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Isolation and Characterization of Cellulolytic Bacteria from Senduro Goat Feces, Lumajang

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Abstract
Cellulolytic bacteria are bacteria that can produce cellulase enzymes. Goat feces can serve as a source for various types of cellulolytic bacteria isolates with diverse cellulose-degrading abilities. The purpose of this study is to isolate and characterize cellulolytic bacterial isolates in Senduro goat feces. This research was an observational analytic study involving isolation using CMC media, testing cellulolytic activity using Congo red, and characterization (including colony morphological characteristics, cell characteristics, and biochemical characteristics) of the cellulolytic bacterial isolates with the highest cellulolytic index. Based on the results, 18 cellulolytic bacterial isolates with varying levels of cellulolytic activity were obtained. Four isolates (BSD5, BSD7, BSA2, and BSA8) was found to have the highest cellulolytic index values of 3.1, 2.9, 2.2, and 2.2, respectively. In conclusion, evaluation of colony morphology, cellular characteristics, and biochemical profiles indicated that isolate BSD5 showed similarity to the genus *Bacillus*, BSD7 to *Alcaligenes*, BSA2 to *Enterococcus*, and BSA8 to *Cellulomonas*.

Keywords: cellulolytic bacteria, goat feces, cellulolytic index, characterization, biodiversity

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INTRODUCTION

Cellulase is among the most widely used industrial enzymes and currently ranks third in global demand for commercial enzyme (Puspitasari & Ibrahim, 2020; Singh *et al.*, 2016). Its broad adoption reflects its functional versatility across various sectors such as textiles, paper and pulp, detergents, food processing, animal feed, biofuels, and chemicals (Anoop *et al.*, 2019). Industrial applications range from softening paper pulp and maintaining fabric brightness to enhancing food quality, improving feed digestibility, facilitating the biodegradation of organic matter, and enabling the bioconversion of cellulose into high-value commodity chemicals, thereby also contributing to the mitigation of environmental pollution (Nababan *et al.*, 2019).

Market projections further indicate sustained growth, with global revenue expected to increase from USD 1.72 billion in 2023 to approximately USD 1.83 billion in 2024 (Research and Markets, 2024). This expansion underscores its strong commercial relevance and continued demand within the industrial enzyme sector (Jayasekara & Ratnayake, 2019). Nevertheless, high production and market costs remain a significant limitation, constraining its economic profitability for large-scale applications (Gradiana & Kasimir, 2024).

Cellulase enzymes can be produced by various microorganisms, including fungi and bacteria (Nababan *et al.*, 2019). Among these, bacteria offer a practical advantage due to their faster growth rates, allowing more rapid enzyme production than other microbial sources (Rakhmawati *et al.*, 2014). Cellulolytic bacteria produce cellulase enzymes and have the ability to degrade cellulose substrates (Murtiyaningsih & Hazmi, 2017). These bacteria produce cellulase enzymes that break down cellulose into simpler compounds such as oligosaccharides and glucose, which can be utilized as an energy source for other microbes or applied in industrial fermentation processes (Patel *et al.*, 2019). Cellulolytic bacteria can be obtained from various sources, including animal feces. In ruminants, microbial communities in the rumen produce cellulase to assist in the digestion of fibrous feed. However, some cellulose is not completely decomposed and is excreted in feces, creating a suitable environment for the growth of cellulolytic bacteria (Vaz-Moreira *et al.*, 2010).

Senduro goats, as herbivores that rely on high-fiber diets, are likely to host diverse communities of cellulolytic microbes in their digestive system. As a result, goat feces can serve as a potential source

of cellulolytic bacterial isolates capable of producing high-activity cellulase enzymes (Irfan *et al.,* 2012). Similar findings have been reported in other studies. For example, Rahayu *et al.* (2018) revealed cellulolytic bacteria in mongoose feces and identified 9 genera, including *Xylophilus*, *Caryophanon*, *Aeromicrobium*, *Exiguobacterium*, *Brochotrix*, *Alcaligenes*, *Alteromonas*, *Halomonas*, *Chromobacterium*, *Corynebacterium*, and *Cellulomonas*. In another study, Satwika *et al.* (2021) successfully isolated 30 bacterial strains, including 7 cellulolytic strains, from environmental samples such as soil, cow dung, and kitchen waste. More recently, Suharti *et al.* (2023) reported that cellulolytic bacteria isolated from the feces of endemic tropical herbivores, including anoa and cattle, exhibited notable cellulose-degrading ability, with cellulolytic indices around 1.2, highlighting their potential as efficient cellulose-degrading agents.

The isolation process for cellulolytic bacteria in this study use Carboxymethyl Cellulose (CMC) as a selective substrate. Cellulolytic activity is detected using the Congo red staining method; the presence of a clear zone around the colony indicates cellulolytic activity. The discovery of bacteria with high cellulolytic activity can contribute to the development of feed fermentation technology, bioethanol production, and more efficient management of organic waste (Mojsov, 2012; Biswas *et al.,* 2020).

Additionally, the use of cellulolytic bacteria from Senduro goat feces can support the implementation of sustainability principles in animal husbandry. By optimizing the utilization of fecal waste, the potential for environmental pollution from manure accumulation can be reduced, and by-products, such in enzymes or value-added feed fermentation products, can be produced (Fitrihidajati *et al.,* 2015). Cellulolytic bacteria help increase the efficiency of ruminant feed fermentation. The success of fermented feed depends on the ability of bacteria to degrade cellulose; bacteria with the highest cellulose-degrading ability can be used as a starter in the fermentation process (Raharjo & Isnawati, 2022). Several studies have been conducted on Senduro goats, including research on the bacterial diversity isolated from their raw milk (Trimulyono *et al.,* 2024). Nevertheless, there was currently no research on the isolation of cellulolytic bacteria from Senduro goat feces.

Based on this exposure, this research is an observational study examining the type of cellulolytic bacteria present in raw materials containing cellulose, specifically goat feces. This study aims to isolate and characterize cellulolytic bacteria from Senduro goat feces in Lumajang. The results of this study are expected to significantly contribute to the utilization of organic waste and the development of microbial-based technologies for applications in the livestock, environmental, and industrial sectors.

MATERIALS AND METHODS

This research is a descriptive observational study involving the isolation, characterization, and testing ofcellulolytic activity in the obtained bacterial isolates. The study was conducted from August 2024 to March 2025. The feces samples were collected directly from Senduro goat farm in Senduro District, Lumajang Regency, East Java, Indonesia. Isolation, characterization, and cellulolytic activity tests were carried out at the Microbiology Laboratory, Building C10, FMIPA, Universitas Negeri Surabaya. The research targets were cellulolytic bacterial isolates derived from the feces of two adult goats (4-5 years) and two Senduro lambs (1-2 months old). Adult goats were fed green fodder (leaves and grass), concentrate, and cassava dregs, while the lambs were fed green fodder (leaves and grass), concentrate, cassava dregs, and cow's milk.

The isolation process began with serial dilutions up to 10^{-8} and was then inoculated using the pour plate method onto selective Carboxy Methyl Cellulose (CMC) solid media in a serial dilution (Yunita *et al.,* 2015). The growth media for cellulolytic bacteria contains CMC as a substrate, which can be broken down by the cellulase enzyme (CMCase). The growth of bacteria on the media indicated that they possess cellulolytic activity (Murtiyaningsih & Hazmi, 2017).

The isolation method used was the pour plate technique, using CMC selective media with serial dilutions up to $10^{-8,}$ prepared in 0.85% NaCl solution. The isolated colonies were incubated for 48 hours at 37^{o}C. After incubation, colonies were purified based on their morphological features. Colony morphological characterization included observing the colony shape (from above), the colony surface (from the side), the colony edge (from above), and the color of the colony. Bacterial isolates were tested for their ability to degrade cellulose, as indicated by the diameter of the clear zone formed around the colony on CMC media after staining with 0.1% Congo red and rinsing with 1 M NaCl. Four bacterial isolates with the highest cellulolytic index were characterized microscopically in the form of cell morphology (cell shape, Gram stain, motility, and endospores). Next, biochemical tests were performed, including the catalase test, carbohydrate fermentation test, TSIA test, indole test, citrate test, and Methyl Red-Voges-Proskauer (MR-VP) test.

Cellulolytic activities and characteristics of cellulolytic bacterial isolates were analysed descriptively and quantitatively. Cellulolytic activity was compared to cellulolytic index: low (≤ 1), medium (1-2), and high (>2) (Choi *et al.,* 2005). Meanwhile, data on the characteristics of bacterial isolates, including colony morphology, cell and biochemical characters, were analyzed descriptively and presented in tabular form (Arifin *et al.,* 2019). Genus-level identification used Bergey's Manual of Determinative Bacteriology, 9th edition (Holt *et al.,* 1994).

RESULTS

Based on the isolation results, a total of 18 bacterial isolates were obtained in the feces of Senduro lambs and adult goats. Nine bacterial isolates from Senduro lamb feces samples with isolate codes BSA1, BSA2, BSA3, BSA4, BSA6, BSA7, BSA8, BSA9, and BSA10. Meanwhile, from the adult Senduro goat feces sample, nine bacterial isolates were identified and coded as BSD2, BSD3, BSD3, BSD4, BSD5, BSD6, BSD7, BSD8, BSD9, and BSD10

The nine isolates with the BSA code have colony morphological characteristics that vary in each isolate (Table 1). Variations in colony morphological characters include the shape, optics, elevation, surface, edge, and color of the colonies.

Table 1. Colony morphologies of BSA Isolates

Code	Shape	Optics	Elevation	Surface	Edge	Color
BSA1	Circular	Opaque	Raised	Smooth and shiny	Lobate	White
BSA2	Circular	Opaque	Raised	Smooth and shiny	Entire	White
BSA3	Circular	Translucent	Raised	Smooth	Entire	White
BSA4	Irregular	Transparent	Flat	Smooth	Undulate	White
BSA6	Irregular	Transparent	Flat	Smooth	Entire	White
BSA7	Irregular	Opaque	Raised	Smooth	Entire	White
BSA8	Irregular	Translucent	Flat	Smooth	Entire	White
BSA9	Circular	Opaque	Raised	Smooth	Entire	White
BSA10	Circular	Opaque	Convex	Smooth	Entire	White

All the isolates have white coloration. White isolates with circular colony shapes consist of isolates BSA1, BSA2, BSA3, BSA9, and BSA10, while irregular colonies consist of isolates BSA4, BSA6, BSA7, and BSA8. Optical characteristics of the isolates include opaque (isolates BSA1, BSA2, BSA7, BSA9, and BSA10), translucent (isolates BSA3 and BSA8) and transparent (isolates BSA4 and BSA6). Colony elevations on the isolates are raised (isolates BSA1, BSA2, BSA3, BSA7, and BSA9), flat (isolates BSA4, BSA6 and BSA8) and convex (BSA10). Colony surface characteristics: seven isolates have a smooth texture, while isolates BSA1 and BSA2 have a shiny smooth texture. Four types of colony edge were observed among the isolates: lobate (BSA1), entire (BSA2, BSA3, BSA6, BSA7, BSA8, BSA9, BSA10), and undulate (BSA4).

A total of nine bacterial isolates, designated by the BSD code, exhibited diverse colony morphologies (Table 2). The observed morphological differences encompassed colony shape, optics, elevation, surface, edge, and color.

Table 2. Colony morphology characteristics of BSD isolates

Code	Shape	Optics	Elevation	Surface	Edge	Colour
BSD2	Irregular	Opaque	Convex	Smooth	Entire	White
BSD3	Circular	Translucent	Flat	Smooth and shiny	Entire	White
BSD4	Irregular	Translucent	Flat	Smooth and shiny	Entire	White
BSD5	Irregular	Translucent	Raised	Smooth	Entire	White
BSD6	Irregular	Opaque	Raised	Smooth and shiny	Entire	White
BSD7	Irregular	Transparent	Flat	Smooth	Entire	White
BSD8	Circular	Translucent	Convex	Smooth and shiny	Entire	White
BSD9	Circular	Opaque	Raised	Smooth and shiny	Entire	White
BSD10	Circular	Translucent	Raised	Smooth	Entire	White

All isolates from the BSD group have a similar color to the BSA isolates, which was white (Table 2). Circular colony morphology was observed in isolates BSD3, BSD8, BSD9, and BSD10, whereas BSD2, BSD4, BSD5, BSD6, and BSD7 exhibited irregular forms. Based on optical characteristics, colonies were classified as opaque (BSD2, BSD6, BSD9), translucent (BSD3, BSD4, BSD5, BSD8, BSD10), or transparent (BSD7). Variation in elevation was also recorded, with raised colonies in BSD5, BSD6, BSD9, and BSD10; flat profiles in BSD3, BSD4, and BSD7; and convex structures in BSD2 and BSD8. Surface texture was predominantly smooth across all isolates, although BSD3, BSD4, BSD6, BSD8, and BSD9 displayed a

distinctly glossy appearance. The colony margins of all isolates were entire, characterised by smooth, uninterrupted edges.

Based on the results of cellulolytic activity of 18 bacterial isolates isolated from the feces of Senduro lambs and adult goats, the isolates exhibited diverse abilities to degrade cellulose. Figure 1 shows the cellulolytic activity from lamb feces isolates while Figure 2 shows the cellulolytic activity of adult goat feces isolates. According to Choi *et al.* (2005), cellulolytic index values are grouped into three categories, low (index<1.0), medium (index 1.0-2.0), and high (index > 2.0). Of the total isolates (Table 3), 7 (38.9%) were classified as medium, 9 (50%) as medium, and 2 (11.1%) as low.

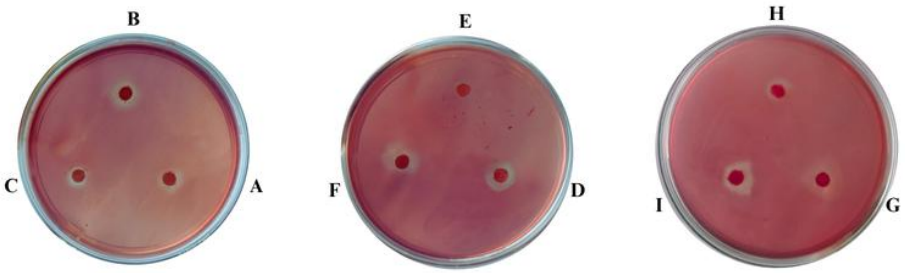

Figure 1. Cellulolytic activity of bacterial isolates from Senduro lamb feces. (A) BSA1, (B) BSA2, (C) BSA3, (D) BSA4, (E) BSA6, (F) BSA7, (G) BSA8, (H) BSA9, and (I) BSA10.

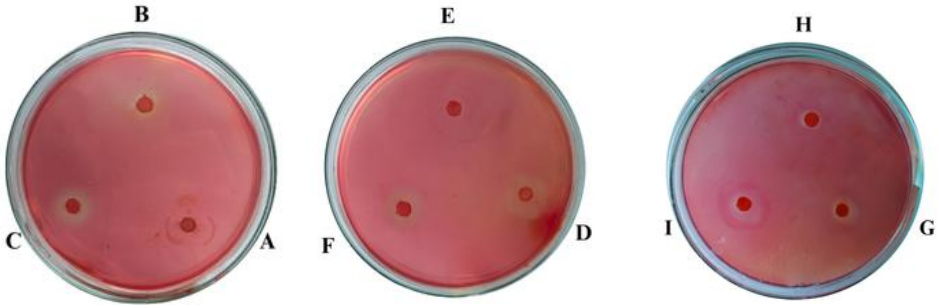

Figure 2. Cellulolytic activity of bacterial isolates from adult Senduro goat feces: (A) BSD2, (B) BSD3, (C) BSD4, (D) BSD5, (E) BSD6, (F) BSD7, (G) BSD8, (H) BSD9, and (I) BSD10.

Table 3. Activity of cellulolytic bacteria isolated from Senduro goat feces

Isolate Code	Cellulolytic Index (cm)	Category (Choi *et al.*, 2005)
BSD5	3,1	High
BSD7	2,9	High
BSA2	2,2	High
BSA8	2,2	High
BSD4	2,2	High
BSD9	2,2	High
BSD10	2,1	High
BSA6	2,0	Medium
BSA10	2,0	Medium
BSA7	1,8	Medium
BSA9	1,8	Medium
BSA4	1,4	Medium
BSD8	1,4	Medium
BSD3	1,2	Medium
BSA1	1,0	Medium
BSA3	1,0	Medium
BSD6	0,3	Low
BSD2	0,2	Low

Notes: BSA = isolated from feces of Senduro lamb; BSD = isolated from Senduro adult goat

As presented in Table 3, the isolate exhibiting the highest cellulolytic activity was BSD5, with an index value of 3.1, followed by BSD7 (2.9) and BSA2, BSA8, BSD4, BSD9, and BSD10, each with an index of 2.2. Based on the origin of the isolates, the BSA group obtained from goat feces showed highly diverse cellulolytic activity. In this group, BSA2 and BSA8 belonged to the high-activity category while

BSA1, BSA3, BSA4, BSA6, BSA7, BSA9, and BSA10 in the medium category. In addition, there were no isolates with low cellulolytic activity.

The group of BSD isolates obtained from adult goat feces showed a more diverse distribution of activity. Five isolates (BSD4, BSD5, BSD7, BSD9, and BSD10) showed high activity, while BSD3 and BSD8 were classified as medium, and BSD2 and BSD6 as low. The four isolates with the highest index values were further characterized based on their cellular and biochemical characteristics. Table 4 presents the result of characterization tests performed to the isolates.

Table 4. Characteristics of 4 isolates with the highest cellulolytic activity

Characteristics	Isolates			
	BSA2	**BSA8**	**BSD5**	**BSD7**
Colony Characteristics				
Shape	Circular	Irregular	Irregular	Irregular
Optic	Opaque	Translucent	Translucent	Transparent
Elevation	Raised	Flat	Flat	Flat
Texture	Smooth	Smooth	Smooth	Smooth
Margin	Entire	Entire	Entire	Entire
Color	White	White	White	White
Cell Characteristics				
Shape	*Coccus*	*Bacil*	*Bacil*	*Coccus*
Gram	Positive	Positive	Positive	Negative
Motility	Non-motile	Motile	Motile	Motile
Endospore	Absent	Absent	Present	Absent
Biochemical Characteristics				
Catalase	-	+	+	+
Glucose	+	+	+	+
Sucrose	+	+	-	+
Lactose	+	+	-	-
TSIA	A/A	A/A	K/A	A/A
H_2S	-	-	-	-
Indole	+	+	-	-
Citrate	-	+	+	+
MR	+	+	+	+
VP	-	-	-	-

Based on the analysis, the four selected bacterial isolates exhibited variations in cell shape, Gram reaction, motility, and catalase enzyme production (Table 4). Isolates BSA2 and BSD7 have coccus-shaped cell morphology, whereas BSA8 and BSD5 are rod-shaped (bacilli). Gram staining results indicate that BSA2, BSA8, and BSD5 belong to the Gram-positive group, as shown by their purple staining. In contrast, BSD7 is the only isolate classified as Gram-negative, indicated by the red coloration of its cells under microscopic observation. In terms of motility, isolates BSA8, BSD5, and BSD7 are motile (+), while BSA2 is non-motile (-). The catalase test revealed that BSA8, BSD5, and BSD7 produce catalase (+). Conversely, BSA2 exhibited a negative catalase reaction, as indicated by the absence of bubble formation. Observation of endospore formation was performed using Schaeffer–Fulton staining, which employs Malachite Green as the primary dye for spores and safranin as a counterstain for vegetative cells. The results showed that only BSD5 formed endospores, indicated by green staining of the spore structures and red staining of the vegetative cells.

Carbohydrate fermentation tests showed that BSA2 and BSD7 could ferment glucose, sucrose, and lactose, as indicated by positive (+) results for all three sugars. In contrast, BSA8 and BSD5 could ferment only glucose. In the other hand, in results of TSIA test showed that BSA2, BSA8, and BSD7 produced A/A results, indicating their ability to ferment both glucose and lactose/sucrose, whereas BSD5 showed a K/A result, indicating glucose fermentation only.

The indole test, performed using SIM medium containing tryptophan and Kovac's reagent, revealed that BSA2 and BSA8 tested positive (+) for indole production, as shown by the formation of a red ring on the medium's surface. BSD5 and BSD7 tested negative (–), indicated by a yellow ring.

In the citrate test with Simmons' Citrate Agar, isolates BSA8, BSD5, and BSD7 showed positive results, as indicated by a change in media color from green to blue. At the same time, isolate BSA2 showed negative results, as indicated by the media remaining green. On the other hand, the four isolates showed positive results in the MR test, marked by a change in colour to red after the addition of methyl red. In the VP test, all four isolates showed no change thus they were all considered negative.

DISCUSSION

Cellulolytic bacteria were isolated from feces of two different types of Senduro goat ages, lambs and adult goats. The abundance of bacterial colonies in kid goat feces samples was 6.45×10^7 CFU/g, while the abundance of bacterial colonies in adult goat feces samples was 8.15×10^7 CFU/g. Adult goats generally have a more developed and diverse digestive system compared to kid goats. As they age, goats undergo dietary changes and adapt to different feed types, which can increase the diversity and abundance of microorganisms in their digestive tracts. Adult goats tend to consume a more varied and fiber-rich diet, which supports the growth of cellulolytic bacteria that play a role in digesting cellulose. The rumen microbial community is known to be influenced by various factors, including diet, age, genetics, race, and geography (Ahmad *et al.,* 2020; Henderson *et al.,* 2015; Li *et al.,* 2019). Goat lambs have higher bacterial community diversity in the rumen and lower diversity in feces compared to adult goats (Luo *et al.,* 2022).

The results of the cellulase enzyme activity test qualitatively showed that the purified bacterial isolate formed a clear zone on CMC medium using the Congo red method. The clear zone produced on CMC media is due to the reaction of sodium benzidineindiazo-bis-1-naphthylamine-4-sulfonate (congo red), which binds strongly to β-1,4-glycosidic bonds in CMC (Arifin *et al.,* 2019). Cellulose hydrolysis products are simple monosaccharide sugars that do not form complex bonds with Congo red dye. The red color surrounding the clear zone indicates residual cellulose that has not been degraded. Optimal clear zone formation occurred after the media were rinsed with 1 M NaCl. The higher the cellulolytic activity index produced by the isolate, the greater its ability to degrade cellulose (Andriani *et al.,* 2020). The greater the hydrolytic ability of the isolate culture, the higher the cellulase enzyme production (Naresh *et al.,* 2019). Four isolates, namely BSD5, BSD7, BSA2, and BSA8, were selected for their ability to produce the highest cellulase levels, each showing a cellulolytic index above 2 (Choi *et al.,* 2005), at 3.1, 2.9, 2.2, and 2.2, respectively.

Based on the characterization results, isolate BSA2 has a coccus cell shape, is Gram-positive, is non-motile, does not form endospores, is negative for catalase, is positive for glucose, sucrose, and lactose, is TSIA A/A with a yellow slant and butt, is negative for H_2S, is positive for indole, is negative for citrate, is positive for MR, and is negative for VP. These characters have similarities with the genus of *Enterococcus*. According to research by Ismail *et al.* (2018), the genus of *Enterococcus* has characteristics such as Gram-positive, non-motile, coccus cells, negative catalase, TSIA with slopes and yellow media base (A/A) not accompanied by the presence of H_2S, positive sucrose, positive lactose, positive glucose, positive MR, and negative VP. *Enterococcus* is a facultative anaerobe; this bacterium uses free oxygen in the intestine to create anaerobic conditions that obligate intestinal anaerobic bacteria require (Malmuthuge *et al.,* 2015). This is in line with the statement of Holt *et al.* (1994) that bacteria with the genus *Enterococcus* have spherical or ovoid cells, endospores are not formed, gram positive, sometimes motile with few flagella, facultatively anaerobic, various kinds of carbohydrates are fermented, negative catalase, optimum temperature of 37 degrees, and widespread in various environments, one of which is vertebral feces.

Isolate BSA8 has characteristics including bacillus cell shape, Gram-positive, motile, does not form endospores, positive catalase, positive glucose, positive sucrose, positive lactose, TSIA A/A with yellow slant and yellow butt, positive indole, positive citrate, positive MR, and negative VP. The characteristics of the BSA8 isolate are similar to those of the genus *Cellulomonas*. *Cellulomonas* has characteristics such as Gram-positive, bacillus cell shape, positive catalase, positive motility, positive indole production, positive fermentation in glucose, lactose, and sucrose, negative H_2S production, and positive citrate utilization (Rahayu *et al.,* 2018; Ananda *et al.,* 2023). Based on Holt *et al.* (1994), young cultures of bacteria with the genus Cellulomonas in the form of slender, irregular, straight or slightly curved rods; rods are paired or form V formations, and occasionally branch. In old cultures, the stem shortens and a coccus forms. Gram-positive, sometimes motile with one or several flagella, does not form spores, facultatively anaerobic, able to produce acid from glucose and other carbohydrates, catalase positive, and cellulolytic.

Isolate BSD5 has characteristics including bacillus cell shape, Gram-positive, motile, forming endospores, positive catalase, positive glucose, negative sucrose, negative lactose, TSIA K/A with red slant and yellow butt, negative indole, positive citrate, positive MR, and negative VP. The characteristics of the BSD5 isolate are similar to those of the genus *Bacillus*, namely Gram-positive, motile, bacillus cells, negative catalase, negative indole, positive citrate, TSIA K/A with gas and no H_2S, negative sucrose, negative lactose, positive glucose, positive MR and negative VP (Fauziah & Ibrahim, 2020; Diarti, *et al.,* 2017). This is in line with the characteristics described by Holt *et al.* (1994), which describe

the genus Bacillus as having rod-shaped, straight cells, Gram-positive bacteria, motile, oval, round, or cylindrical endospores, and being either aerobic or facultatively anaerobic, with positive catalase activity. Endospores are a characteristic of the *Bacillus* genus that distinguishes it from other bacteria (Mukamto *et al*., 2015). In general, the *genus Bacill*us exhibits macroscopic characteristics such as white or cream-colored colonies, round or irregular shapes, and elevations that are usually flat or convex (Napitupulu *et al*., 2019).

Isolate BSD7 has characteristics including a coccus cell shape, Gram-negative, motile, does not form endospores, positive catalase, positive glucose, positive sucrose, negative lactose, TSIA A/A with a yellow slant and butt, negative Indole, positive citrate, positive MR, and negative VP. These characters are similar to those of the genus Alcaligenes, which has motile, coccus-shaped cells, positive catalase, positive glucose, negative lactose, negative sucrose, no gas production and H_2S, and positive citrate (Nisa *et al*., 2020). Based on Holt *et al.* (1994), the genus Alcaligenes is rod-shaped, Gram-negative, motile, obligately aerobic, catalase-positive, and does not produce indole.

CONCLUSION

Based on the results, eighteen isolates were obtained from feces samples of Senduro lambs and adult goats showing varying cellulolytic indices. Isolates BSD5, BSD7, BSA2, and BSA8 were the four isolates with the highest cellulolytic indices of 3.1, 2.9, 2.2, and 2.2, respectively. Based on the observed colony and cellular morphology, supported by biochemical characterisation, isolate BSD5 was similar to members of the genus *Bacillus*, BSD7 to *Alcaligenes*, BSA2 to *Enterococcus*, and BSA8 to *Cellulomonas*. Further study can be performed to identify the species of the isolates using molecular methods.

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CONFLICT OF INTEREST

There is no conflict of interest.

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