

**MOLECULAR IDENTIFICATION OF 16S RNA OF PATHOGENIC BACTERIA FROM THE WINGS OF FLESH FLIES (*Sarcophaga* sp.)  
INSPIRED BY THE HADITH OF THE PROPHET SAW,  
BUKHARI'S HISTORY ABOUT FLIES**

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**Abstract:** Meat flies (*Sarcophaga* sp.) are one of the vectors of infection. Meat flies often fly by using contact wings with legs so that the fly's flying area is very wide. This study uses qualitative and exploratory methods aimed at knowing the types of bacteria that can be found on the wings of meat flies (*Sarcophaga* sp.) through molecular identification. Samples were taken from the body parts of the right and left wings of meat flies, which were coded (B1) left wing of fly 1; (A2) right wing of fly 2; (B2) left wing of fly 2; (A3) right wing of fly 3; (B3) left wing of fly 3; (A4) right wing of fly 4; (B4) left wing of fly 4; (A5) right wing of fly 5; (B5) left wing of fly 5. Meat fly wings (*Sarcophaga* sp.) were inoculated on BHIB day NA medium, molecular identification day was done using 16S RNA. Based on molecular data, pathogenic bacteria were found in sample A5: *Bacillus cereus*, *B. anthracis*, and *B. tropicus*; and in sample B5, *Moellerella wisconsensis* was found. This research can provide a biological explanation of the hadith of the Prophet Muhammad (peace be upon him) about flies, indicating the presence of pathogenic bacteria on the wings of flesh flies (*Sarcophaga* sp.).

**Keywords:** Molecular identification; pathogenic bacteria; *Sarcophaga* sp.; fly wings

**Abstrak:** Lalat daging (*Sarcophaga* sp.) merupakan salah satu vektor berbagai penyakit infeksi. Lalat daging banyak bergerak dengan menggunakan sayap dibandingkan dengan kaki, sehingga area terbang lalat sangat luas. Penelitian ini menggunakan metode kualitatif dan eksploratif yang bertujuan untuk mengetahui jenis bakteri yang terdapat pada sayap lalat daging (*Sarcophaga* sp.) melalui identifikasi molekuler. Sampel diambil dari bagian tubuh lalat daging sayap kanan dan kiri yang diberi kode (B1) sayap kiri lalat 1; (A2) sayap kanan lalat 2; (B2) sayap kiri lalat 2; (A3) sayap kanan lalat 3; (B3) sayap kiri lalat 3; (A4) sayap kanan lalat 4; (B4) sayap kiri lalat 4; (A5) sayap kanan lalat 5; (B5) sayap kiri lalat 5. Sayap lalat daging (*Sarcophaga* sp.) diinokulasi pada medium BHIB dan NA, dan identifikasi molekuler menggunakan 16S RNA. Berdasarkan data molekuler ditemukan bakteri patogen pada sampel A5, yaitu *Bacillus cereus*, *B. anthracis*, dan *B. Tropicus*; pada sampel B5 ditemukan *Moellerella wisconsensis*. Hasil penelitian ini dapat membuktikan kebenaran hadits Rasulullah SAW tentang lalat dari

perspektif biologis dengan membuktikan adanya bakteri patogen yang ditemukan pada sayap lalat daging (*Sarcophaga* sp.).

**Kata kunci:** Identifikasi molekuler; Bakteri patogen; *Sarcophaga* sp; sayap lalat

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## Introduction

Inspired by the hadith contained in the Sahih Bukhary No. 5336, two studies have been carried out in the biology department of UIN Alauddin Makassar in 2016, concerning the identification of biochemical, microbiological, and molecular bacteria found on the left and right wing of house flies (*Musca domestica*), and research on bacterial identification in biochemistry, microbiology and molecular found on the left and right wings of green flies (*Chrysomya* sp.).

The fact that we obtained from the first study was that *B. cereus* bacteria were identified from the wings of the house fly (*M. domestica*). *Bacillus cereus* bacteria are pathogenic bacteria that can cause disease in human, these bacteria are able to produce spores that are resistant to heat and dehydration. Cases of poisoning that have occurred and have been reported to date are often associated with processed foods from vegetable flour such as pasta, rice, potatoes, bread and noodles (Ehling-Schulz, Lereclus, & Koehler, 2019). Another species, the flesh fly, or *Sarcophaga*, is a member of the family Sarcophagidae and the order Diptera, primarily distributed in Asia, including China, Thailand, Laos, and Sri Lanka (Monyama *et al.*, 2023; Nayduch *et al.*, 2023). Adults are potential vectors for the spread of pathogens, important in medicine and sanitation (Wang *et al.*, 2020).

In the second study, the results of 3 types of bacteria in the wings of green flies (*Chrysomya* sp.), namely *Acinetobacter baumannii*, *Escherichia coli* and *Pantoea agglomerans*. These 3 species of bacteria are pathogenic bacteria, which act as carrier vectors of a disease (Giermasińska-Buczek *et al.*, 2024; Kumar *et al.*, 2023; Yehya *et al.*, 2025). *A. baumannii* cause pneumonia, meningitis, septicemia, burns or surgical wounds (Li *et al.*, 2017). *E.coli* cause acute diarrhea (Zhou, 2018). *P. agglomerans* cause bacteremia, lower respiratory tract infections, skin infections, soft tissue infections, urinary tract infections, endocarditis, intraabdominal infections, septic arthritis, osteomyelitis, and eye infections (Hammed *et al.*, 2023; Kaur *et al.*, 2020; Mirtella *et al.*, 2021; Yamada *et al.*, 2017).

Based on the two studies, then an inspired exploration study of the Bukhary hadith was conducted on fly so many pathogenic bacteria that can cause disease in humans, while on the one hand flies are very close to human life . Bukhary Hadith seems to be an enlightenment that behind the pathogenic bacteria found in flies, it turns out that Allah has entrusted anti-bacteria to the other wing of the fly (Claresta

*et al.*, 2020; Mufid & Sattar, 2023). Scientifically this is very acceptable, given the fact that flies can live even with bacteria in their wings, meaning that the true designer has prepared anti-bacteria on the other wing.

This research is a The Development of Department because it is closely related to the Biology Department Vision, which is to become a place for civilization in the development of Biology science and its application based on biodiversity, imbued with the values of the Qur'an and Al-Hadith so that it gives birth to biologists who believe, have faith, are intelligent, independent and achievers ( <http://bio.fst.uin-alauddin.ac.id/visi> ).

## Methods

### Sample Preparation

The sample uses the right and left wings parts of the flesh fly body part of Meat flies (*Sarcophaga* sp.) The morphological characteristics of the flesh fly are a gray body with three longitudinal black lines on the thorax (back) and a checkered pattern on the abdomen (stomach), has striking red eyes, and a hairy body. Sampling was carried out in a sterile way. The fly wing is inserted into an eppendorf tube containing phosphate-buffered saline (PBS). The purpose of this technique in principle is to dissolve or release microbes from the substrate (Kumar *et al.*, 2023).

### Preparation Media

Nutrien Agar (NA) media is by dissolving 23 grams of NA powder into one liter of distilled water, the solution formed is put into a Schott bottle then mixed to homogeneous. Media NA was sterilized in autoclave for 15 minutes at 121 °C (C Idibie, 2018).

Media BHI (Brain Heart Infusion Broth). The manufacture of this media is by dissolving 7.4 grams of BHI powder into the 200 ml of distilled water, then homogenized. After that, put in test tube then the mouth of the tube is closed using dry cotton then put in clear plastic then tied tightly and labeled. After then sterilized for 15 minutes at 121°C in an autoclave then cooled and put in the refrigerator (Shankar *et al.*, 2018 ; Park *et a.l.*, 2019).

### Isolation of bacteria

A total of 5 flies, each fly separated from its body right wing and left wing so that 10 samples of fly wings are obtained meat (*Sarcophaga* sp.). The determination of the right and left wings is determined by following the direction of the fly's body. Samples were taken from the body parts of right and left wing flesh flies coded (B1) left wing fly 1; (A2) right wing of fly 2; (B2) left wing of fly 2; (A3) right wing of fly 3; (B3) left wing of fly 3; (A4) right wing of fly 4; (B4) left wing of fly 4; (A5) right wing of fly 5; (B5) left wing of fly 5. Each fly wing sample was put into an Eppendorf tube containing PBS is then inserted into the tube eppendorf containing BHI media. After that, it was incubated at 37°C for 24 hours. The culture of BHI will experience turbidity indicates bacterial growth. Samples

were propagated into the prepared media (NA media) to identify growing microbes (Troha & Buchon, 2019; Tonner, 2018).

## Molecular Identification

### *Polymerase Chain Reaction (PCR) Amplification*

The process includes 3 stages, namely denaturation at 95 °C for 30 seconds, annealing at 55 °C for 30 seconds and extension at 72 °C for 1 minute. 46 This procedure was performed on isolated DNA samples, extracting DNA from the sample and aquadest as a negative control. "PCR mix" is inserted into the PCR tube:

**Table 1.** Property of Primer Mix

Reaction	( $\mu$ l)
ddH <sub>2</sub> O	34.75
10X PCR buffer	5
25 mM MgCl	2.2
5 mM Dntp	1
Reverse primer (20pmol)	1
Forward primer (20pmol)	1
Hotstart DNA pol.	0.25
DNA sample	5
Total premix	50

Amplification is done using a PCR machine (DNA thermal Cycler). For PCR amplification, the initial stages of denaturation at 95 °C for 15 minutes, then 94 °C for 1 minute, annealing at 55 °C for 30 seconds, extension of 72 °C for 1 minute as many as 40 cycles followed by a final extension of 72 °C for 5 minutes and 12°C  $\pm$  30 minutes for storage (Mordechai, 1999).

### *Agarose gel electrophoresis*

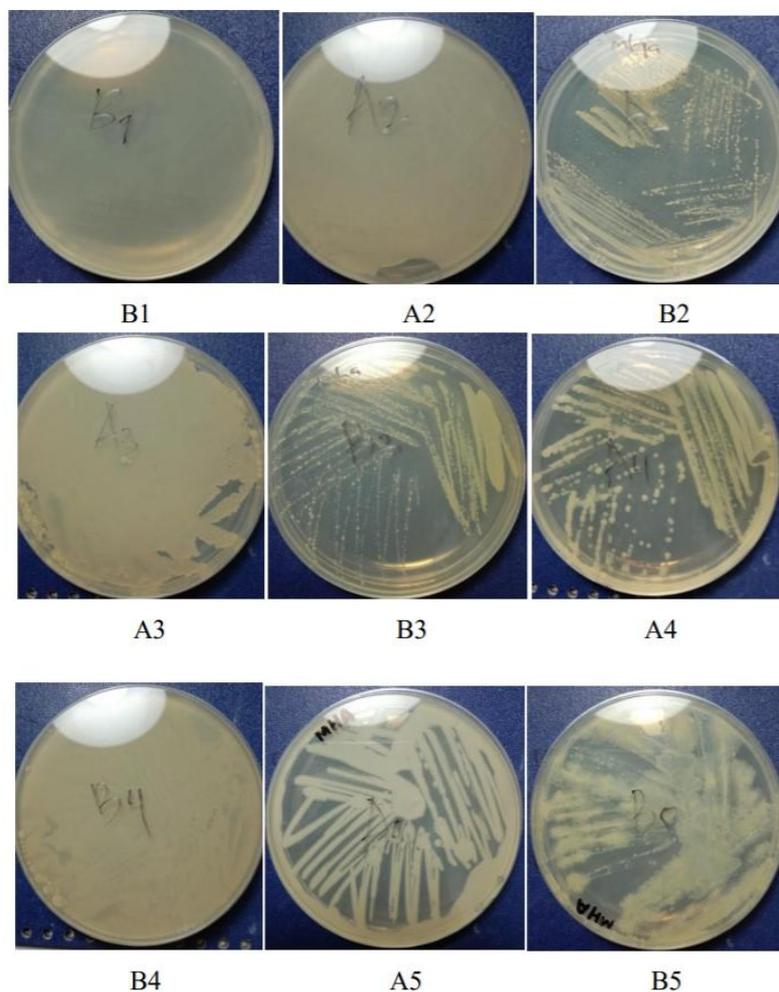
Agarosa is made by dissolving 2 g of agarose (BioRad) in 100 ml of 0.5 x Tris borate EDTA (100 g Tris base, 27.5 g boric acid, 20 ml 0.5 M EDTA pH 8.047 in 1 liter of water). Then it is heated to boiling and dissolves. Then added 1  $\mu$ l of ethidium bromide (0.2  $\mu$ g / ml) and put it in a comb-mounted gel printer. After agarose solidifies (about 30 minutes) then put it in an electrophoresis tank containing 0.5% TBE solution. Enter the sample DNA which has been mixed with a "loading dye" liquid into the well with a ratio of 2: 1, then put a 100 bp marker after the entire sample is inserted. The electrode is connected to the power supply and then turned on for 1 hour + voltage of 100 volts, 400 Ampere. After that, the electrophoresis device is turned off then the gel from the device is taken. The gel is transferred into the UV trans illuminator then the results are observed on the computer. The size of the PCR amplification fragment was determined by comparing the position of the DNA marker size (Marker) with the size of the sample fragment. Positive results are indicated by the presence of a band at 996 bp (Mordechai, 1999).

### Sequencing Data Analysis

Sequencing data analysis is done using DNA star software program. For sequence alignment analysis, it is done by comparing the queries obtained with those already in the Gene Bank with the NCBI internet searches database (<http://www.ncbi.nlm.nih.gov> ) using BLAST (Basic Local Alignment Search Tool).

### Results and Discussion

Bacteria isolation in wings of flesh flies *Sarcophaga* sp. The results obtained were 9 isolates, namely B1, A2, B2, A3, B3, A4, B4, A5, B5 and 1 sample had no bacterial colony growth, namely A1.



**Figure 1.** The results of the bacterial culture of the wings of the flesh fly (*Sarcophaga* sp.) on media NA: (B1) left wing of fly 1; (A2) fly right wing 2; (B2) fly left wing 2; (A3) fly right wing 3; (B3) fly's left wing 3; (A4) fly right wing 4; (B4) fly's left wing 4; (A5) right wing fly 5; (B5) fly left wing 5.

A total of 5 meat flies (*Sarcophaga* sp.) were separated from the right wing (A) and left wing (B) so that 10 samples of the meat fly wing (*Sarcophaga* sp.) were

obtained. Then each sample was dipped into an Eppendorf tube containing PBS (Phosphate Buffer Saline). PBS is a solution containing Potassium Chloride, Potassium Phosphate, Sodium Chloride, Sodium Phosphate dissolved in distilled water. PBS is a buffer solution that functions to maintain and maintain cell pH and osmolarity levels, a physiological solution that is isotonic and non-toxic to cells (Mai-Prochnow *et al.*, 2016).

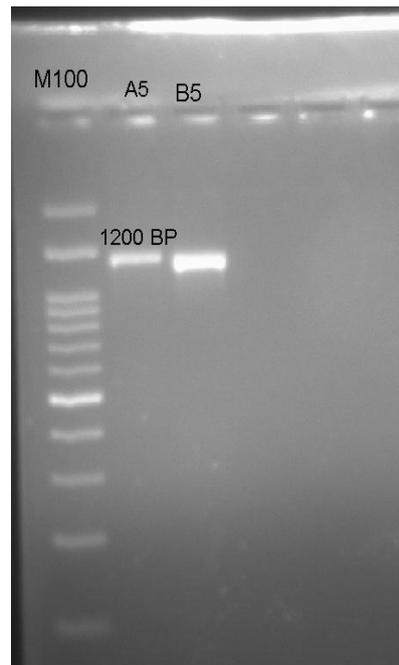
Based on the observation of bacterial isolation, it was found that there was bacterial growth on NA media, namely isolates B1, A2, B2, A3, B3, A4, B4, A5, B5. This is because NA media contains the main compounds that support the growth and development of bacterial cells. Meat extract and peptone are broken down into glucose, amino acids and minerals which are the main components of bacterial cell membranes and organelles (Mohamed *et al.*, 2016).

After the isolation of the bacteria, the colony morphology was observed by looking at the shape and color of each sample, then Gram staining was performed and observed under a microscope with a certain magnification. Gram staining is carried out with the aim of identifying the bacteria obtained so that they can be distinguished from Gram positive bacteria or Gram negative bacteria (Bayonova, 2018; Chandrakasan *et al.*, 2026; Lainjong *et al.*, 2021; Yanestria *et al.*, 2019).

Based on observations of colony morphology and gram staining, the suspected bacteria obtained were isolates B1, A3, B3, A4, A5 and B5, suspected to be *Bacillus* sp. Meanwhile, isolates A2, B2 and B4 were suspected to be *Staphylococcus* sp.

#### *Molecular Identification of Pathogenic Bacteria*

The results of the analysis of the molecular weight of bacterial DNA contained in the wings of the meat fly (*Sarcophaga* sp.) can be shown in Figure 2. The success of the DNA and PCR isolation processes will be seen in the electrophoresis results, where the DNA sequences will have bright bands after being visualized using UV light. The results of electrophoresis obtained on samples A5 and B5 are the presence of DNA bands that have the same size with a length of 1200 bp, so that the bacterial DNA amplification process was successfully carried out.



**Figure 2.** Electrophoresis results visible on Gel doc: M (marker); A5 (left-wing sample); B5 (right wing sample)

The next identification is molecular identification where the steps taken are extraction, amplification and electrophoresis. The purpose of extraction is to obtain high-quality DNA through several stages, namely sample preparation, cell splitting (lysis), DNA binding, DNA washing, and DNA elution. The purpose of amplification using the PCR technique is to multiply pieces of DNA up to millions of times in a relatively short time with several stages, namely denaturation, annealing and extension. The purpose of electrophoresis using agarose gel is to determine the size of DNA fragments from PCR products (Godbey, 2022; Roume *et al.*, 2013; Wittmeier & Hummel, 2022).

After that, the sequencing process was carried out on the results of DNA amplification. To see the bacterial species, a sequencing process was carried out on the amplification results obtained. Sequencing data from Malaysia in the form of an electropherogram which will be translated into a sequence of nucleotide bases for bacterial samples using the DNA start program. The results of this analysis are the nucleotide base sequences of the 16S rRNA gene from bacterial isolates on the wings of the meat fly (*Sarcophaga* sp.). In the amplification process, the 16S rRNA gene primer was used which served as a limiter for the specific sequence of the 16S rRNA gene that initiated the polymerization reaction (Jagielski, 2018; Kundu *et al.*, 2024; Santosa *et al.*, 2024;). The sequence of nucleotide results can be seen in Figure 4 (a-b), and Figure 5 (a-b).

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*Bacillus cereus* strain VBE41 16S ribosomal RNA gene, partial sequence  
Sequence ID: [MG027637.1](#) Length: 1456 Number of Matches: 1

Range 1: 33 to 1302 [GenBank](#) [Graphics](#) [Next Match](#) [Prev](#)

Score	Expect	Identities	Gaps	Strand
2244 bits(1215)	0.0	1252/1270(99%)	6/1270(0%)	Plus/Plus
Query 12	CTTCTCTTATGAA-TTAAAGGGGGACGGGTGAGTAAACAGTGGTAACCTGCCATAAG	70		
Sbjct 33	CTTCTCTTATGAAAGTTAGCGGGACGGGTGAGTAAACAGTGGTAACCTGCCATAAG	92		
Query 71	ACTGGGATAACTCCGGGAAACC GGGGCTAAATACCGGATACATTTTGAACCGCATGGTTC	130		
Sbjct 93	ACTGGGATAACTCCGGGAAACC GGGGCTAAATACCGGATACATTTTGAACCGCATGGTTC	152		
Query 131	GAAATGAAAGCGGCTTCGGCTGCTACTTATGGATGGACCCGCTGCATTAGCTAGT	190		
Sbjct 153	GAAATGAAAGCGGCTTCGGCTGCTACTTATGGATGGACCCGCTGCATTAGCTAGT	212		
Query 191	GGTGGGTAACGGCTCACCAAGGCAACGATCGTAGCCGACCTGAGAGGGGTGATCGGCCA	250		
Sbjct 213	GGTGGGTAACGGCTCACCAAGGCAACGATCGTAGCCGACCTGAGAGGGGTGATCGGCCA	272		
Query 251	CAC TGGGACTGAGACAGCCCGACCTCTACGGGAGGACGATAGGGAATCTTCCGCA	318		
Sbjct 273	CAC TGGGACTGAGACAGCCCGACCTCTACGGGAGGACGATAGGGAATCTTCCGCA	330		
Query 311	ATGGACGAAAGTCTGACGGAGCAACCGCCGCTGAGTGAAGGCTTCGGGCTGTAATA	370		
Sbjct 333	ATGGACGAAAGTCTGACGGAGCAACCGCCGCTGAGTGAAGGCTTCGGGCTGTAATA	392		
Query 371	CTCTGTGTAGGGAGAAAGCTAGTGTGTAATAAGCTGGACCTTGCAGCTACCTAA	430		
Sbjct 393	CTCTGTGTAGGGAGAAAGCTAGTGTGTAATAAGCTGGACCTTGCAGCTACCTAA	452		
Query 431	CCAGAAGCCACGGCTAACCTAGCTGCACAGCCGGGTAAATACGTAGTGGCAAGCGTT	490		
Sbjct 453	CCAGAAGCCACGGCTAACCTAGCTGCACAGCCGGGTAAATACGTAGTGGCAAGCGTT	512		
Query 491	ATCCGGAATATTGGGCGTAAAGCGCCGCGAGGTGGTTCTTAAGTCTGATGTGAAAGCC	550		
Sbjct 513	ATCCGGAATATTGGGCGTAAAGCGCCGCGAGGTGGTTCTTAAGTCTGATGTGAAAGCC	572		
Query 551	CACGGCTCAACGGTGGAGGCTATGGAACTGGGAGCTTGAAGTGCAGAGGAAAGT	610		
Sbjct 573	CACGGCTCAACGGTGGAGGCTATGGAACTGGGAGCTTGAAGTGCAGAGGAAAGT	632		
Query 611	GGAAATTCATGTAGCGGTAATCGTAGAGATATGGAGAACACCGTGGCGAAGGC	670		
Sbjct 633	GGAAATTCATGTAGCGGTAATCGTAGAGATATGGAGAACACCGTGGCGAAGGC	692		
Query 671	GACTTTCTGGTCTGTAACGACACTGAGCGCGCAAGGCTGGGGAGCAACAGGATAGA	730		
Sbjct 693	GACTTTCTGGTCTGTAACGACACTGAGCGCGCAAGGCTGGGGAGCAACAGGATAGA	752		
Query 731	TACCTCTGTAGTCAACGGTAAAGCATGAGTGTAAAGTGTAGAGGGTTTCCGCCCTT	790		
Sbjct 753	TACCTCTGTAGTCAACGGTAAAGCATGAGTGTAAAGTGTAGAGGGTTTCCGCCCTT	812		
Query 791	AGTCTGAAATTAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	850		
Sbjct 813	AGTCTGAAATTAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	872		
Query 851	CAAAGGAATTTGACGGGGCCCGCACAAAGCGGTGGAGCATGGTTAATTGCAAGCAAC	910		
Sbjct 873	CAAAGGAATTTGACGGGGCCCGCACAAAGCGGTGGAGCATGGTTAATTGCAAGCAAC	932		
Query 911	CGAAGAACCTTACAGGCTTGCATCTCTGACAAACCTAGAGATAGGGCTTCTCTTC	970		
Sbjct 933	CGAAGAACCTTACAGGCTTGCATCTCTGACAAACCTAGAGATAGGGCTTCTCTTC	992		
Query 971	GGGAGCAGAGTACAGGTTGGTATGGTTGCTGACGCTGCTGCTGAGATGTTGGGT	1030		
Sbjct 993	GGGAGCAGAGTACAGGTTGGTATGGTTGCTGACGCTGCTGCTGAGATGTTGGGT	1052		
Query 1031	AAAGTCCCGCAAGCGGCGCAACCTTGAATCTAGTTGCTCATTAAGTTGGGCACTTAA	1090		
Sbjct 1053	AAAGTCCCGCAAGCGGCGCAACCTTGAATCTAGTTGCTCATTAAGTTGGGCACTTAA	1112		
Query 1091	GGTACTGCGCGTACAAACCGGAGGAAAG-GGGGATGACGCT-AATCATCTGCCCT	1148		
Sbjct 1113	GGTACTGCGCGTACAAACCGGAGGAAAGTGGGATGACGCTCAATCATCTGCCCT	1172		
Query 1149	TATGACCTGGGCTACCAAGGTGTACAATGGACGGTACAAAAGCTGCAAGACC-CG	1207		
Sbjct 1173	TATGACCTGGGCTACCAAGGTGTACAATGGACGGTACAAAAGCTGCAAGACC-CG	1232		
Query 1208	GGGAACATAATCCA-AAAAAGCTTCCAGTTCGGATGGAGGCTGCANNITCCGCTAC-TG	1265		
Sbjct 1233	GGGAACATAATCCA-AAAAAGCTTCCAGTTCGGATGGAGGCTGCANNITCCGCTAC-TG	1292		
Query 1266	AAACTGGAAT 1275			
Sbjct 1293	AAGCTGGAAT 1302			

a.

*Bacillus anthracis* strain ES-12 16S ribosomal RNA gene, partial sequence  
Sequence ID: [KY649403.1](#) Length: 1439 Number of Matches: 1

Range 1: 31 to 1300 [GenBank](#) [Graphics](#) [Next Match](#) [Prev](#)

Score	Expect	Identities	Gaps	Strand
2244 bits(1215)	0.0	1252/1270(99%)	5/1270(0%)	Plus/Plus
Query 11	ACTTGTCTTATGAA-TTAAAGGGGGACGGGTGAGTAAACAGTGGTAACCTGCCATAA	69		
Sbjct 31	ACTTGTCTTATGAAAGTTAGCGGGACGGGTGAGTAAACAGTGGTAACCTGCCATAA	90		
Query 70	GACTGGGATAACTCCGGGAAACC GGGGCTAAATACCGGATAAATTTTGAACCGCATGGT	129		
Sbjct 91	GACTGGGATAACTCCGGGAAACC GGGGCTAAATACCGGATAAATTTTGAACCGCATGGT	150		
Query 130	CGAATGAAAGCGGCTTCGGCTGCTACTTATGGATGGACCCGCTGCATTAGCTAGT	189		
Sbjct 151	CGAATGAAAGCGGCTTCGGCTGCTACTTATGGATGGACCCGCTGCATTAGCTAGT	210		
Query 190	TGTTGAGTAAACGGCTCACCAAGGCAACGATCGTAGCCGACCTGAGAGGGGTGATCGGCC	249		
Sbjct 211	TGTTGAGTAAACGGCTCACCAAGGCAACGATCGTAGCCGACCTGAGAGGGGTGATCGGCC	270		
Query 250	ACACTGGGACTGAGACAGCCCGACCTTACGGGAGGACGATAGGGAATCTTCCGC	309		
Sbjct 271	ACACTGGGACTGAGACAGCCCGACCTTACGGGAGGACGATAGGGAATCTTCCGC	330		
Query 310	AATGGACGAAAGTCTGACGGAGCAACCGCCGCTGAGTGAAGGCTTCGGGCTGTAATA	369		
Sbjct 331	AATGGACGAAAGTCTGACGGAGCAACCGCCGCTGAGTGAAGGCTTCGGGCTGTAATA	390		
Query 370	ACTCTGTTGTAGGGAAAGCAAGTGTAGTGAATAAGCTGGACCTTGCAGCTACCTA	429		
Sbjct 391	ACTCTGTTGTAGGGAAAGCAAGTGTAGTGAATAAGCTGGACCTTGCAGCTACCTA	450		
Query 430	ACCAGAAGCCACGGCTAACCTAGCTGCACAGCCGGTAAATACGTAGTGGCAAGCGT	489		
Sbjct 451	ACCAGAAGCCACGGCTAACCTAGCTGCACAGCCGGTAAATACGTAGTGGCAAGCGT	510		
Query 490	TATCCGGAATATTGGGCGTAAAGCGCCGCGAGGTGGTTCTTAAGTCTGATGTGAAAGCC	549		
Sbjct 511	TATCCGGAATATTGGGCGTAAAGCGCCGCGAGGTGGTTCTTAAGTCTGATGTGAAAGCC	570		
Query 550	CCACGGCTCAACGGTGGAGGCTATTGGAACCTGGGAGCTTGAAGTGCAGAGGAAAG	609		
Sbjct 571	CCACGGCTCAACGGTGGAGGCTATTGGAACCTGGGAGCTTGAAGTGCAGAGGAAAG	630		
Query 610	TGGAATTCATGTAGCGGTAAATGCTAGAGATATGGAGAACACCGTGGCGAAGG	669		
Sbjct 631	TGGAATTCATGTAGCGGTAAATGCTAGAGATATGGAGAACACCGTGGCGAAGG	690		
Query 670	CGACTTTCTGGTCTGTAACGACACTGAGCGCGCAAGGCTGGGGAGCAACAGGATAG	729		
Sbjct 691	CGACTTTCTGGTCTGTAACGACACTGAGCGCGCAAGGCTGGGGAGCAACAGGATAG	750		
Query 730	ATACCTCTGTAGTCAACGGTAAAGCATGAGTGTAAAGTGTAGAGGGTTTCCGCCCTT	789		
Sbjct 751	ATACCTCTGTAGTCAACGGTAAAGCATGAGTGTAAAGTGTAGAGGGTTTCCGCCCTT	810		
Query 790	TAGTCTGAAATTAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	849		
Sbjct 811	TAGTCTGAAATTAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	870		
Query 850	TCAAAGGAATTTGACGGGGCCCGCACAAAGCGGTGGAGCATGGTTAATTGCAAGCAAC	909		
Sbjct 871	TCAAAGGAATTTGACGGGGCCCGCACAAAGCGGTGGAGCATGGTTAATTGCAAGCAAC	930		
Query 910	GCAGAAGAACCTTACAGGCTTGCATCTCTGACAAACCTAGAGATAGGGCTTCTCTTC	969		
Sbjct 931	GCAGAAGAACCTTACAGGCTTGCATCTCTGACAAACCTAGAGATAGGGCTTCTCTTC	990		
Query 970	GGGAGCAGAGTACAGGTTGGTATGGTTGCTGACGCTGCTGCTGAGATGTTGGGT	1029		
Sbjct 991	GGGAGCAGAGTACAGGTTGGTATGGTTGCTGACGCTGCTGCTGAGATGTTGGGT	1050		
Query 1030	TAAGTCCCGCAAGCGGCGCAACCTTGAATCTAGTTGCTCATTAAGTTGGGCACTTAA	1089		
Sbjct 1051	TAAGTCCCGCAAGCGGCGCAACCTTGAATCTAGTTGCTCATTAAGTTGGGCACTTAA	1110		
Query 1090	AGGTACTGCGCGTACAAACCGGAGGAAAGGGGATGACGCT-AATCATCTGCCCT	1148		
Sbjct 1111	AGGTACTGCGCGTACAAACCGGAGGAAAGTGGGATGACGCTCAATCATCTGCCCT	1170		
Query 1149	TATGACCTGGGCTACCAAGGTGTACAATGGACGGTACAAAAGCTGCAAGACC-CG	1207		
Sbjct 1171	TATGACCTGGGCTACCAAGGTGTACAATGGACGGTACAAAAGCTGCAAGACC-CG	1230		
Query 1208	GGGAACATAATCCA-AAAAAGCTTCCAGTTCGGATGGAGGCTGCANNITCCGCTAC-TG	1265		
Sbjct 1231	GGGAACATAATCCA-AAAAAGCTTCCAGTTCGGATGGAGGCTGCANNITCCGCTAC-TG	1290		
Query 1266	AAACTGGAAT 1275			
Sbjct 1291	AAGCTGGAAT 1300			

b.

**Figure 4.** Comparison of the base sequence of sample (a). A5 with *Bacillus cereus* and (b). *Bacillus anthracis*

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Bacillus tropicus strain ISP161A 16S ribosomal RNA gene, partial sequence  
Sequence ID: [MT611943.1](#) Length: 1467 Number of Matches: 1

Range 1: 66 to 1334 [GenBank](#) [Graphics](#) [Next Match](#)

Score	Expect	Identities	Gaps	Strand
2242 bits(1214)	0.0	1251/1269(99%)	5/1269(0%)	Plus/Plus
Query 12	CTTGTCTTATGAA-TTAGCGCCGACGGGTGAGTAAACGTGGGTAACTGCCATAAG	70		
Sbjct 66	CTTGTCTTATGAA-TTAGCGCCGACGGGTGAGTAAACGTGGGTAACTGCCATAAG	125		
Query 71	ACTGGGTAACCTCCGGAAACGGGGCTAATACCGGATACCAATTTGAACCGCATGGTTC	130		
Sbjct 126	ACTGGGTAACCTCCGGAAACGGGGCTAATACCGGATACCAATTTGAACCGCATGGTTC	185		
Query 131	GAATTGAAGGCGGCTTGGCTGTCACTTATGATGACCCGCGCATAGTGTAGTT	190		
Sbjct 186	GAATTGAAGGCGGCTTGGCTGTCACTTATGATGACCCGCGCATAGTGTAGTT	245		
Query 191	GGTGAAGTAAACGGCTCAACAGGCAACGATGCTGAGCCGACCTGAGAGGGTATCGCCCA	250		
Sbjct 246	GGTGAAGTAAACGGCTCAACAGGCAACGATGCTGAGCCGACCTGAGAGGGTATCGCCCA	305		
Query 251	CACCTGGCACTGAGACACGGCCAGACTCCACGGGAGGACAGTAGGGAATCTCCCGCA	310		
Sbjct 306	CACCTGGCACTGAGACACGGCCAGACTCCACGGGAGGACAGTAGGGAATCTCCCGCA	365		
Query 311	ATGGACGAAGTCTGACGGAGCAACCCCGCTGAGTGAATGAAGGCTTTCGGTCTGAAAA	370		
Sbjct 366	ATGGACGAAGTCTGACGGAGCAACCCCGCTGAGTGAATGAAGGCTTTCGGTCTGAAAA	425		
Query 371	CTCTGTTTAGGGAAGAACAGTGTCTGTAATAAGCTGGCACTTACGGTACCTAA	430		
Sbjct 426	CTCTGTTTAGGGAAGAACAGTGTCTGTAATAAGCTGGCACTTACGGTACCTAA	485		
Query 431	CCAGAAGCAACGGCTCAACTACGTGCAGCAGCCGCTAATACGTAGGTGGCAAGCGTT	490		
Sbjct 486	CCAGAAGCAACGGCTCAACTACGTGCAGCAGCCGCTAATACGTAGGTGGCAAGCGTT	545		
Query 491	ATCCGGAAATTAATGGGCTAAAGCCGCGCAGGTGTTCTTAAGTCTGATGTAAGGCC	550		
Sbjct 546	ATCCGGAAATTAATGGGCTAAAGCCGCGCAGGTGTTCTTAAGTCTGATGTAAGGCC	605		
Query 551	CACGGCTCAACCTGGAGGGCTATTGAAACTGGAGACTTGAAGTCAGAAAGGAAAGT	610		
Sbjct 606	CACGGCTCAACCTGGAGGGCTATTGAAACTGGAGACTTGAAGTCAGAAAGGAAAGT	665		
Query 611	GGAAATTCATGTGATAGCGTAATGCGTAGAGATATGGAGAAACCAAGTGGCAAGGC	670		
Sbjct 666	GGAAATTCATGTGATAGCGTAATGCGTAGAGATATGGAGAAACCAAGTGGCAAGGC	725		
Query 671	GACTTTCTGGTCTGTAATGACACTGAGGCGCGAAAGCGTGGGAGCAACAGGATAGA	730		
Sbjct 726	GACTTTCTGGTCTGTAATGACACTGAGGCGCGAAAGCGTGGGAGCAACAGGATAGA	785		
Query 731	TACCTGGTAGTCCACCGCTAAACGATGATGCTAAGTGTAGAGGGTTTCGCCCTTT	790		
Sbjct 786	TACCTGGTAGTCCACCGCTAAACGATGATGCTAAGTGTAGAGGGTTTCGCCCTTT	845		
Query 791	AGTCTGAAGTAAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	850		
Sbjct 846	AGTCTGAAGTAAACGATTAAGCACTCCGCTGGGGAGTACGGCCGCAAGGCTGAAACT	905		
Query 851	CAAAGGAATTGACGGGGCCCGCAACAGCGGTGGAGCATGTGGTTAAATTCGAAGCAACG	910		
Sbjct 906	CAAAGGAATTGACGGGGCCCGCAACAGCGGTGGAGCATGTGGTTAAATTCGAAGCAACG	965		
Query 911	CGAAGAACCTTACAGGCTTGGACATCTCTGACAAACCTAGAGATAGGGCTTCTCCCTC	970		
Sbjct 966	CGAAGAACCTTACAGGCTTGGACATCTCTGACAAACCTAGAGATAGGGCTTCTCCCTC	1025		
Query 971	GGGAGCAGAGTGACAGGTGGTGTGATGGTGTCTGCTGCTGCTGCTGAGATGTTGGGTT	1030		
Sbjct 1026	GGGAGCAGAGTGACAGGTGGTGTGATGGTGTCTGCTGCTGCTGCTGAGATGTTGGGTT	1085		
Query 1031	AAGTCCCGCAACGAGCGCAACCTTATCTTAGTGGCATCATTAAAGTTGGGCACTCAA	1090		
Sbjct 1086	AAGTCCCGCAACGAGCGCAACCTTATCTTAGTGGCATCATTAAAGTTGGGCACTCAA	1145		
Query 1091	GGTGACTGCCGTTGACAAACGGGAAAGGGGGGATGACGTC-AATCATCATECCCTT	1149		
Sbjct 1146	GGTGACTGCCGTTGACAAACGGGAAAGGGGGGATGACGTC-AATCATCATECCCTT	1205		
Query 1150	ATGACTGGGCTACCAACGCTGCTACAATGGACGGTACAAAAGCTGCAAGACCGC-AGGG	1208		
Sbjct 1206	ATGACTGGGCTACCAACGCTGCTACAATGGACGGTACAAAAGCTGCAAGACCGC-AGGG	1265		
Query 1209	GGAACTAATTC-AAAACCGTCCAGTTCGGATTGGAGGCTGCANNITGCTAC-TGA	1266		
Sbjct 1266	GGAACTAATTC-AAAACCGTCCAGTTCGGATTGGAGGCTGCANNITGCTAC-TGA	1325		
Query 1267	AACCTGGAAAT 1275			
Sbjct 1326	AGCTGGAAAT 1334			

Moellerella wisconsensis strain 95B-1 16S ribosomal RNA gene, partial sequence  
Sequence ID: [KY400229.1](#) Length: 1403 Number of Matches: 1

Range 1: 17 to 1253 [GenBank](#) [Graphics](#) [Next Match](#) [Pr](#)

Score	Expect	Identities	Gaps	Strand
2206 bits(1194)	0.0	1225/1240(99%)	4/1240(0%)	Plus/Plus
Query 7	GAA-AAGCTTGTCTTTTCTGACGAGCGGGGACGGGTGAGTAAATGATGGGATCTGC	65		
Sbjct 17	GAAGAAGCTTGTCTTTTCTGACGAGCGGGGACGGGTGAGTAAATGATGGGATCTGC	76		
Query 66	CTGACAGAGGGGATAACTACTGGAACGGTAGCTAATACCGATAATCTTAAGGACCA	125		
Sbjct 77	CTGACAGAGGGGATAACTACTGGAACGGTAGCTAATACCGATAATCTTAAGGACCA	136		
Query 126	AAGCAGGGGACCTTCCGGCTCCGGCTGTCGGATGAACCATATGGGATAGCTAGTAGG	185		
Sbjct 137	AAGCAGGGGACCTTCCGGCTTCCGGCTGTCGGATGAACCATATGGGATAGCTAGTAGG	196		
Query 186	TGAGTAAATGGCTCACTAGGCGACGATCTAGCTGGTCTGAGAGGATGATCAGCCACA	245		
Sbjct 197	TGAGTAAATGGCTCACTAGGCGACGATCTAGCTGGTCTGAGAGGATGATCAGCCACA	256		
Query 246	CTGGACTGACACACGGCCAGACTCCCTACGGGAGGACAGTGGGGAATATGCAACAT	305		
Sbjct 257	CTGGACTGACACACGGCCAGACTCCCTACGGGAGGACAGTGGGGAATATGCAACAT	316		
Query 306	GGGCGCAAGCTGATGACGATCCGCGCTGATGAAGAAGGCCCTAGGGTGTAAAGTA	365		
Sbjct 317	GGGCGCAAGCTGATGACGATCCGCGCTGATGAAGAAGGCCCTAGGGTGTAAAGTA	376		
Query 366	CTTTCACTGGGAGGAGGGCTTGATATTAATCTATCAGCGATTGACGTTACCGACAGA	425		
Sbjct 377	CTTTCACTGGGAGGAGGGCTTGATATTAATCTATCAGCGATTGACGTTACCGACAGA	436		
Query 426	AGAAGCACCGGCTAACTCCGTCGACAGCCGCGGTAATACGGGGGTGCAAGCGTTAAT	485		
Sbjct 437	AGAAGCACCGGCTAACTCCGTCGACAGCCGCGGTAATACGGGGGTGCAAGCGTTAAT	496		
Query 486	CGGAATTAATGGGCAAAAGCCAGCGAGCGGGTGGATTAAGTGTAGATGAAATCCCG	545		
Sbjct 497	CGGAATTAATGGGCAAAAGCCAGCGAGCGGGTGGATTAAGTGTAGATGAAATCCCG	556		
Query 546	GGCTTAACTGGGAAATGCACTAAAACCTGGTCAAGTAGAGTCTTGAAGGGGGTAGA	605		
Sbjct 557	GGCTTAACTGGGAAATGCACTAAAACCTGGTCAAGTAGAGTCTTGAAGGGGGTAGA	616		
Query 606	ATTCATGTAGTGGGTAAGTCCGTAGAGATGTTGGAGAAATCCGGTGGCAAGCGGC	665		
Sbjct 617	ATTCATGTAGTGGGTAAGTCCGTAGAGATGTTGGAGAAATCCGGTGGCAAGCGGC	676		
Query 666	CCCCGGCAAAAGCTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATAGATAC	725		
Sbjct 677	CCCCGGCAAAAGCTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATAGATAC	736		
Query 726	CCTGTAGTCCACGCTGATAAAGATGCTGATTTGGAGTGTCCCTTGGAGGTGGCTT	785		
Sbjct 737	CCTGTAGTCCACGCTGATAAAGATGCTGATTTGGAGTGTCCCTTGGAGGTGGCTT	796		
Query 786	CCGGAGCTAACCGGTTAAATGACCGCTGGGAGTACGGCCGCAAGGTTAAAACCTAAA	845		
Sbjct 797	CCGGAGCTAACCGGTTAAATGACCGCTGGGAGTACGGCCGCAAGGTTAAAACCTAAA	856		
Query 846	TGAAATGACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTAAATTCGATGCAACGGAA	905		
Sbjct 857	TGAAATGACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTAAATTCGATGCAACGGAA	916		
Query 906	GAACCTTACTACTCTTGACATCCAGAGAATTAAGCAGAGATGCTTAGTGCTCCGGGA	965		
Sbjct 917	GAACCTTACTACTCTTGACATCCAGAGAATTAAGCAGAGATGCTTAGTGCTCCGGGA	976		
Query 966	ACTCTGAGCAGGTGCTGATGGCTGTCTGCTGCTGCTGCTGAGATGTTGGGTTAAGT	1025		
Sbjct 977	ACTCTGAGCAGGTGCTGATGGCTGTCTGCTGCTGCTGCTGAGATGTTGGGTTAAGT	1036		
Query 1026	CCCCCAACGAGCGCAACCTTATCTTTGTTGCGCAGCATGCTGGTGGGAACCAAGGG	1085		
Sbjct 1037	CCCCCAACGAGCGCAACCTTATCTTTGTTGCGCAGCATGCTGGTGGGAACCAAGGG	1096		
Query 1086	AGACTGCCGTTGATAAACCAGGAGGAGTGGGATGACGCTCAAGTCAATCGGCCCTTAC	1145		
Sbjct 1097	AGACTGCCGTTGATAAACCAGGAGGAGTGGGATGACGCTCAAGTCAATCGGCCCTTAC	1156		
Query 1146	GAGTAGGGCTACCAACGTGCTCAATGGCGCATACAANGAAGAAACAAATTCGAGAA	1205		
Sbjct 1157	GAGTAGGGCTACCAACGTGCTCAATGGCGCATACAANGAAGAAACAAATTCGAGAA	1214		
Query 1206	CCAGCGGAACCTTAAAGTGGCTCTAATCCCGGATTTGGA 1245			
Sbjct 1215	CCAGCGGAACCTAATAAGTGGCTCTAATCCCGGATTTGGA 1253			

a.

b.

Figure 5. Comparison of base sequences of A5 sample with *Bacillus tropicus* bacteria (a), and sample B5 with *Moellerella wisconsensis* bacteria (b).

The isolate from sample A5 (Figure 4.a) obtained ranging from the order of 70 to 1275 corresponds to the sequence of *B. cereus* strains of the order of 92 to 1302. The strain of sample A5 (Figure 4.b) obtained ranging from the order of 69 to 1275 corresponds to the sequence of the *B. anthracis* strain of the order of 90 to 1300. The sample A5 strain (Figure 5.a) obtained from the order of 70 to 1275 corresponds to the sequence of the *B. tropicus* strain of the order of 125 to 1334. Meanwhile, the sample B5 obtained from the order of 66 to 1245 corresponds to the strain of *M. wisconsensis* in the order of 76 to 1253 (Figure 5.b). Matches between species are indicated by the sign “|” while the “\_” sign indicates the gap associated with the insertion or deletion process in that section. While the nucleotide base is replaced with “N” indicates that the N can be replaced by one of the four existing base sequences (<http://www.ncbi.nlm.nih.gov/>; Kim *et al.*, 2017).

The sequencing results obtained are then used as a basis for analysis on Gen Bank using BLAST analysis with the aim of comparing the results obtained with DNA sequence results from around the world from the results deposited in the public sequence Gen Bank database. BLAST analysis was conducted online through the NCBI website (<http://www.ncbi.nlm.nih.gov>). After BLAST was performed, the results showed the similarity of the nucleotide sequence of the 16S rRNA gene of the isolate obtained with the nucleotide sequence of the bacterial 16S rRNA gene in Gen Bank. BLAST results can be seen in Figure 6 and Figure 7 (<http://www.Ncbi.Nlm.Nih.Gov/>, n.d.).

The screenshot shows the BLAST results interface for sample A5. The title is "Sequences producing significant alignments". At the top right, there are options for "Download", "Select columns", and "Show 10". Below the title, there are links for "GenBank", "Graphics", "Distance tree of results", and "MSA Viewer". A checkbox for "select all" is present, with "0 sequences selected" below it. The main table lists the following data:

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/> <a href="#">Uncultured bacterium clone nck217a03c1 16S ribosomal RNA gene, partial sequence</a>	<a href="#">uncultured bacterium</a>	2248	2248	99%	0.0	98.66%	<a href="#">KF095984.1</a>
<input type="checkbox"/> <a href="#">Bacillus cereus strain VBE41 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus cereus</a>	2244	2244	99%	0.0	98.58%	<a href="#">MG027637.1</a>
<input type="checkbox"/> <a href="#">Bacillus anthracis strain ES-12 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus anthracis</a>	2244	2244	99%	0.0	98.58%	<a href="#">KY649403.1</a>
<input type="checkbox"/> <a href="#">Bacillus cereus strain DFT-1 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus cereus</a>	2244	2244	99%	0.0	98.58%	<a href="#">KY750685.1</a>
<input type="checkbox"/> <a href="#">Bacillus anthracis strain SCD7 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus anthracis</a>	2244	2244	99%	0.0	98.58%	<a href="#">KF476035.1</a>
<input type="checkbox"/> <a href="#">Bacillus cereus strain MD152 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus cereus</a>	2242	2242	99%	0.0	98.58%	<a href="#">MT642947.1</a>
<input type="checkbox"/> <a href="#">Bacillus tropicus strain ISP161A 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Bacillus tropicus</a>	2242	2242	99%	0.0	98.58%	<a href="#">MT611943.1</a>
<input type="checkbox"/> <a href="#">Bacillus anthracis strain FDAARGOS_695 chromosome</a>	<a href="#">Bacillus anthracis</a>	2242	24589	99%	0.0	98.58%	<a href="#">CP054816.1</a>
<input type="checkbox"/> <a href="#">Bacillus anthracis strain FDAARGOS_702 chromosome</a>	<a href="#">Bacillus anthracis</a>	2242	24589	99%	0.0	98.58%	<a href="#">CP054800.1</a>
<input type="checkbox"/> <a href="#">Bacillus anthracis strain FDAARGOS_703 chromosome</a>	<a href="#">Bacillus anthracis</a>	2242	24589	99%	0.0	98.58%	<a href="#">CP054797.1</a>

**Figure 6.** Results of BLAST analysis of sample A5

Mashuri Masri, Hajrah, Asfiana, Rusny & Syafrina Sari Lubis : Molecular Identification of 16S RNA of Pathogenic Bacteria From The Wings of Flesh Flies (*Sarcophaga* sp.) Inspired by The Hadith of The Prophet SAW, Bukhari's History About Flies

Sequences producing significant alignments Download  Select columns  Show 10

select all 0 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [New MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis strain 95B-1 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2206	2206	99%	0.0	98.79%	<a href="#">KY400229.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis strain X 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2206	2206	99%	0.0	98.79%	<a href="#">KP159747.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis strain NTS31501793 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2202	2202	99%	0.0	98.71%	<a href="#">KR339013.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis strain E3-4 16S ribosomal RNA gene, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2202	2202	99%	0.0	98.87%	<a href="#">KP058388.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis JCM 5896 gene for 16S ribosomal RNA, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2193	2193	99%	0.0	98.70%	<a href="#">LC462161.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis JCM 5894 gene for 16S ribosomal RNA, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2193	2193	99%	0.0	98.70%	<a href="#">LC462160.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis partial 16S rRNA gene, isolate M38</a>	<a href="#">Moellerella wisconsensis</a>	2189	2189	98%	0.0	98.78%	<a href="#">LT986671.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis strain 2896-78 16S ribosomal RNA, partial sequence</a>	<a href="#">Moellerella wisconsensis</a>	2189	2189	99%	0.0	98.55%	<a href="#">NR_104939.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis 16S rRNA gene, type strain DSM 5676T</a>	<a href="#">Moellerella wisconsensis</a>	2185	2185	99%	0.0	98.47%	<a href="#">AMD40754.1</a>
<input type="checkbox"/>	<a href="#">Moellerella wisconsensis partial 16S rRNA gene, strain Marseille-P296</a>	<a href="#">Moellerella wisconsensis</a>	2182	2182	99%	0.0	98.46%	<a href="#">LT223600.1</a>

Figure 7. Results of BLAST analysis of B5 sample

The results of the BLAST analysis obtained from sample A5 are that there are 3 species of bacteria from the genus *Bacillus*, each of which has the same Max Store, Total Store, Query Coverage and Ident values. The bacteria in question are *B. cereus* strain VBE41 16S ribosomal RNA gene, partial sequence, *B. anthracis* strain ES-12 16S ribosomal RNA gene, partial sequence, and *B. tropicus* strain ISP.161A 16S ribosomal RNA gene, partial sequence. This strain was taken from the results that most closely match the strain obtained with the same Max Store and Total Score value of 2244, Query Coverage which is closest to 100%, which is 99%, E-Value is equal to 0 and ident is 98.58% (Figure 6).

While the results of the BLAST analysis obtained from sample B5, namely the bacterium *M. wisconsensis* strain 95B-1 16S ribosomal RNA gene, partial sequence. This strain was taken from the results that best match the strain obtained with the same Max store value and Total score is 2206, Query Coverage which is closest to 100% is 99%, E-Value is equal to 0 and ident is 98.79% (Figure 7).

Based on the results of the BLAST analysis, the bacterial species in sample A5 were *B. cereus*, *B. anthracis*, and *B. tropicus*. While the sample B5 is *M. wisconsensis*. *B. cereus* is a Gram-positive bacterium that is rod-shaped, can form spores that are resistant to heat and radiation. These bacteria can grow well with an average temperature of 28.8°C on NA media. *B. cereus* is a type of bacteria that is commonly found in food so that it can cause poisoning in humans so that it is

classified as a pathogenic bacterium (Abdul & Pavoni, 2025; Dietrich *et al.*, 2021; Eom and Choi, 2015; Griffiths and Schraft, 2017).

Bizani *et al.*, (2005) said that *B. cereus* produces bacteriocins as antibacterial against *Listeria monocytogenes*. Amin *et al.*, (2015) said that *B. cereus* No. 3-7 produced antibacterial with a minimum inhibitory concentration of 8.34 mg/mL against *Shigella dysenteriae*, 20.67 mg/mL against *Staphylococcus aureus*, 16.67 mg/mL against *Salmonella typhi* and 25.00 mg/mL against *Corynebacterium diphtheria*. Feliatra *et al.*, (2021) said that *B. cereus* can produce antimicrobial compounds that can inhibit pathogenic bacteria; *Vibrio alginolyticus*, *Aeromonas hydrophila* and *Pseudomonas* sp. which was marked by the formation of a clear zone during the antagonist test. This ability is thought to be because these bacteria produce antibiotic compounds. The compounds produced are in the form of a collection of chemical substances produced by microorganisms including fungi and bacteria which have the function of inhibiting the growth or killing of other microorganism (Liu *et al.*, 2017)

*B. anthracis* is a Gram-positive, rod-shaped, aerobic, non-flagellated bacterium with a size of approximately 1-1.5 times 3-5 micrometers. These bacteria are easy to grow on a variety of media with a pH of 7.0-7.4, the growth temperature ranges from 12-45°C for the optimum temperature of 37°C. Colonies will appear as large, grayish-white colonies with irregular edges after 24 hours of incubation (Verma *et al.*, 2020). *B. anthracis* can cause anthrax disease, which is a disease in animals, especially warm-blooded and grass-eating animals (herbivores) such as buffalo, cows, horses, goats and sheep. This disease can infect humans through direct or indirect contact with infected animals (Carlson *et al.*, 2019).

*B. tropicus* is a suspected species from the *B. cereus* group, including Gram positive bacteria, facultative anaerobes, can form spores, and are motile. This bacterium is rod-shaped with pale white, circular, opaque, and 2-3 mm diameter colonies after being incubated at 32°C for 48 hours on LB media. The growth temperature is 15-45°C (optimal 30°C), pH 5-9 (optimal pH 6) (Liu *et al.*, 2017). Ayuningrum *et al.*, (2019) said that the endophytic isolate of TSB 47 tunicate (*Polycarpa aurata*) from Lease Sea, Maluku, Indonesia has the ability as an antibacterial. The endophytic isolate TSB 47 was identified molecularly with similarity 99% as *B. tropicus*. The isolate produced an inhibition zone of 17.46 mm against *Virgibacillus massiliensis*. Based on the above, it is known that *B. tropicus* is one of the bacteria that acts as an antibacterial.

*M. wisconsensis* is a new member of the family Enterobacteriaceae which belongs to the group of Gram-negative, facultative anaerobes and bacilli-shaped bacteria. Bacterium *M. wisconsensis* was first found in human feces with symptoms of diarrhea. *Moellerella* is a genus of bacteria that belongs to the Coliform, which is commonly found in human and animal feces (Anastácio & Leão, 2016).

## Conclusion

The results of this study showed that on the right and left wings of the meat fly (*Sarcophaga* sp.) several types of pathogenic bacteria were found. However, from this study it has not been confirmed that there is an anti-bacterial or anti-toxin as an antidote/drug on the right wing or on the left wing of the fly as stated by Rasulullah SAW in HR. Bukhari. However, this research can strengthen the Prophet's hadith about flies from a biological perspective by proving the presence of bacteria found on the wings of the meat fly.

The results of this study prove that on the wings of flesh flies. There are several types of bacteria on the right and left wings of these flies. And in this study, several pathogenic bacteria were found on the wings of these flies, but it is not certain that the presence of antibacterial or anti-poison (drugs) on the wings of flies as in the hadith of the Prophet Muhammad. narrated by Al Bukhari from Abu Hurairah, namely "If a fly falls on your drink, then drown it and then lift it, because on one wing it is a disease and the other wing has the cure." So that research to prove this hadith still needs to be developed in terms of research on the bacteria found on the right and left wings of flies. Even so, this research can also strengthen the Hadith of the Rasulullah saw. about these flies by proving that there are bacteria found on the flesh fly's wings from the side of biology.

## Conflict of Interest

In this section, the authors may specify the individual contributions of each author as well as the extent and role of any limited assistance obtained from Artificial Intelligence (AI) tools. Mashuri Masri: Conceptualization, methodology, investigation, writing original draft. Hajrah and Asfiana: Data curation, validation, visualization, writing review & editing. Rusny: Supervision, resources, writing review and editing. Syafrina Sari Lubis: Supervision, writing review & editing. All authors have read and agreed to the published version of the manuscript.

## Acknowledgements

This then inspired us to do the Grand Design Multy Years Research No. 89/UIN Allauddin/2020. Form of Letter of Guarantee UIN Alauddin's Rector, which is broadly divided into: Supporting the data of the first stage of the Grand Design Multy Years Research.

## References

- Abdul, M.-E., & Pavoni, E. (2025). *Bacillus cereus* in food safety: a bibliometric analysis. *Frontiers in Microbiology*, 16(June), 1–13. <https://doi.org/10.3389/fmicb.2025.1574802>
- Akhmawati, A. *Media Penyiapan Mikroorganisme, Pelatihan Laboratorium*. Universitas Negeri Yogyakarta: Yogyakarta; 2012

- Anastácio, S., & Leão, H. (2016). *Moellerella wisconsensis*: What's its role in cattle disease? *Experimental Pathology and Health Sciences*, 8(1), 35–36. <https://www.researchgate.net/publication/293825285>
- Amin, M., Rakhisi, Z., & Zarei Ahmady, A. (2015). Isolation and identification of *Bacillus* species from soil and evaluation of their antibacterial properties. *Avicenna Journal of Clinical Microbiology and Infection*, 2(1), e23233. <https://doi.org/10.17795/ajcmi-23233>
- Ayuningrum, D., Kristiana, R., Nisa, A. A., Radjasa, S.K., Muchlissin, S. I., Radjasa, O. K., Sabdono, A., & Trianto, A. (2019). Bacteria associated with tunicate, *Polycarpa aurata*, from Lease Sea, Maluku, Indonesia exhibiting anti-multidrug-resistant bacteria. *Biodiversitas*, 20(4), 956–964. <https://doi.org/10.13057/biodiv/d200404>
- Boyanova, L. (2018). Direct Gram staining and its various benefits in the diagnosis of bacterial infections. *Postgraduate Medicine*, 130(1), 105–110. <https://doi.org/10.1080/00325481.2018.1398049>
- Bizani, D., Motta, A. S., Morrissy, J. A. C., Terra, R. M. S., Souto, A. A., & Brandelli, A. (2005). Antibacterial activity of cerein 8A, a bacteriocin-like peptide produced by *Bacillus cereus*. *International Microbiology*, 8(2), 125–131. <https://pubmed.ncbi.nlm.nih.gov/16052461/>
- Carlson, C. J., Kracalik, I. T., Ross, N., Alexander, K. A., Hugh-Jones, M. E., Fegan, M., Elkin, B. T., Epp, T., Shury, T. K., Zhang, W., Bagirova, M., Getz, W. M., & Blackburn, J. K. (2019). The global distribution of *Bacillus anthracis* and associated anthrax risk to humans, livestock and wildlife. *Nature microbiology*, 4(8), 1337–1343. <https://doi.org/10.1038/s41564-019-0435-4>
- Chandrakasan, G., Soto-Zarazúa, G. M., Toledano-Ayala, M., Flores-Aguilar, P. S., & Rodríguez-Romero, S. A. (2026). Purification, Structural Characterization, and Antibacterial Evaluation of Poly- $\gamma$ -Glutamic Acid from *Bacillus subtilis*. *Polymers*, 18(2), 172. <https://doi.org/10.3390/polym18020172>
- Claresta, I., Sari, D. D., Nurohmi, S., Fatimah, & Damayanti, A. Y. (2020). The Right-Wing of Fly (*Musca domestica*) as a Neutralization of Drinks Contaminated by Microbe. *Journal of Nutritional Science and Vitaminology*, 66(Supplement), S283–S285. <https://doi.org/10.3177/jnsv.66.S283>
- Dietrich, R., Jessberger, N., Ehling-Schulz, M., Märtilbauer, E., & Granum, P. E. (2021). The Food Poisoning Toxins of *Bacillus cereus*. *Toxins*, 13(2), 98. <https://doi.org/10.3390/toxins13020098>
- Ehling-Schulz, M., Lereclus, D., & Koehler, T. M. (2019). The *Bacillus cereus* group: *Bacillus* species with pathogenic potential. *Gram-Positive Pathogens*, 875–902. <https://doi.org/10.1128/microbiolspec.GPP3-0032-2018>
- Eom, J. S., & Choi, H. S. (2015). Inhibition of *Bacillus cereus* growth and toxin production by *Bacillus amyloliquefaciens* RD7-7 in fermented soybean

- products. *Journal of Microbiology and Biotechnology*, 26(1), 44–55. <https://doi.org/10.4014/jmb.1509.09090>
- Feliatra, F., Batubara, U. M., Nurulita, Y., Lukistyowati, I., & Setiaji, J. (2019). The potentials of secondary metabolites from *Bacillus cereus* SN7 and *Vagococcus fluvialis* CT21 against fish pathogenic bacteria. *Microbiology Pathogenesis*, 158, 105062. <https://doi.org/10.1016/j.micpath.2021.105062>
- Giermasińska-Buczek, K., Gawor, J., Stefańczyk, E., Gaęła, U., Żuchniewicz, K., Rekosz-Burlaga, H., Gromadka, R., & Łobocka, M. (2024). Interaction of bacteriophage P1 with an epiphytic *Pantoea agglomerans* strain—the role of the interplay between various mobilome elements. *Frontiers in Microbiology*, 15. <https://doi.org/10.3389/fmicb.2024.1356206>
- Godbey, W. T. (2022). Agarose gels. In *Biotechnology and its Applications* (pp. 203–218). Elsevier. <https://doi.org/10.1016/B978-0-12-817726-6.00009-5>
- Griffiths, M. W., & Schraft, H. (2017). *Bacillus cereus* food poisoning. In *Foodborne Diseases* (3rd ed., pp. 395–405). Elsevier. <https://doi.org/10.1016/B978-0-12-385007-2.00020-6>
- Hammed, Z. N., Taha, A. M., & Alabdali, T. A. (2023). A Review Articles: *Pantoea agglomerans* in UTI- It is Bacteria Caused Urinary Tract Infection and Genomic Analysis related with Bacterial Resistance. *Journal for Research in Applied Sciences and Biotechnology*, 2(4), 142–150. <https://doi.org/10.55544/jrasb.2.4.20>
- <http://bio.fst.uin-alaud-din.ac.id/visi>.
- <http://www.ncbi.nlm.nih.gov/>.
- Idibie, O. C., Oviojie, O. E., Isalar, O. F., & Emoghene, A. O. (2018). Comparative microbial analysis of borehole water and other sources of water in Benin Metropolis, Edo State. *Journal of Environmental Science and Public Health*, 2, 232–242. <https://doi.org/10.26502/jesph.96120042>
- Jagielski, T., Gawor, J., Bakuła, Z., Decewicz, P., Maciszewski, K., & Karnkowska, A. (2018). *Cytb* as a new genetic marker for differentiation of *Prototheca* species. *Journal of Clinical Microbiology*, 56(10), e00584-18. <https://doi.org/10.1128/JCM.00584-18>
- Kaur, I. P., Inkollu, S., Prakash, A., Gandhi, H., Mughal, M. S., & Du, D. (2020). *Pantoea agglomerans* Bacteremia: Is It Dangerous? *Case Reports in Infectious Diseases*, 2020(September 2019), 1–4. <https://doi.org/10.1155/2020/7890305>
- Kim, Y. B., Komor, A. C., Levy, J. M., Packer, M. S., Zhao, K. T., & Liu, D. R. (2017). Increasing the genome-targeting scope and precision of base editing with engineered Cas9–cytidine deaminase fusions. *Nature Biotechnology*, 35(4), 371–376. <https://doi.org/10.1038/nbt.3803>
- Kumar, R., Bauri, S., Sahu, S., Chauhan, S., Dholpuria, S., Ruokolainen, J., Kesari, K. K., Mishra, M., & Gupta, P. K. (2023). In Vivo Toxicological Analysis of MnFe2O4@poly(tBGE-alt-PA) Composite as a Hybrid Nanomaterial for

- Possible Biomedical Use. *ACS Applied Bio Materials*, 6(3), 1122–1132. <https://doi.org/10.1021/acsabm.2c00983>
- Kundu, S., Varshney, R., & Sulabh, S. (2024). Exploration of isothermal nucleic acid amplification techniques in the biomedical field. *Gene and Genome Editing*, 7, 100032. <https://doi.org/10.1016/j.ggedit.2024.100032>
- Lainjong, E., Sompah, N. P., & Hasania, O. (2021). Identification of air bacteria using gram stying method. *Jurnal Ilmiah Dr Aloei Saboe*, 8(2), 1–10.
- Li, Y. J., Pan, C. Z., Fang, C. Q., Zhao, Z. X., Chen, H. L., Guo, P. H., & Zhao, Z. W. (2017). Pneumonia caused by extensive drug-resistant *Acinetobacter baumannii* among hospitalized patients: Genetic relationships, risk factors, and mortality. *BMC Infectious Diseases*, 17(1), 2471. <https://doi.org/10.1186/s12879-017-2471-0>
- Liu, Y., Du, J., Lai, Q., Zeng, R., Ye, D., Xu, J., & Shao, Z. (2017). Proposal of nine novel species of the *Bacillus cereus* group. *International journal of systematic and evolutionary microbiology*, 67(8), 2499–2508. <https://doi.org/10.1099/ijsem.0.001821>
- Liu, Y., Lai, Q., Du, J., & Shao, Z. (2017). Genetic diversity and population structure of the *Bacillus cereus* group bacteria from diverse marine environments. *Scientific reports*, 7(1), 689. <https://doi.org/10.1038/s41598-017-00817-1>
- Mai-Prochnow, A., Clauson, M., Hong, J., & Murphy, A. B. (2016). Gram-positive and Gram-negative bacteria differ in their sensitivity to cold plasma. *Scientific Reports*, 6, 38610. <https://doi.org/10.1038/srep38610>
- Mirtella, D., Fedeli, P., Scendoni, R., Cannovo, N., & Cingolani, M. (2021). A Case of Nosocomial Outbreak of *Pantoea agglomerans* Related to Parenteral Nutrition Procedures. *Healthcare*, 9(6), 684. <https://doi.org/10.3390/healthcare9060684>
- Mohamed, E. F., Awad, G., Andriantsiferana, C., & El-Diwany, A. I. (2016). Biofiltration technology for the removal of toluene from polluted air using *Streptomyces griseus*. *Environmental Technology*, 37(10), 1197–1207. <https://doi.org/10.1080/09593330.2015.1107623>
- Monyama, M. C., Taioe, O. M., Nkhebenyane, J. S., van Wyk, D., Ramatla, T., & Thekiso, O. M. M. (2023). Bacterial Communities Associated with Houseflies (*Musca domestica* L.) Inhabiting Hospices in South Africa. *Microorganisms*, 11(6), 1440. <https://doi.org/10.3390/microorganisms11061440>
- Mordechai, E., 1999. *Application of PCR The Methodologies in Molecular Diagnostic*. Burlington Country, USA.
- Mufid, A., & Sattar, A. (2023). Track Dating Hadith Fly Wings. *ESENSIA: Jurnal Ilmu-Ilmu Ushuluddin*, 24(1), 15–29. <https://doi.org/10.14421/esensia.v24i1.4362>

- Nayduch, D., Neupane, S., Pickens, V., Purvis, T., & Olds, C. (2023). House Flies Are Underappreciated Yet Important Reservoirs and Vectors of Microbial Threats to Animal and Human Health. *Microorganisms*, *11*(3), 583. <https://doi.org/10.3390/microorganisms11030583>
- Park, M., Sutherland, J. B., & Rafii, F. (2019). Effects of nano-hydroxyapatite on the formation of biofilms by *Streptococcus mutans* in two different media. *Archives of oral biology*, *107*, 104484. <https://doi.org/10.1016/j.archoralbio.2019.104484>
- Rohde M. (2019). The Gram-Positive Bacterial Cell Wall. (May):1-21. <https://doi.org/10.1128/microbiolspec.GPP3-0044-2018>.
- Roume, H., Heintz-Buschart, A., Müller, E. E. L., & Wilmes, P. (2013). Sequential isolation of metabolites, RNA, DNA, and proteins from the same unique sample. In *Methods in Enzymology* (Vol. 531, pp. 219–236). Elsevier. <https://doi.org/10.1016/B978-0-12-407863-5.00011-3>
- Santosa, A. I., Hilmany, T., Dewi, N. A., Rahmawati, N. E., Putri, E. A., Hafidsya, T., Setyaningrum, A. V., Dewi, R. E., Sari, G. N. P., Nubatonis, M. B. F. M., & Widyawan, A. (2024). Cross amplification of 16S rRNA bacterial primer 27F/1492R on horticultural crop chloroplast genome. *Agricultural Science*, *7*(2), 172–183. <https://doi.org/10.55173/agricscience.v7i2.132>
- Shankar, S., Pangeeni, R., Park, J. W., & Rhim, J. W. (2018). Preparation of sulfur nanoparticles and their antibacterial activity and cytotoxic effect. *Materials Science and Engineering C*, *92*, 508–517. <https://doi.org/10.1016/j.msec.2018.07.015>
- Shokrpoor, S., Baghkheirati, A. A., Yazdani, A., & Razmyar, J. (2019). Cutaneous xanthogranuloma associated with *Klebsiella pneumoniae* in a budgerigar (*Melopsittacus undulatus*). *Veterinary Research Forum*, *10*(4), 365–367. <https://doi.org/10.30466/vrf.2019.102621.2445>
- Troha, K., & Buchon, N. (2019). Methods for the study of innate immunity in *Drosophila melanogaster*. *Wiley Interdisciplinary Reviews: Developmental Biology*, *8*(5), e344. <https://doi.org/10.1002/wdev.344>
- Tonner, M. (2018). *Axenic amastigotes of Leishmania tarentolae as drug testing system* [Master's thesis, FH Campus Wien]. <https://pub.fh-campuswien.ac.at/obvfcwhsacc/.download/pdf/2676624>
- Verma, D. K., Mohapatra, B., Kumar, C., et al. (2019). Molecular techniques for detection of foodborne pathogens: *Salmonella* and *Bacillus cereus*. In *Microbiology of Food and Health* (pp. 231–296). CRC Press. <https://doi.org/10.1201/9780429276170-7>
- Wang, W., Wang, C., She, Y., Zeng, Q., Mao, W., Gu, X., Yuan, H., Pan, X., & Wang, Y. (2020). The complete mitochondrial genome of *Sarcophaga scopariiformis* (Diptera: Sarcophagidae). *Mitochondrial DNA Part B: Resources*, *5*(3), 2701–2702. <https://doi.org/10.1080/23802359.2020.1787269>

- Wittmeier, P., & Hummel, S. (2022). Agarose Gel Electrophoresis to Assess PCR Product Yield: Comparison with Spectrophotometry, Fluorometry and qPCR. *BioTechniques*, 72(4), 155–158. <https://doi.org/10.2144/btn-2021-0094>
- Yanestria, S. M., Rahmaniar, R. P., Wibisono, F. J., Effendi, M. H. (2019). Detection of *invA* gene of Salmonella from milkfish (*Chanos chanos*) at Sidoarjo wet fish market, Indonesia, using polymerase chain reaction technique. *Veterinary World*. 12(1):170-175. <https://doi.org/10.14202/vetworld.2019.170-175>
- Yamada, K., Kashiwa, M., Arai, K., Satoyoshi, K., & Nishiyama, H. (2017). *Pantoea calida* bacteremia in an adult with end-stage stomach cancer under inpatient care. *Journal of infection and chemotherapy : official journal of the Japan Society of Chemotherapy*, 23(6), 407–409. <https://doi.org/10.1016/j.jiac.2017.01.001>
- Yehya, A., Ezzeddine, Z., Chakkour, M., Dhaini, Z., Bou Saba, M. S., Bou Saba, A. S., Nohra, L., Nassar, N. B., Yassine, M., Bahmad, H. F., & Ghssein, G. (2025). The intricacies of *Acinetobacter baumannii*: a multifaceted comprehensive review of a multidrug-resistant pathogen and its clinical significance and implications. *Frontiers in Microbiology*, 16. <https://doi.org/10.3389/fmicb.2025.1565965>
- Zhou, Y., Zhu, X., Hou, H., Lu, Y., Yu, J., Mao, L., & Sun, Z. (2018). Characteristics of diarrheagenic *Escherichia coli* among children under 5 years of age with acute diarrhea: A hospital-based study. *BMC Infectious Diseases*, 18(1), 2936. <https://doi.org/10.1186/s12879-017-2936-1>