clarity of fruit juices. During this study the bacterial strain was isolated using dilutions of 10-1 and 10-7 of rotten oranges. Isolated organisms were identified supported staining and biochemical tests. the pectinolytic activity decided using pectin containing pectinase screening agar well diffusion method at the temperature is 35 + 2 degree C. Supported gram staining and biochemical tests, the bacterial strain was isolated and identified as Bacillus cereus. The strain showed different pectinolytic zones counting on the concentration of inoculum and therefore, the largest pectinolytic zones was observed by the strain. This strain was efficient and have potential to be implicated commercially to extend the clarity and quality of fruit juices.

**KEYWORDS** – Pectinolytic activity, pectin, pectinase screening agar medium, *Bacillus cereus*, polygalacturonic acid.

### **1. INTRODUCTION**

Most of the critical life processes are established on the functions of enzymes in which Pectinase enzymes are mostly used in processes involving the degradation of plant materials, commonly referred to as pectic enzymes. The biotechnological significance of pectinolytic enzymes from microbial sources has pulled in the consideration of numerous scientists because of its various applications in different industrial processes. These enzymes are one of the most important groups of biological catalysts that have been established for usage in increasing juice yield and clarification in fruits and vegetable industries. It is used in the treatment and degumming of natural fibers used in the paper and textile industry.

Pectinase plays a significant role in coffee and tea fermentations. They are used in animal feed production for reducing feed viscosity, nutrients absorption, releasing increasing nutrients by hydrolysis of non-biodegradable fibers or by releasing nutrients blocked by these fibers and reducing the amount of nutrients in faeces. Microbial enzymes are produced either through submerged fermentation (SmF) or solid state fermentation (SSF) techniques.Medium is used for the detection of pectinolytic microorganisms especially those producing polygalacturonase.

Several types of conditions and media have been used to detect organisms capable of producing soft rots and degrading pectin. This general medium has been designated as MP medium. Murashige and Skoog Medium (MS) provide all the essential macroelements and microelements. Amongst citrus wastes, the waste of Citrus reticulata is a well-studied substrate for the enzyme and ethanol production under solid-state and submerged fermentation Pectin is a type of watersoluble fiber found inside plant cells. Many vegetables are excellent sources of pectin. Some fruits and vegetables are more pectin-rich than others. For example, apples, carrots, oranges, grapefruits, and lemons contain more pectin than cherries, grapes, and other small berries with citrus fruits containing the most pectin. The potential isolate was further identified using the molecular tool of 16S rRNA sequencing. In this method, a DNA purification kit was used for the extraction of genomic DNA of the selected isolate. The sequencing results were then processed using BioEdit software. The amplified PCR products were purified and sequenced. The obtained sequence data were blasted in the NCBI database and the likely microorganisms (with lower E value, higher identity percentage and maximum total score) were identified.

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# 2. Materials and methods: Sample collection:

For the isolation of pectinase producing bacterial strains, partially decayed fruit (oranges) were taken from the local market of Pallavaram, Chennai. The sample was collected aseptically using sterilized polythene bags. The physical characterization of the sample was analysed.



Fig 1: Rotten Orange Sample

### Isolation of bacterial strain:

The 1g of rotten orange sample was crushed into presterile mortar and pestle with distilled water to form suspension, 1 ml of rotten pulp was added in 0.9% saline as a diluent and made 7 fold serial dilutions (10-1 to 10-7).100µl of the diluted samples from 10-3, 10-5, and 10-7 was plated onto nutrient agar plates by spread plate method. The plates were observed for colonies after an incubation of 24 hours at 37°C in the incubator. The colonies (P1, P2, P3) was chosen and maintained as pure culture in a rotatory shaker at 150rpm and 37°C.



Fig 2: Serial dilution

# Screening of pectinolytic bacteria:

Screening the bacterial isolates for pectinase activity was carried out by inoculating the cultures in pectinase screening agar medium (PSAM) and observing the zone of clearance. The pH of the medium is 7.0. The plates with PSAM were prepared and a loopful of bacterial cultures was inoculated at the respective wells of the plate and incubated at 37°C. After 48 hours, the plate was flooded with gram's iodine solution for 10 minutes and then washed with distilled water. A clear halo zone around the well indicates pectinase enzyme activity. The zone diameter was measured. The colony, which forms a large clear zone diameter, was used for further biochemical test and molecular identification processes.

# Identification of pectinolytic bacteria:

Identification of strains was done on the basis of gram staining and biochemical testing (catalase, IMViC-Indole, Methyl Red, Voges Proskauer and Citrate).

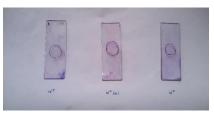


Fig 3: Gram Strained Slides

# Molecular identification of pectinolytic strain:

Genomic DNA was extracted from screened strain (P2) by ethanol precipitation method.

After extraction,  $2 \mu l$  of DNA fragments was mixed with Novel Juice dye contains 3 pursuit dyes like bromophenol blue, resolvent Cyanol FF and Orange 5.The gel was then electrophoresed at 100 volts for 45 minutes and it absolutely was determined in an exceedingly gel documentation system.

PCR was employed to amplify the DNA sequence in between two known sequences (forward primer 27F (5'-(AGA GTT TGA TCM TGG CTC AG)-3') and reverse primer 1492R (5'-(CGG TTA CCT TGT TAC GAC TT)-3') which are complementary to the known 16S rDNA sequences, were used).

The PCR sequence products were purified and sequenced. The obtained sequence data was compared with known sequences within the GenBank using the Basic local alignment search tool (BLAST) of the national center for biotechnology information (NCBI). Species that were identified supported the shared similarity with the known species sequences within the database.

# 3. Results and discussion:

From the various observations recorded during experimentation, the relevant results are being compiled and represented below.

### Isolation of bacteria:

The orange sample was partially decayed. The top part of the orange was rotten, it was appeared as soft brown coloured texture with sour smell.





Fig 4: Crushed orange paste

To isolate microorganisms from the collected rotten orange sample, serial dilution (Fig 2), Spread plating (Fig 5) isolation techniques were used. Subsequently, the selected isolates (P1, P2, P3) was subcultured into nutrient medium until pure culture (Fig 6) were isolated .In total, seven (7) white isolates were identified from the 1gm of rotten orange sample. From seven isolated white colonies, Three colonies were selected namely P1, P2, P3 for screening of pectinase activity.



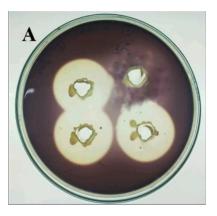


Fig 5: Spread Plate

Fig 6: Pure colony

PLATE ASSAY METHOD FOR PECTINASE QUALITATIVE ASSAY:

Subsequent to isolation and purification, the selected isolates (P1, P2, P3) were assessed for pectinase activity using pectinase screening agar medium (PSAM).



# Fig 7: PSAM plate showing zone of inhibition

Table 1: Zone Measurement				
S.No	Colony	Diamete		
		cm)		

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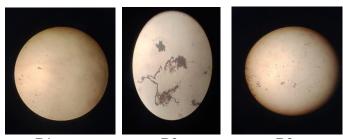
3.110	Colony	Diameter(III		
		cm)		
1.	Control	-		
2.	P1	1.5		
3.	P2	1.8		
4.	P3	1.6		

The control did not show any clear zone while the welldefined clear zones are visible around well (colonies) having pectinase activity. The diameter of the clear zone is directly proportional to the pectinase activity. It means that colonies with large clear zones possess high pectinase quantity while those with low diameter clear zone have low activity. Therefore, the P2 colony shows larger clear zone of 1.8cm and it possess higher pectinase activity when compared to other two colonies (P1 & P3).

#### **Biochemical tests:**

#### **GRAM STRAINING**

The Gram strained slides were observed under microscope. The screened bacteria (P2) was viewed as purple colored colonies. It indicates the isolated colonies were Gram Positive Bacteria (Fig 8).



P1 P2 P3 Fig 8: Gram Strained Colonies under Microscope (Purple colored colonies)

### IMViC TEST INDOLE TEST:

After adding Kovac's reagent to the culture broth, formation of a red color ring in the reagent layer on top of the medium within seconds of adding the reagent indicated the positive result (Fig 9).





Fig 9: Indole Test (Red ring formation)

### METHYL RED (MV) TEST:

After the addition of methyl red indicator, the culture broth turns red because of a pH at or below 4.4 from the fermentation of glucose. This indicates the positive result of methyl red test (Fig 10).

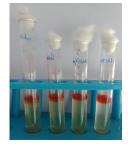


Fig 10: Methyl Red Test (Red color formed)

# **VOGES-PROSKAUER (VP) TEST:**

After the addition of Barritt's reagent A and Barritt's reagent B. The culture broth turns Pink red color on the surface. This indicates the positive result of Voges-Proskauer test (Fig 11).



Fig 11: Voges-Proskauer Test (Pink red color formed)

### CITRATE TEST:

The results of citrate test are indicated by a change in color in the medium. The medium was appeared as growth with a color change from green to intense blue along the slant. This shows the positive result in citrate test (Fig 12).



Fig 12: Citrate Test

(Blue color changes)

#### Table 2: IMViC Test Results

Colonies	Indole	Methyl Red	Voges- Proskauer	Citrate
Control	+ve	+ve	-ve	-ve
1	+ve	+ve	+ve	+ve
2	+ve	+ve	+ve	+ve
3	+ve	+ve	+ve	+ve

### CATALASE TEST

The immediate appearance of bubbles in the slide demonstrated the positive result in catalase test (Fig 13).



Fig 13: Catalase Test (Bubbles Formed)

The P2 strain was identified as Large, irregular and colonies with Higher clear zone diameter appeared on pectinase screening agar medium (PSAM). Grampositive, rod-shaped on Gram staining, arranged in short chains. The strain was catalase, indole, methyl red, Voges-Proskauer, and citrate tests positive (Table 3). Although, the P2 strain shows positive results in biochemical and staining test but 16S rRNA sequence analysis is required for confirmation. The P2 strains was further analysed for molecular characterization.

Table 3:	<b>Biochemical test</b>	results o	f screened	strain
(P2) with	pectinolytic activ	ity		

Str ain	Gra m Stain ing	ole	hyl	Voges - Prosk auer	ate	Catal ase	Pecti nase
P2	+	+	+	+	+	+	+



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Molecular identification isolated bacterial strain: Genomic DNA extraction methods was performed to isolate genomic DNA away from screened strain (P2). Finally, the DNA is isolated by ethanol precipitation.

#### **Agarose Gel Electrophoresis:**

After separation, the resulting DNA fragments are visible as clearly defined bands after running in agarose gel electrophoresis. The DNA standard or ladder should be separated to a degree that allows for the useful determination of the sizes of sample bands (Fig 14).

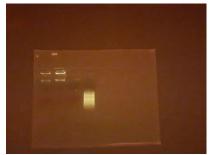


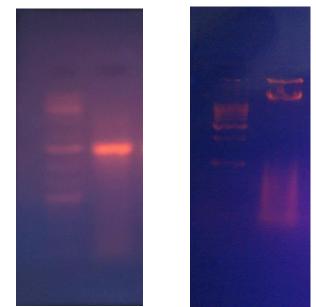
Fig 14: Bands appeared on **Agarose Gel Electrophoresis** 

#### PCR:

The isolated bacterial strain DNA was used to perform colony PCR. The strain was selected for 16S rRNA analysis and for this purpose colony PCR was done and the amplified product was run in agarose gel against ladder, both the bands (a) and (b) appeared on the same level in the agarose gel thus indicating the similarity of newly isolated bacterial strain (Fig 15).

**(a)** 

**(b**)



Lane 1 – 1KB DNA Ladder

Lane 1 – Ladder

Lane 2 – Bacterial genomic Lane 2 – Bacteria DNA 16srRNA

Fig 15: PCR Bands

Sequencing:

#### Sequence:

#### >VS Pec01

TGGGAGACTTGAGTGCAGAAGAGGAAAGTGGA ATTCCATGTGTAGCGGTGAAATGCGTAGAGATA TGGAGGAACACCAGTGGCGAAGGCGACTTTCTG GTCTGTAACTGACACTGAGGCGCGAAAGCGTGG GGAGCAAACAGGATTAGATACCCTGTCCACGCC GTAAACGATGAGTGCTAAGTGTTAGAGGGTTTC CGCCCTTTAGTGCTGACCGCCTGGGGAGTACGG CCGCAAGGCTGAAACTCAAAGGAATTGACGGG GGCCCGCACAAGCGGTGGAGCATGTGGTTTAAT TCGAAGCAACGCGAAGAACCTTACCAGGTCTTG ACATCCTCTGAAAACCCTAGAGATAGGGCTTCT CCTTCGGGAGCAAAATGACAGGTGGTGCATGGT TGTCCTCACCTCCTGTCGTGAAGTTGCCACCATT AAATTGGGCACTCTAAGGTGACGGCCGGTGACA AAACCAAGGAAGGGGGGGGGGGATGAACTCAAATCA TAATGCCCCTTATAACCGGGGGCTACACCATGCT ACAATGGGCTACAAAACCCCCAGGGGGGGGGCTA ATCTCATAAAACCTTCTCAGTTCGGATTGGAGG CTGCCTCCCTACATGAAACTGAAAGCGTAGAAA TCGAGAGAAGCATACCCCGCGGAAAAAGTTCC CGGCTTTAACACAGCCGCACACACGGAAATTTA

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#### AATCCCAAGAATGGGGGGGACCTGTGGACCCAA CGAAAATAGGAGGAAGGAAACGAACAGGAGG AGAGAAG

Later on 16S rRNA sequencing confirmed the Bacillus status of the strain (P2). The 16S rRNA sequence was submitted Basic local alignment search tool (BLAST) of the national center for biotechnology information (NCBI).Colony PCR is an efficient way for identification of species (P2).

### **BLAST:**

The **BLAST** result was interpreted as

~	select all 100 sequences selected	GenBank	Gra	phics	Dista	ance tree	e of resu	lits New	MSA Vie
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accessi
	Bacillus cereus ATCC 14579 165 ribosomal RNA gene, partial sequence	Bacillus cereus ATCC 14579	660	1241	100%	0.0	94.75%	975	MG70817
~	Bacterium TLCL8 16S ribosomal RNA gene, partial sequence	bacterium TLCL8	658	658	54%	0.0	94.85%	1471	EU086575
~	Bacilus nitratireducens strain SKC-2a 16S ribosomal RNA gene, partial sequence	Bacillus nitratireducens	649	649	54%	0.0	94.79%	1447	MT225575
~	Bacilus anthracis strain TC-3 16S ribosomal RNA gene, partial sequence.	Bacillus anthracis	643	643	54%	5e-180	94.21%	1554	GU939628
~	Bacilius cereus C1L chromosome, complete genome	Bacilius cereus C1L	640	8486	55%	6e-179	94.02%	5312355	CP022445
~	Bacillus wiedmannii R5a gene for 16S ribosomal RNA, partial sequence	Bacillus wiedmannie	638	638	54%	2e-178	93.82%	1538	LC501432
~	Bacillus cereus strain MGC4 16S ribosomal RNA gene: partial sequence	Bacillus cereus	636	636	54%	8e-178	93.81%	1511	MH266413
~	Bacillus sp. (in: Bacteria) strain AP1 16S ribosomal RNA gene, partial sequence	Bacillus sp. (in. Bacteria)	630	630	54%	4e-176	93.58%	1491	MN480586
~	Bacilus thuringiensis strain A1B3 16S ribosomal RNA gene , partial sequence	Bacilius thuringiensis	628	628	54%	1e-175	93.56%	1504	MG779636
~	Bacilus pacificus strain RI-A8 16S ribosomal RNA gene, partial sequence	Bacillus pacificus	627	627	54%	5e-175	93.56%	1480	MN704775
~	Proteobacteria bacterium strain BS120.16S ribosomal RNA gene, santial sequence	Proteobacteria bacterium	625	625	54%	20-174	93.35%	1473	MH061190
~	Bacifus thuringiensis strain SDY-3 16S ribosomal RNA gene, partial sequence	Bacillus thuringiensis	619	619	54%	8e-173	93.32%	1412	JX015365
~	Bacillus sp. (in: Bacteria) NGB-R138 gene for 16S ribosomal RNA, partial sequence	Bacillus sp. (in: Bacteria)	612	612	54%	1e-170	92.89%	1062	LC482487
~	Bacillus halotolerans strain Boillus 16S ribosomal RNA pene, partial sequence	Bacillus halotolerans	610	610	54%	5e-170	92.97%	1473	MN160225
~	Bacillus sp. OSS 8 16S ribosomal RNA gene, partial sequence	Bacillus sp. OSS 8	610	610	54%	5e-170	93.18%	1401	EU124557
~	Bacillus cereus strain CC3 16S ribosomal RNA gene partial sequence	Bacillus cereus	695	595	54%	1e-165	92,41%	1164	MK652869
•	Bacillus megalerium strain DC4 16S ribosomal RNA gene, partial sequence	Priestia megaterium	693	593	54%	5e-165	92.27%	1402	ME576262

Fig 16: Tabular Representation



Fig 17: Graphical Representation

Download      GenBank Graphics		Vext Previous ADescriptions
Bacillus cereus ATCC 14579 165 ribosomal RNA gene, part	tial sequence	
Requence ID: MG708176.1 Length: 975 Number of Matches: 1		
Range 1: 141 to 975 GenBank Graphics	🐨 Heat Match 🛓 Pravicus Match	
Score         Expect         Identities         Gaps           1214         bits(1346)         0.0         759/835(91%)         76/835(9%)	Strand Plus/Plus	
Query 1 Topostar I los for a sub-source for an I control of the second state of the se		
Durry 61 AGATATGGAGGAACACCAGTGGCGAAGGCGACTTCTGGTCTGTAACTGA		
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Query 278  Goldcalging   AA  GoldgeAdigidadadci  Adiabel    3bjet 441  GoldgeAdigidadadci   Adiabel   A		
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Query 477 gggATGAACTCAAATCATAATGCCCCTTATAACCGGGGTACACCATGCTA Sbjet 681 000ATGAACTCAAATCATAATGCCCCTTATAACCGGGGTACACCATGCT	ACAATGGACG 740	
Query 534	tead tead see	
Duery SES Hondooc Tote Coc Acta Game Towards Addam Concentration Sejet Bei Hondooc fote Coc Acta Game Towards Addam Concentration	LATACCCCGC 860	
Duery 645 COMMAND CCCCCC II ACCA ACCOMMAND CCCCCC ACCA COMMAND CCCCCCC ACCA COMMAND CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CAAGAATGGG 920	
Query 705 GOMCCIGIGGACCCAR GAMALAGAACGAACGAACGAACGAACGAACGAACGAACGAACG	AGAAG 759	



<b>Bacterial Strain</b>	Bacillus cereus
	ATCC 14579
Max Score	660
Total Score	1241
Query Cover	100%
Percentage Identification	94.75%
Accession Length	975

The amplified PCR products were purified and sequenced. The obtained sequence data were blasted in NCBI database and the likely microorganisms (with lower *E* value, higher identity percentage and maximum total score) was identified as *Bacillus cereus* ATCC **14579** with max score - 660, total score - 1241 and percentage identification - 94.75% (Table 4).

### 4. CONCLUSIONS

*Bacillus cereus* was isolated from the rotten fruit and was found as efficient pectinase producing bacterial strains which will be used for various industrial applications including extraction and clarification of fruit juices, processing of cotton fabric in textile industries, bleaching of paper, removal of pectic waste water and maceration of tea leaves. In future, the further studies to identify some other microorganisms to be used in the industries for fruit juice clarification process and perform a comparative study by performing a pairwise alignment to know their activity levels.

# ACKNOWLEDGEMENT

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