Characteristics of Raw–Starch Degrading Amylase Bacteria from Natar Hot Spring Lampung

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**Abstract**

Indonesia has a diversity of hot springs as a habitat of bacteria. One of the hot springs is Natar hot spring, Lampung. This study is to report the characteristics of a bacterium called Nati isolate that produces amylase to degrade raw starch from Natar hot spring. Water samples were taken from hot springs with a temperature of 45°C and a pH of 7.0. Nati was isolated by screening on the medium of Starch–Luria Bertani at 37°C. Its amylase–producing bacteria showed an optimum amylolytic activity of a crude enzyme of Nati isolate in soluble starch was 267.2774 U/mL at 60°C. Genotypic identification results using the 16S rRNA gene showed that the Nati isolate is identified as *Panninobacter phragmatetus*. A crude enzyme of Nati isolate showed a novel amylase ability and could degrade the raw starch substrates, such as corn and sago, with the amount of reducing sugar for each raw starch, 37.0688 µmol/mg, and 24.2697 µmol/mg. In conclusion, Nati amylase is potentially used in industry for its ability to degrade raw starch directly.

1. Introduction

Acid hydrolysis of starch is considered a simple method, as the acid is cheap and quickly obtained [1]. The result of starch hydrolysis by acid are glucose, xylose, arabinose as the main products. On the other hand, furans (furfural and hydroxymethylfurfural) as undesirable byproducts are also obtained [2]. Acid hydrolysis of the starch industry, especially the food and beverage industry, is considered unsafe if consumed [3]. Therefore, enzymatic hydrolysis was developed using α-amylase as an alternative to starch hydrolysis.

Starch hydrolysis using α-amylase does less production of unwanted byproduct, has specific and higher yield, approximately obtained 95% more of glucose [4]. Starch hydrolysis by amylase is also used in the detergent industry for stain removal applications [5]. Based on Business Communication Company (BCC) Research, the global enzyme market for the detergent industry is projected to increase to 1.3 billion in 2021 [6].Amylase production in the world is 30% of the total production of all enzymes [7].

Amylase bacteria are used predominantly in industrial applications because their production is more accessible, cheaper, and faster than other amylase microbes [8]. Furthermore, bacterial amylase is easily performed for genetic engineering studies. A large number of amylase bacteria species have been isolated, mostly are *Bacillus* species [9]. Amylase, which is involved in the thawing step in the starch processing industry, requires thermostable amylase in a high-temperature process [7]. The study of thermostable amylase-producing–thermophilic bacteria from hot springs is one of the trends of screening thermophilic bacteria that produce thermostable amylase. Some of the thermophilic
bacteria produce thermostable amylase have been reported [10, 11, 12, 13, 14, 15].

Furthermore, α-amylase is widely known for degrading various substrates [16], which could be a recent study of amylase, there are some raw starch degrading α-amylases; α-amylase from Bacillus aquimaris MKSC 6.2 (BaqA) [17], Geobacillus thermoleovorans (GTA) [18], and Geobacillus thermoleovorans (Gt-amyl II) [19] have been reported. The ability of some α-amylases, as mentioned above, that can directly hydrolyze a raw starch is considered useful in the starch-processing industry. The initial step causes gelatinization is to introduce amylase and amylpectin to be easily degraded by amylase. This step requires high temperature and can be neglected if using raw starch degrading α-amylases to reduce the industrial cost.

Indonesia has a diversity of natural hot spring as a habitat for thermophilic bacteria. One of the hot springs is Natar hot spring in Lampung. Limited information about the identification of thermophilic bacteria that can produce α-amylase from Natar is the basis of research on the screening of thermophilic bacteria that produce amylase in Natar. Based on the previous study, one bacterium (Nati isolate) with amylolytic activity has been screened from Natar hot spring in Lampung. The purpose of this study is to determine the characteristics of Nati isolate.

2. Methodology

This research was divided into three steps to determine the characteristics of Nati isolates. Bacterial characteristics were determined in the form of (i) morphology and physiology of Nati isolates, (ii) identification of Nati isolate genotypes based on 16S ribosomal RNA analysis, and (iii) determination of amylolytic activity in soluble and raw starches and (iv) scanning electron microscopy of raw starch granules treated by Nati isolates.

2.1. Equipment and Materials

In this research, the tools used were incubator (Memmert), water bath (Memmert), autoclave SA-232X (Tomy, Japan), Genesys 10S UV-Vis spectrophotometer (Thermo Scientific), and micropipettes (Eppendorf, Germany). While the materials used were tryptone (Himedia), yeast extract (Criterion), NaCl (Merck), bacto agar (Himedia), soluble starch (Merck), I₂ (Merck), and dinitrosalicylic acid/DNS (Himedia). Commercial grade corn and sago starch granule were purchased from a local market in Bandar Lampung, Indonesia.

2.2. Bacterial Identification

Nati isolate was inoculated on Luria Bertani agar plates (1% w/v tryptone, 0.5% w/v yeast extract, 1% w/v NaCl, 2% w/v agar, 1% w/v soluble starch). Nati isolate was grown at a temperature of 37°C for 24 hours and then sent into Genetika Science Laboratorium, PT. Genetika Science Indonesia, Jakarta for bacterial species barcoding. Bacteria were identified based on the identification of full-length 16S rRNA. The bacterial identification included extraction of genomic DNA with quick-DNA Fungal/Bacterial Miniprep Kit (Zymo Research, D6005), PCR amplification with MyTaq HS Red Mix (BIO-25047) and purification, then bidirectional PCR product sequencing [20]. The resulting fragment of 1.3 kb was compared to other 16S rRNAs in the GenBank database using the NCBI BLAST tool. A phylogenetic tree was constructed using neighbor-joining by NCBI BLAST Tree Method with 1000 bootstraps. The morphology and physiology properties of bacteria were determined at the Laboratory of Bacterial Diagnostic, Balai Veteriner Lampung, Bandar Lampung, Indonesia.

2.3. Determination of Amylolytic Activity on Soluble Starch

Nati isolate was grown in 50 mL Luria Bertani (1% w/v tryptone, 0.5% w/v yeast extract, 1% w/v NaCl) on shaker at temperature of 37°C and 150 rpm for 24 hours. The amylolytic activity was determined by measuring the amount of reducing sugar using the DNS method [21]. Amylase assay was performed from a mixture of 25 μL α-amylase bacterial crude and 25 μL 1% w/v of soluble starch. A 50 μL DNS solution stopped the activity. The mixture was incubated in the water bath at 50°C for 10 minutes, and then the reaction stopped in the boiling water for 10 minutes. As a control reaction, DNS reagent was added before adding amylase. All reaction was performed triplicates. The absorbance was measured at 500 nm. The protein concentration was determined using the Bradford method with the absorbance measured at 595 nm [22]. One unit of amylase activity is defined as the amount of amylase needed to produce 1 μmol reducing sugar under specified conditions.

2.4. Determination of Amylolytic Activity on Raw Starch

The amylolytic activity of Nati isolate on corn and sago raw starch granule was determined by incubating 1% w/v of each raw starch with 1 mL of crude in a shaker at a temperature of 37°C and 150 rpm for 24 hours. Followed by 5000 rpm centrifugation for 10 min, the supernatant’s amylolytic activity was measured by the DNS method as it was observed that the amylolytic activity of soluble starch [21]. The activity was performed triplicates. Meanwhile, the crude pellets were sent into Laboratorium Terpadu dan Sentra Inovasi Teknologi, Universitas Lampung, Bandar Lampung, Indonesia, for scanning electron microscopy of hydrolysis amylase of the raw starch granule.

3. Results and Discussion

Based on the previous study, one Nati isolate was screened for their amylase activity when growing in selective media containing soluble starch. The appearance of the clear zone after staining with KI/I₂
solution around the Natl colony indicating the ability to hydrolyze soluble starch. Natl isolate has a crude amylolytic activity of 240.7267 U/mL in a 1% soluble starch substrate using DNS reagents at a temperature of 50°C. Hot springs are a common source of bacteria that produce enzymes, one of which is amylase. Several hot springs in Indonesia can be the source of bacterial growth and have potential applications in the starch-processing industry. *Bacillus megaterium* has been isolated from Hatuasa hot spring in Tubuh Village Ambon, which excreted amylase after being screened on a starch agar plate [10]. *Bacillus licheniformis* BT5.9 has been identified as a potential bacterial producer in Malang [11]. Two isolates (BR 002 and BR 015) of thermostable α-amylase were isolated from Bora Hot Springs, Central Sulawesi [12]. *Anoxybacillus flavigerus* AE3 was isolated as an α-amylase-producing bacterium from Bukit Kilii hot spring in Solok, West Sumatera [13]. Amylase producing bacteria have been isolated from Donand hot spring in Muara Jawa Sub District, Kalimantan [14]. One colony was identified as *Thermoactinomyces saachari* based on morphology and physiology identification as α-amylase bacteria from Singgahan hot spring, Tuban, East Java [15].

### 3.1. Morphology and Physiology Characteristics of Natl Isolate

The morphological analysis results showed that the Natl isolate produced circular, flat, light yellow colonies on agar plates. It has pink-red rods, cocccobacilli, Gram-negative bacteria, positive for catalase and oxidade production, and γ-hemolytic on blood agar plates. The physiological tests for Natl isolate were carried out with Microbact GN 12A/BYE, 24 E. The results of the Natl isolate physiological test, are shown in Table 1.

**Table 1.** The result of physiology characteristic of Natl isolate

<table>
<thead>
<tr>
<th>Test</th>
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<tbody>
<tr>
<td>Lysine</td>
<td>Positive</td>
<td>Gelatine</td>
<td>Negative</td>
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<tr>
<td>Ornithine</td>
<td>Negative</td>
<td>Malonate</td>
<td>Negative</td>
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<tr>
<td>H2S</td>
<td>Negative</td>
<td>Inositol</td>
<td>Neutral</td>
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<td>Glucose</td>
<td>Positive</td>
<td>Sorbitol</td>
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<tr>
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<td>Rhamnose</td>
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<tr>
<td>Xylose</td>
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<td>Succrose</td>
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<td>ONPG</td>
<td>Positive</td>
<td>Lactose</td>
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<td>Positive</td>
<td>Salicin</td>
<td>Positive</td>
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<tr>
<td>TDA</td>
<td>Negative</td>
<td>Arginine</td>
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</table>

### 3.2. Identification of Natl Isolate

Fragments of 1322 base pairs of Natl isolate DNA were amplified and determined (Figure 1). The nucleotide sequence of 16S rRNA gene fragment Natl isolates (Figure 2) was aligned and compared to the 16S rRNA of various bacteria from GenBank data. The phylogenetic tree was constructed and showed that Natl isolate belongs to *Pannibacter phragmatetus* (Figure 3). It is suggested that amylase bacterial from Natl hot spring in Lampung, be identified as *Pannibacter phragmatetus* with strain name Natl.

**Figure 1.** Electropherogram of 16S rRNA gene fragment Natl isolate. Line M, molecular marker; line 1, 16S rRNA gene fragment Natl isolate.

**Figure 2.** The nucleotide sequence of the 16S rRNA gene from Natl isolate.
3.3. Amylolytic Activity on Soluble Starch

The crude enzyme of *Panninobacter phragmatetus* strain Nati shows amylase activity in soluble starch and raw starch. The crude enzyme of Nati isolate can hydrolyze soluble starch at a temperature range 40–80°C (Figure 4). Nati isolate displayed an optimum amylase activity in soluble starch at a temperature of 60°C, with the amylolytic activity of 267.2774 U/mL determined by the DNS method [21]. Nati shows the amylolytic activities in soluble starch at a temperature of 60°C, and 50°C is 131.435 U/mL and 240.7267 U/mL, respectively. Nati can still actively hydrolyze soluble starch at temperature 70°C and 80°C, in which the amylase activities are 114.0236 U/mL and 23.5817 U/mL, respectively. Previous studies reported that several hot spring bacteria produce amylase, each of which had optimum amylolytic activity at 70°C[10], 50°C[11], 50°C and 70°C[12].

![Figure 4. Amylolytic activities of Nati isolate on 1% soluble starch](image)

3.4. Amylolytic Activity on Raw Starch

The determination of Nati amylase activity in raw starch has been carried out by measuring the supernatant adsorption after incubating a mixture of the Nati crude enzyme with corn and sago starch for 24 hours at 37°C. The amylolytic activities of Nati on corn and sago raw starch granule are 37.0688 µmol/mg and 24.2697 µmol/mg, respectively, determined by the DNS method [21]. The results of scanning electron microscopy of amylase treated corn granules by the Nati crude enzyme show that corn granules have small pores on the surface (Figure 5A), compared to corn granules starch, which had not been applied to amylase hydrolysis (Figure 5B).

![Figure 5. Result of scanning electron microscopy of corn granule. A. amylase treated corn granule by the crude enzyme of Nati. B. amylase untreated corn granule](image)

Amylase treated corn granules were incubated with Nati crude enzyme. Small pores on the surface of amylase treated corn granules by Nati show that Nati crude enzyme can hydrolyze a corn raw starch granule. The results compared to the untreated corn granules which have no small pores on the surface. This indicates that Nati crude amylase can directly hydrolyze raw corn starch. Previous studies reported that α-Amylase from *Bacillus aquimaris* MKSC 6.2 and *B. amylophilificiens* ABBD showed the same hydrolyze pattern to raw corn starch, that holes were found on the surface of corn raw starch [17, 25].

The crude enzyme of *Panninobacter phragmatetus* strain Nati can be a novel amylase because of its ability to hydrolyze raw starch directly along with other strains that had been reported previously [26]. The study reported that *Bacillus aquimaris* MKSC 6.2 could degrade various raw starch granules, such as corn, cassava, sago, potato, and rice[17]. *Geobacillus thermoleovorans* (GT–amy II) had the optimum ability to directly hydrolyze a corn raw starch granule [19]. Amylase from Anoxybacillus
strains SK3-4, (ASKA) and Anoxybacillus strains DT3-1 could degrade sago and potato granule starch [27]. The gelatinization step in the starch industry needs high temperature and could be abolished if using α-amylases to directly degrade raw starch [17][17][17][17][17]. The advantage of using raw starch degrading α-amylases can save the cost. Natti isolate has the ability as a raw starch degrading α-amylases so that it becomes promising and potentially used as an enzyme in the starch industry.

4. Conclusion

The result shows that Natti isolate as a moderate thermostable bacterium from Natar hot springs in Lampung Province produces amylase that degrades soluble starch and raw starch granules, such as corn and sago. A novel amylase from Natti isolate has the potential to be use in the starch-processing industry.

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References

[11] Darah Ibrahim, Han Lj Zhu, Nuraqilah Yusof, Bacillus licheniformis BT5. 9 isolated from Charing Hot spring, Malang, Indonesia, as a potential producer of thermostable α-amylase, Tropical Life Sciences Research, 24, 1, (2013), 71-84
[19] Deepika Mehta, T. Satyanarayana, Domain C of thermostable α-amylase of Geobacillus thermoeleovorans mediates raw starch adsorption,


