

Quantitative Estimation of Protease Produced by Bacterial Isolates from Food Processing Industries

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Abstract - To quantitatively estimate the protease produced by bacterial isolates from soil and water samples collected from food processing industries. In the present study, quantitative estimation of protease produced by selected bacterial isolates from soil and water samples collected from food processing industries was carried out and best protease producing organism can be used for the degradation of proteinaceous waste material from food manufacturing units leading to recycling of food industry waste. Protease activity was qualitatively determined using Gelatine clear zone method. Quantitative estimation of protease was performed for five bacterial isolates such as *Cedecea davisae* (TKMFT8), *Staphylococcus intermedius* (TKMFT10), *Proteus mirabilis* (TKMFT19), *Enterobacter asburiae* (TKMFT25) and *Alloiooccus otitis* (TKMFT61). Among all studied bacterial isolates, the maximum protease activity (138.23 ± 1.50) was recorded in *Cedecea davisae* (TKMFT8).

Key-Words: Protease, Protease activity, Quantitative estimation

1. INTRODUCTION

Proteases can be defined as enzymes which catalyze the breakdown of hydrolytic bonds in proteins thereby releasing amino acids and/or peptides (Louwrens W. Theron & Benoit Divol, 2014). Proteases represent a distinct subgroup of hydrolytic enzymes which catalyze the peptide bond breakdown in proteinous substrates (Younes Ghasemi et al, 2011; Bhatnagar et al., 2010; Yadav et al., 2011; Sankeerthana et al., 2013). Among enzymes, proteases are one of the major classes occupying 60% of total enzyme market (Chu W.H 2007; Kunamneni et al, 2003; Merheb-Dini et al, 2009, Verma O D et al.2011). Proteases are involved in every aspect of function of organisms and are among the oldest and most diverse enzyme families known.

Owing to their broad substrate specificity, proteases have tremendous applications in baking, brewing, waste treatment, leather processing, detergent formulations, meat tenderization, peptide synthesis, cheese manufacture, protein hydrolysate, soysauce production, pharmaceutical industry, silk industry, organic synthesis, silver recovery from waste photographic film and analytical tools in basic research and have prominent commercial value (Emtiazi et al.2005; Beheshti et al.2009; Sumantha et al.2006; Ward et al.2009). Moreover, baking industries use wheat flour (or Bakery dough) as a prime component in baking processes. This compound consists of an insoluble protein called

gluten which is hydrolyzed by protease (Sumantha et al., 2005). In addition, the addition of proteases decreases the mixing time and results in 4 increased loaf volumes (Leng and Xu, 2011).

Generally, proteolytic enzymes (proteases) are categorized into peptidases and proteinases. Protein degradation into smaller peptide fractions is catalyzed by proteinases; while hydrolysis of specific peptide bonds or completely breakdown peptides to amino acids are catalyzed by peptidases or peptide bond hydrolase (Michael G. Ga'nzle et al, 2008; Anita, 2010; Vasantha and Subramanian, 2012). Proteases are classified under the subgroup 4 of Group 3 (hydrolases) and this classification is according to the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology. Proteases are grouped as endo- or exo-enzymes based on their site of action on protein substrates (Rao et al, 1998). Depending on their catalytic mechanism, they are further classified (Enzyme Commission (E.C.) 3.4. 21- 25) as aspartic proteases, serine proteases, cysteine proteases or metalloproteases (Barett, 1994; Barett, 1995). Based on the p^H optima, there are 3 different types of proteases such as acidic, neutral and alkaline and among these, alkaline protease is the most commonly used industrial enzyme due to their stability and activity at alkaline PH (Onkar Nath Tiwari et al, 2015).

Proteases are present in all forms of life such as plants, animals and microorganisms. The major sources of proteases were from plants (eg. pineapple, fig and papaya), animals (eg. calf stomach) and microbes (eg. *Pseudomonas spp.*, *Bacillus spp.*). Plant proteases composed of zingibain, papain, ficin and bromelain (Adulyatham and Owusu- Apenten, 2005) and animal proteases include chymotrypsin, pepsin, Rennin, Trypsin etc. Microbial proteases are distributed in diverse microbial population viz. bacteria, fungi, viruses and actinomycetes. Microorganisms serve as a preferred source of protease and account for around two-thirds of commercial protease production worldwide. Current world demand for microbial protease are increasing due to their cost effectiveness, rapid growth and the ease with generating high yielding genetically modified strains (Sankeerthana et al.2013). The major bacterial genera which contribute to proteases include *Aeromonas*, *Alcaligenes*, *Arthrobacter*, *Bacillus*, *Halomonas*, *Pseudomonas* and *Serratia* (Shafee N et al,

2005; Rao et al.1998).In addition to this ,other bacteria producing protease include *Alteromonas* sp.(Yeo, I.O., et al,1995), *Brevibacterium linens*(Rattray, F.P., 1995), *Hyphomonasjannaschiana* VP 3(Shi, J., et al,1997) *Lactobacillus helveticus*(Valasaki, K., et al.2008) *Microbacterium* sp. (Gessesse, A. and Gashe, B.A. (1997))*Pimelobacter* sp.z-483(Oyama, H., et al.1997) *Salinivibrio* sp. Strain AF-2004 (Heidari, H.R.K., et al.2007) *Streptomyces* isolate EGS-5(Ahmad, S.M. (2011)) *Streptomyces microflavus* (Rifaat, H.M., et al.2006) *Streptomyces rimosus* (Yang, S.S. and Wang, J.Y. 1999) *Thermoactinomyce* ssp. (Lee, J.K., et al.1996) *Thermoactinomycesthalpophilus* THM1 (Anderson, J.K., et al.1997).In the present study ,quantitative estimation of protease produced by selected bacterial isolates from soil and water samples collected from food processing industries was carried out and best protease producing organism can be used for the degradation of proteinaceous waste material from food manufacturing units leading to recycling of food industry waste.

2. MATERIALS AND METHODS

Isolation and identification of Protease producing bacteria

Isolation of protease producing bacteria from soil and water samples collected from food processing industries was performed by serial dilution technique (Sjodahl *et al.* (2002)). A total of 87 dissimilar colonies from nutrient agar plates were selected and each isolate was given a reference number (TKMFT 01 to TKMFT87) and each isolate was subjected to primary screening for the production of protease by plate assay using gelatine agar (Abdel Galil, 1992). Selection of protease producing organisms was carried out by measuring the zone diameter on Gelatine agar medium. According to the results obtained, the maximum zone diameter was obtained for

TKMFT25 (15mm) on Gelatine Agar medium which was followed by TKMFT39 (14mm), TKMFT22 (22mm), TKMFT10 (10mm), TKMFT53 (9mm), TKMFT19 (8mm), TKMFT 8 & TKMFT61 (7mm).Selected isolates were identified based on the morphological and biochemical identification using Biomerieux Vitek-2 compact automated system.

Qualitative test for Protease

Proteolytic activities of selected bacterial isolates were detected on the basis of formation of clear zones around the bacterial isolates. Bacterial colonies appeared on agar plates were screened for evaluating their proteolytic potential by inoculating them in gelatin agar medium .Out of 87 isolates, 8 isolates were used in present study for thorough investigation as it exhibited most prominent zones of proteolysis around the colony. Protein hydrolysis was expressed as diameter of clear zone in millimetre (mm). Based on the results obtained in the biochemical identification of 8 isolates using Biomerieux VITEK 2 System, 5 isolates were selected for quantitative test for protease activity.

Quantitative estimation of Protease

The five bacterial isolates were inoculated separately to five conical flasks containing 100 ml MRS (De Man, Rogosa and Sharpe) broth and incubated over a 10 days period at 37⁰ C in a rotary shaker. MRS broth without bacterial inoculation kept as control. The contents of the flasks were collected in a centrifuge tube and it was centrifuged at 10000 rpm for 10 minutes at 4⁰ C in order to get the cell free supernatant containing crude enzyme. The protease assay was carried out from the first day onwards to till 10th day to find out the day with maximum enzyme production.



Fig.II . MRS broth inoculated with bacterial isolates for Quantitative estimation of Protease

Measurement of activity of Enzyme

Protease activity in the culture supernatant was determined according to the method of Tsuchida et al. (1986) by using casein as a substrate. A mixture of 500 μ l of 1% (w/v) of casein in 50 mM phosphate buffer, pH 7 and 200 μ l crude enzyme extract were incubated in a water bath at 40°C for 20 minutes. After 20 minutes, the enzyme reaction was terminated by the addition of 1 ml of 10% (w/v) trichloroacetic acid (TCA) and was kept at room temperature for 15 minutes. Then, the reaction mixture was centrifuged to separate the unreacted casein at 10,000 rpm

for 5 minutes. The supernatant mixed with 2.5 ml of 0.44M Na₂CO₃. 1 ml of 3-fold diluted Follin Ciocalteus phenol reagent was adding. The resulting solution was incubated at room temperature in the dark for 30 minutes and absorbance of the blue colour developed was measured at 660 nm against a reagent blank using a tyrosine standard (Lowry et al. 1951). One unit of protease is defined as the amount of enzyme that releases 1 μ g of tyrosine per ml per minute under the standard conditions of supernatant solution.

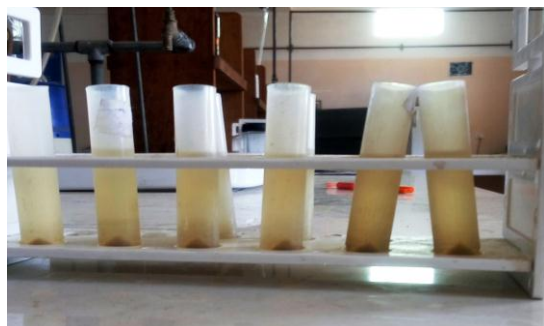


Fig.III. Supernatant solution containing



Fig.IV. Standard Protein assay by Folin Lowry's method crude protease enzyme for quantitative estimation of Protease

Quantitative assay of protein: The total protein content of the samples was determined by by Lowry method using Bovine serum Albumin as standard (Lowry et al. 1951).

3. RESULT AND DISCUSSION

Bacteria were isolated from soil and water samples collected from food processing industries. The proteolysis ability of 87 bacterial isolates from soil and waste water samples were evaluated using Gelatine agar medium.

Following inoculation and incubation of the Gelatine agar plates, organisms secreting protease enzyme exhibited a zone of proteolysis which was shown by a clear area around bacterial colonies. Among 87 isolated bacteria, 27 isolates were protease producer based on zone of hydrolysis and out of them 8 isolates (TKMFT 8, TKMFT10, TKMFT19, TKMFT22, TKMFT25, TKMFT39, TKMFT53, and TKMFT61) were chosen for further studies based on the diameter of zone of hydrolysis.

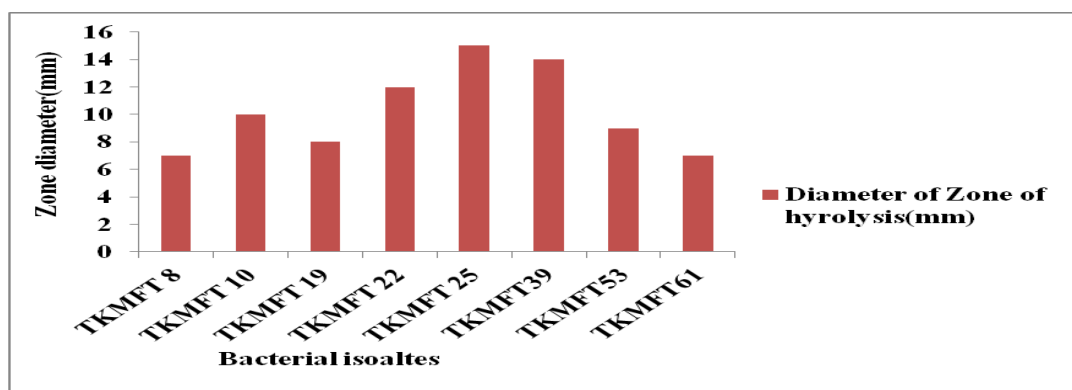


Fig.I. Zone of Diameter of protease producing Bacterial isolates

The selected 8 isolates were identified using cultural characterization, microscopic observation and biochemical identification using Biomerieux VITEK 2 system. Among the 8 isolates, TKMFT22, 10, 53 are representing *Staphylococcus intermedius*, TKMFT25, 39 are representing *Enterobacter asburiae*, and TKMFT8, TKMFT 19, and TKMFT61 are representing *Cedecea davisae*, *Proteus mirabilis* and *Alloiococcus otitis* respectively according to the test results.

The bacterial isolates were screened for their abilities to produce extracellular protease during their growth on protease production medium (Folasade and Joshua 2005). In order to select the bacterial isolate with highest potential of protease production, the selected 5

isolates were tested for extracellular protease production in liquid medium (MRS broth). Protease activity in the crude enzyme extract was determined (Carrie Cupp Enyard, 2008). The selected 5 isolates (TKMFT8, TKMFT10, TKMFT19, TKMFT25, and TKMFT61) were inoculated into MRS broth and incubated over a 10 days period at 37^o C in a rotary shaker and quantitatively determined the production of extracellular protease. The protease assay was carried out from the first day onwards to till 10th day to find out the day with maximum enzyme production. The results and observations are summarized in Table.I.

Table. I. Protease activity (U/ml) of bacterial isolates and protein content mg/ml

Incubation day	Protease activity(u/ml) & protein content mg/ml					
		TKMFT8	TKMFT10	TKMFT19	TKMFT25	TKMFT61
1	PA	6.93±0.75	45.5 ±1.3	15.16±1.98	6.93±0.75	16.46±1.98
	PC	2.73	1.97	2.25	1.89	0.89
2	PA	17.33 ±0.75	57.63 ±0.75	35.1±1.3	14.73±1.98	39±2.25
	PC	2.52	1.95	2.13	2.23	0.85
3	PA	45.06±1.98	70.2±1.3	41.16±0.75	17.76±0.75	46.36±1.50
	PC	2.37	1.75	1.98	1.78	0.72
4	PA	61.1±1.3	80.16±0.75	54.6±1.3	26.86±1.98	83.2±2.25
	PC	1.98	1.32	1.77	1.65	0.65
5	PA	91.43±1.98	88.83±0.75	78.43±2.70	42.03±2.70	103.56±1.98
	PC	1.81	1.1	1.78	1.63	0.64
6	PA	138.23±1.50	125.66±1.98	95.76±0.75	61.53±1.98	97.5±2.25
	PC	1.8	0.95	1.53	1.32	0.63
7	PA	113.06±1.98	117.43±1.98	126.96±1.98	56.33±0.75	91±2.6
	PC	1.79	0.94	0.87	1.31	0.52
8	PA	91 ±1.3	108.76±1.98	114.4±1.3	38.13±2.25	74.96±0.75
	PC	1.78	0.94	0.89	1.05	0.5
9	PA	84.5±1.3	89.26±1.98	109.63±2.70	31.63±0.75	61.96±0.75
	PC	1.59	0.97	0.72	0.97	0.45
10	PA	77.56 ±0.75	83.2 ±1.3	104.43±0.75	22.96±1.98	55.9±1.3
	PC	1.51	0.98	0.75	0.98	0.43

Protease activity expressed in U/ml.

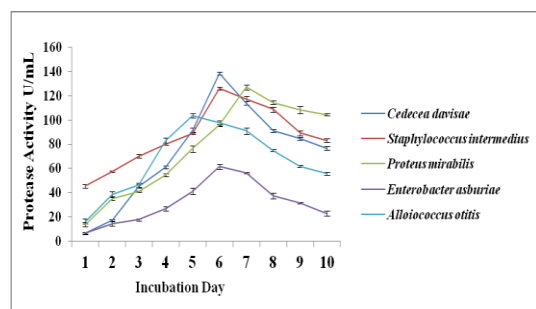


Fig.V.Comparison of Protease activity (U/mL) by different bacterial isolates

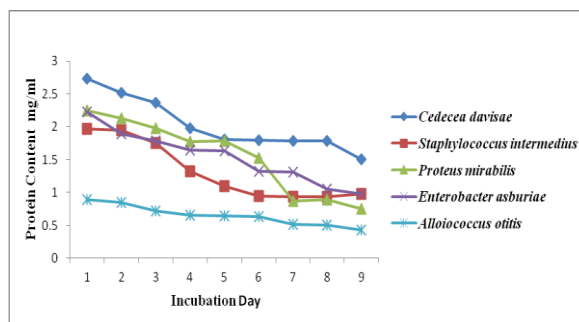


Fig.VI.Comparison of protein content in samples to detect the effect of protease activity

The results shown in Table. I revealed that all the bacterial isolates under study secreted protease enzyme at varied levels. The enzyme activity by *Cedecea davisiae* (TKMFT8), *Staphylococcus intermedius* (TKMFT10) and *Enterobacter asburiae* (TKMFT25) was gradually increased from first day of incubation to sixth day of incubation and the activity were shown in Table. I. It was also clear from the results that the activity of enzyme gradually decreased from sixth day of incubation to tenth day of incubation. It was found that the highest protease activity by these isolates has been observed on sixth day of incubation and it was found to be 138.23±1.50U/mL, 125.66±1.98 U/mL and 61.53±1.98 U/mL respectively. The enzyme activity exhibited by *Proteus mirabilis* (TKMFT19) was gradually increased from first day of

incubation to seventh day of incubation as shown in Table and after seventh day it started decreasing. The highest activity by *Proteus mirabilis* (TKMFT19) was found to be 126.96±1.98 U/mL and it was observed on seventh day of incubation. The activity of enzyme by *Alloicoccus otitis* (TKMFT61) has been increased from first day of incubation to fifth day of incubation and after that it started decreasing and the maximum activity was found on fifth day of incubation and it was found to be 103.56±1.98 U/mL. Protease activity and Protein content are related. It was clear from the data presented in Table. I and Fig. and graphical representation of protein Content in Fig.VI that increased protease activity decreased the protein content in the inoculated media. The decrease in the total protein content was resulted from the degradation of protein due to

the action of proteolysis enzymes secreted by the selected bacterial isolates. Among all studied bacterial isolates, the maximum protease activity (138.23 ± 1.50) was recorded in *Cedecea davisae* (TKMFT8). In a similar screening method in which a total of 118 bacterial strains were isolated from soil and *Bacillus* sp. predominant was used for the production of protease with activity (380U/ml) (Mohsin et al (2011). Sharma et al. (2015) reported the maximum protease activity (37.94 U/ml) by the bacterial isolate No. 2 at 37°C after incubation time of 72 h. The highest extracellular protease production (243 U/ml) by *Bacillus* sp without optimization of culture conditions was reported by Alnahdi (2012). In another study, Sinha et al. (2013) reported maximum protease activity (124.2 U/ml) exhibited by *Bacillus* sp .Sp-5 after 24 h of incubation at 25 °C using different nitrogen and Carbon sources like yeast extract and sucrose respectively. The study conducted by Smita et al (2012) reported highest protease activity (66.23 U/ml) showed by the bacterial species *Serratia liquiefaciens* at 37 °C after 48 h of incubation. In a similar study, Tiwari et al (2015) studied the enzyme activity of the bacterial isolate B2 in a medium (P^H 7.0) without optimization at 37 °C for 48h in a shaker. It was found that the isolate produced

68.05IU/ml enzyme and also checked the bacterial isolates in an alkaline medium for quantitative test of extracellular protease in a liquid medium and were found the production of protease at varying levels. Other works reported that *Bacillus cereus* S-98 and *Bacillus anthracis* S-44 showed their maximum activity for the biosynthesis of proteases within 60h incubation period since the productivity of protease reached up to 240.45U/ml for *Bacillus cereus* S-98 and 126.09U/ml for *Bacillus anthracis* S-44 (Johnvesly B and Naik G R, 2001). These data are in agreement with the present findings and revealed that protease producing organisms are widespread in environment and can be able to produce protease enzyme at varied levels without optimization of the culture conditions.

4.5 Statistical Analysis

Statistical analysis was carried out using a SPSS (Chicago, IL) statistical software package (SPSS for Windows, ver. 17, 2008). The Pearson correlation analysis was performed between protein content and incubation days for selected five bacterial isolates. The statistical analysis shown in Table.4.5 revealed that organisms showed significant positive correlation at different incubation days.

Table. II Pearson's Correlation coefficients between the variables

		<i>Cedecea davisae</i>	<i>Staphylococcus intermedius</i>	<i>Proteus mirabilis</i>	<i>Enterobacter asburiae</i>	<i>Alloiococcus otitis</i>
<i>Cedecea davisae</i>	Pearson Correlation Sig. (2-tailed) N	1 0 30	.971** 0 30	.851** 0 30	.950** 0 30	.865** 0 30
<i>Staphylococcus intermedius</i>	Pearson Correlation Sig. (2-tailed) N	.971** 0 30	1 0 30	.856** 0 30	.953** 0 30	.828** 0 30
<i>Proteus mirabilis</i>	Pearson Correlation Sig. (2-tailed) N	.851** 0 30	.856** 0 30	1 0 30	.750** 0 30	.645** 0 30
<i>Enterobacter asburiae</i>	Pearson Correlation Sig. (2-tailed) N	.950** 0 30	.953** 0 30	.750** 0 30	1 0 30	.874** 0 30
<i>Alloiococcus otitis</i>	Pearson Correlation Sig. (2-tailed) N	.865** 0 30	.828** 0 30	.645** 0 30	.874** 0 30	1 0 30

** Correlation is significant at the 0.01 level (2-tailed).

4. CONCLUSION

Among the five selected isolates, the maximum protease activity (138.23 ± 1.50) was exhibited by *Cedecea davisae* (TKMFT8) followed by *Proteus mirabilis* (TKMFT19), *Staphylococcus intermedius* (TKMFT10), *Alloicoccus otitis* (TKMFT61) and *Enterobacter asburiae* (TKMFT25) and the activity was found to be 126.96 ± 1.98 , 125.66 ± 1.98 , 103.56 ± 1.98 and 61.53 ± 1.98 respectively. The highest protease producing organism (*Cedecea davisae*) can be used for the degradation of proteinaceous waste material from food manufacturing units leading to recycling of food industry waste.

ACKNOWLEDGEMENTS

The author sincerely thanks Cashew Export Promotion Council of India (CEPCI), Mundakkal, Kollam, and Kerala, India for providing experimental facilities to carry out the work.

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