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

Mashuri Masri[*], Hajrah[*], Asfiana[*], Rusny[**], Syafrina Sari Lubis[***]

[*]*Department of Biology, Faculty of Science and Technology, Alauddin State Islamic University Makassar, South Sulawesi, Indonesia, mashuri.masri@uin-alauddin.ac.id, hajrah.sukri@uin-alauddin.ac.id, asfiana.uin.alauddin@gmail.com*

[**]*Department of Animal Science, Faculty of Science and Technology, Alauddin State Islamic University Makassar, South Sulawesi, Indonesia, rusny@uin-alauddin.ac.id*

[***]*Department of Biology, Faculty of Science and Technology, Ar-Raniry State Islamic University, Kopelma Darussalam, Banda Aceh, Indonesia, syafrinasarilbs@ar-raniry.ac.id*

Email Correspondence : mashuri.masri@uin-alauddin.ac.id

Received : September 7, 2022 Accepted : December 27, 2025 Published : December 31, 2025

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

Recommended APA Citation :

Masri, M., Hajrah, Asfiana, Rusny, & Lubis, S. S. (2025). 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. *Elkawnie*, *11*(2), 189-206. https://doi.org/10.22373/ekw.v11i2.14962

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 ^{o}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 ^{0}C for 30 seconds, annealing at 55 ^{0}C for 30 seconds and extention at 72 ^{0}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	(µl)
ddH2O	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 ºC for 15 minutes, then 94 ºC for 1 minute, annealing at 55 ºC for 30 seconds, extension of 72 ºC for 1 minute as many as 40 cycles followed by a final extension of 72 ºC for 5 minutes and 12ºC ± 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 µl of ethidium bromide (0.2 µg / 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.

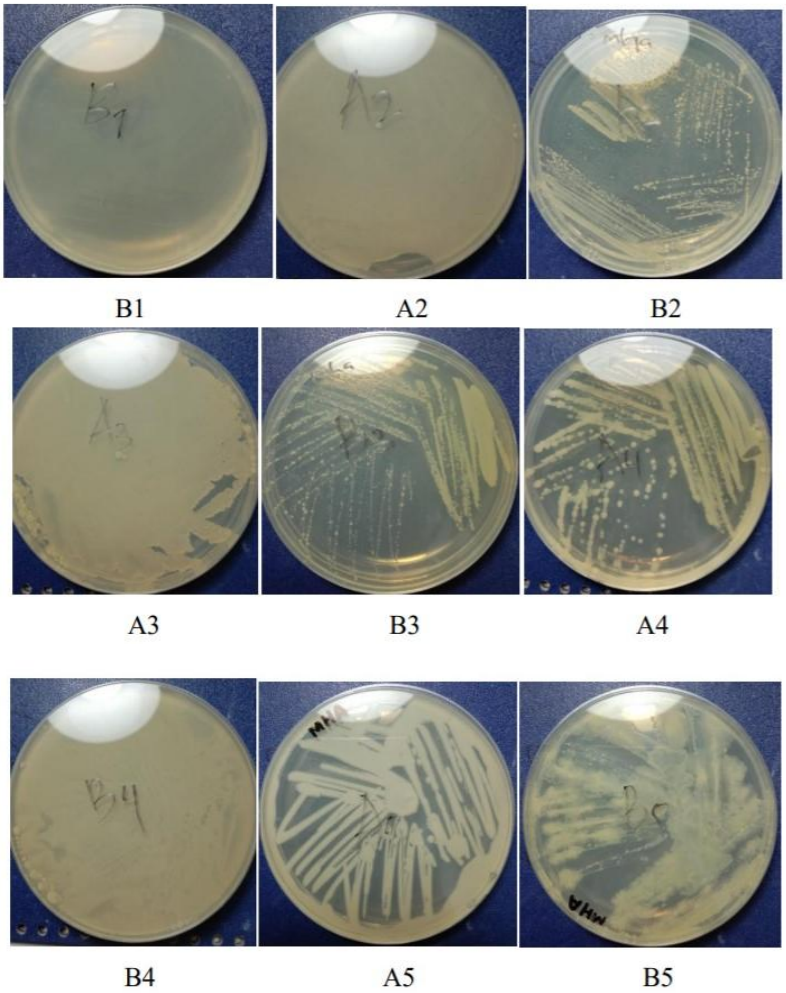


Figure 1. The results of the bacterial culture of the wings of the flesh fly (*Sarcophaga* sp.) on media NA: (B1) left wing of fly 1; (A2) fly right wing 2; (B2) fly left wing 2; (A3) fly right wing 3; (B3) fly's left wing 3; (A4) fly right wing 4; (B4) fly's left wing 4; (A5) right wing fly 5; (B5)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

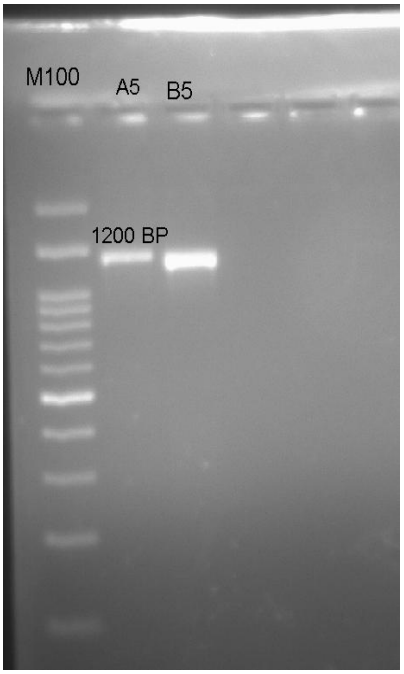


Figure 2. Electrophoresis results visible on Gel doc: M (marker); A5 (left-wing sample); B5 (right wing sample)

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 electropherogam 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).

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

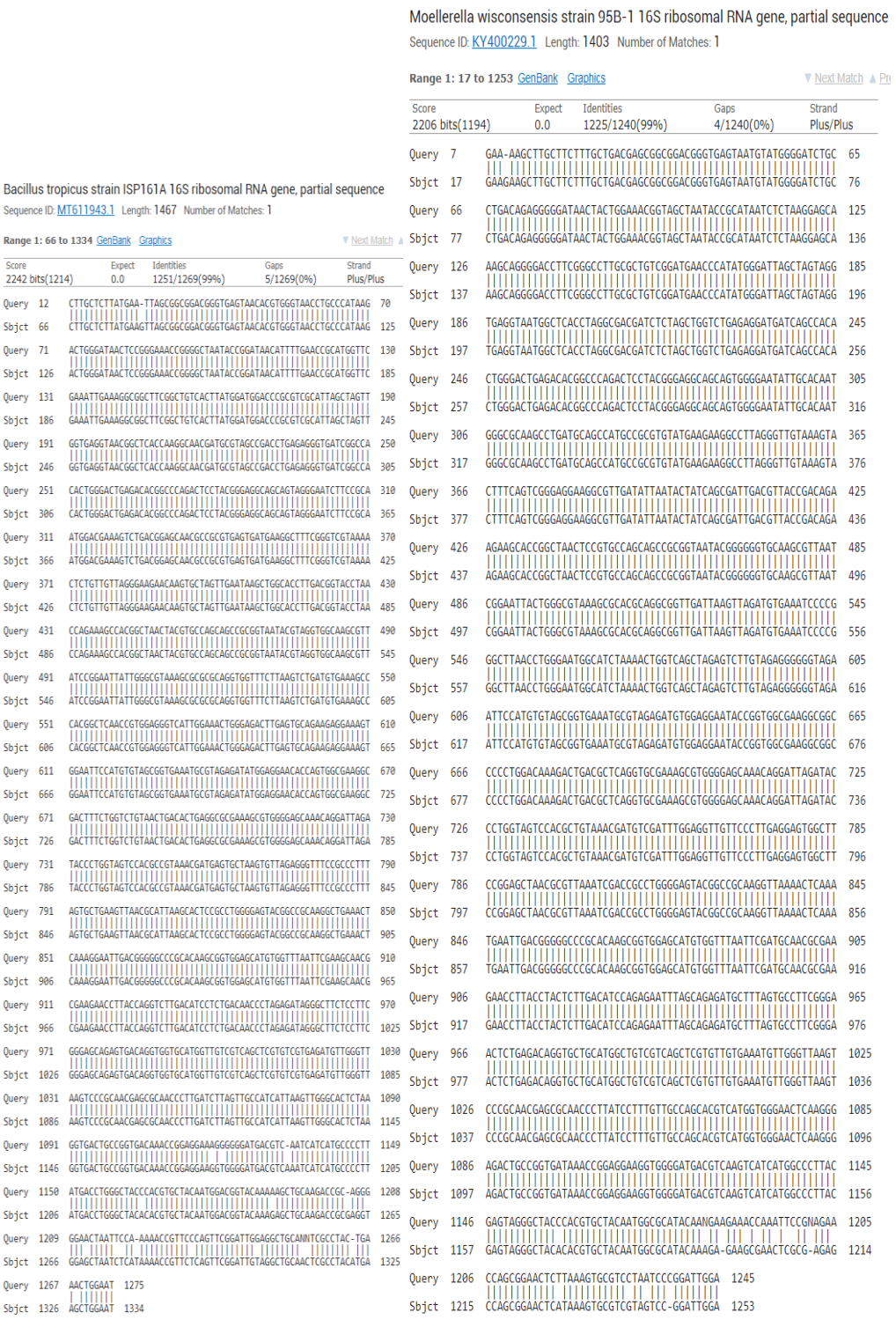
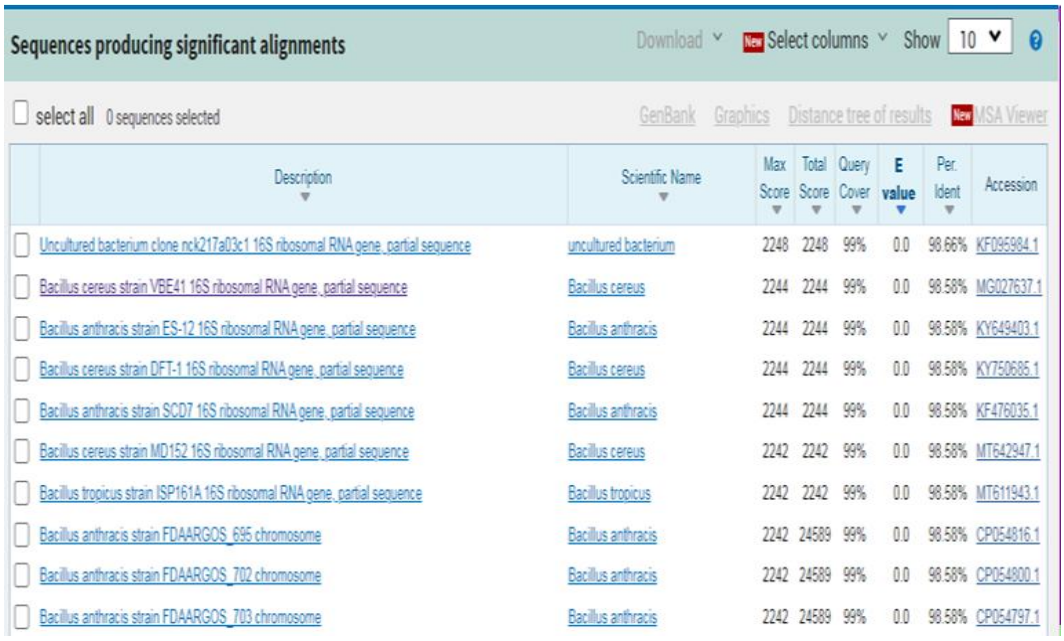


Figure 5. Comparison of base sequences of A5 sample with *Bacillus tropicus* bacteria (a), and ***sample*** B5 with *Moellerella wisconsensis* bacteria (b).

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 corresp.onds 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 corresp.onds 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 ecies 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.).

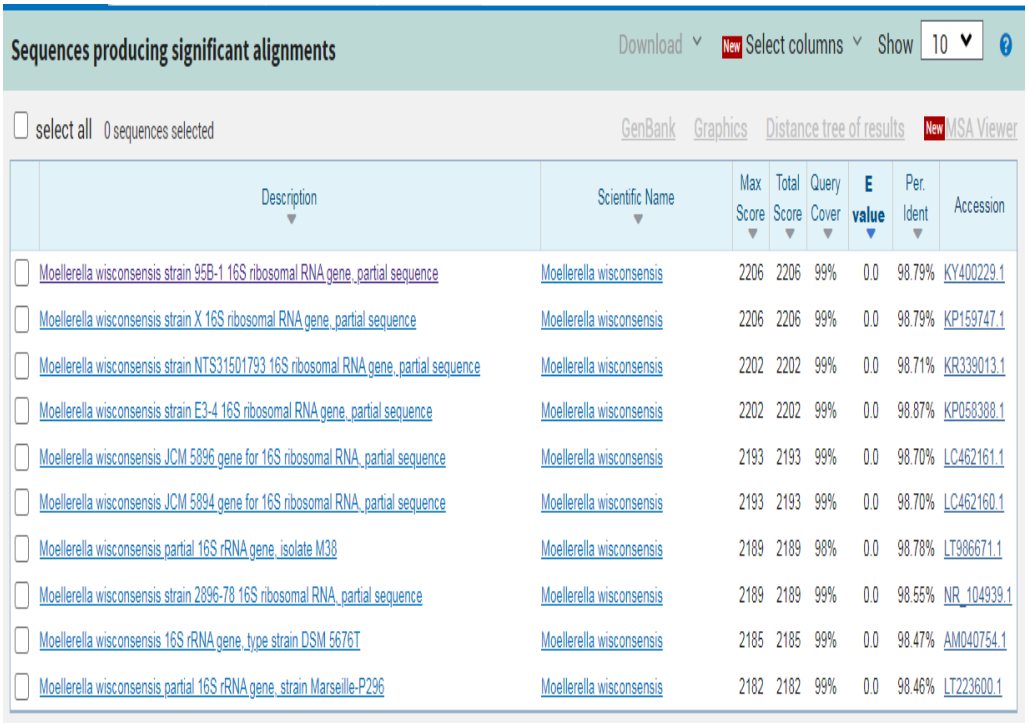


Sequences producing significant alignments Download Select columns Show 10

select all 0 sequences selected GenBank Graphics Distance tree of results MSA Viewer

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

Figure 6. Results of BLAST analysis of sample A5



Sequences producing significant alignments

Download | New 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
Moellerella wisconsensis strain 95B-1 16S ribosomal RNA gene, partial sequence	Moellerella wisconsensis	2206	2206	99%	0.0	98.79%	KY400229.1
Moellerella wisconsensis strain X 16S ribosomal RNA gene, partial sequence	Moellerella wisconsensis	2206	2206	99%	0.0	98.79%	KP159747.1
Moellerella wisconsensis strain NTS31501793 16S ribosomal RNA gene, partial sequence	Moellerella wisconsensis	2202	2202	99%	0.0	98.71%	KR339013.1
Moellerella wisconsensis strain E3-4 16S ribosomal RNA gene, partial sequence	Moellerella wisconsensis	2202	2202	99%	0.0	98.87%	KP058388.1
Moellerella wisconsensis JCM 5896 gene for 16S ribosomal RNA, partial sequence	Moellerella wisconsensis	2193	2193	99%	0.0	98.70%	LC462161.1
Moellerella wisconsensis JCM 5894 gene for 16S ribosomal RNA, partial sequence	Moellerella wisconsensis	2193	2193	99%	0.0	98.70%	LC462160.1
Moellerella wisconsensis partial 16S rRNA gene, isolate M38	Moellerella wisconsensis	2189	2189	98%	0.0	98.78%	LT986671.1
Moellerella wisconsensis strain 2896-78 16S ribosomal RNA, partial sequence	Moellerella wisconsensis	2189	2189	99%	0.0	98.55%	NR_104939.1
Moellerella wisconsensis 16S rRNA gene, type strain DSM 5676T	Moellerella wisconsensis	2185	2185	99%	0.0	98.47%	AM040754.1
Moellerella wisconsensis partial 16S rRNA gene, strain Marseille-P296	Moellerella wisconsensis	2182	2182	99%	0.0	98.46%	LT223600.1

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 sp.ecies 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 sp.ores 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 aereus*, 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 algynolyticus, 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 Rasulluah 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-γ-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., Märtlbauer, 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., Gągała, 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-alauddin.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., & Thekisoe, 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/agriscience.v7i2.132

Shankar, S., Pangeni, 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 Acinsetobacter 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