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IDENTIFIKASI DAN INVENTARISASI JENIS BAKTERI YANG DITEMUKAN DI PANGKALAN DERMAGA SUNGAI SEBANGAU KOTA PALANGKA RAYA

Identification And Inventory of The Types Of Bacteria Found At The Base Of The Sebangau River Pier Palangka Raya City

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ABSTRAK

Penelitian ini dilakukan dengan tujuan untuk mengindentifikasi dan invetarisasi jenis bakteri yang ditemukan di Pangkalan Dermaga Sungai Sebangau Kota Palangka Raya. Waktu pelaksanaan pada bulan Nopember 2021 dengan metode penelitian secaran deskriptif dengan pengambilan sampel di lokasi Pangkalan Dermaga Sungai Sebangau Kota Palangka Raya dan pengujian sampel dilaksanakan di Laboratorium Stasiun Karantina dan Pengendalian Mutu Palangka Raya. Hasil penelitian ini ditemukannya 7 isolat gram positif dan 12 gram negatif dengan 12 jenis bakteri dan karakterisitik bakteri yang berbeda yaitu, *Aeromonas hydrophila, Aeromonas sobria, Aeromonas caviae, Citrobacter freundii, Edwardseilla tarda, Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis, Plesiomonas shigelloides, Bacillus subtilis, Listeria* sp, dan *Enterobacter cloacae.*

ABSTRACT

This research was conducted with the aim to identify and invetarize the types of bacteria found in the Sebangau River Pier Base in Palangka Raya City. The implementation time was in November 2021 with a descriptive research method with sampling at the Sungai Sebangau Pier Base in Palangka Raya City and sample testing was carried out at the Palangka Raya Quarantine and Quality Control Station Laboratory. The results of this study found 7 positive and 12 gram-negative isolates with 12 different types of bacteria and bacterial characteristics, namely, *Aeromonas hydrophila, Aeromonas sobria, Aeromonas caviae, Citrobacter freundii, Edwardseilla tarda, Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis, Plesiomonas shigelloides, Bacillus subtilis, Listeria sp.,* and *Enterobacter cloacae.*

Kata Kunci	*Identifikasi, Invetarisasi, Jenis Bakteri, Sungai Sebangau*
Keywords	*Identification, Inventory, Types of Bacteria, Sebangau River*
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INTRODUCTION

The Sebangau River is one of the large rivers in Central Kalimantan with a length of 198 km. The Sebangau River has the characteristics of being a peat river, because the river water comes from peat swamp forests. Water containing high levels of peat flows from the peat swamp forest (Sulistiyarto, 2017).

The organic substance content in peat water is dominated by humic compounds which are difficult to break down by microorganisms or are non-biodegradable. However, efforts to reform humic and fulvic compounds continue to be developed (Eri et al., 2010).

The content of peat water which contains a lot of organic material makes it possible for amylolytic bacteria to live in environmental conditions with a high organic material content. Amylolytic bacteria are a type of bacteria that produce the amylase enzyme which is able to break down starch, where this enzyme works to hydrolyze starch which can be produced by bacteria, fungi, plants and animals (Ismiati, 2018).

Peat water contains a variety of microorganisms which can be applied for research purposes, namely to look for the potential of these microbes in various aspects such as health, medicine, agriculture, fisheries and so on. Therefore, it is important to isolate microbes from peat water, especially bacteria, to be identified in terms of morphology (Mahdiyah, 2015).

The aquatic environment, surrounding land use and human activities that are directly or indirectly related to rivers. The decline in potential aquatic resources is usually caused by environmental damage. Microorganisms, especially bacteria, have a role in environmental management, often having a symbiotic relationship (both positive and negative) with other organisms, and this relationship affects aquatic ecosystems (Irianto, 2016).

The Sebangau River is a river basin (DAS) in the Sebangau National Park area which is located in the city of Palangka Raya, Central Kalimantan Province. The Sebangau River has quite potential fisheries resources and is one of the fishing grounds for fishermen and supports the economy of the community in the Kereng Bangkirai sub-district.

According to Badjoeri (2018) research on public waters in Kalimantan is still limited, because the research carried out is mostly about the inventory and biodiversity of freshwater fish species, but on the other hand, not much research has been done on the ecology of the waters. Therefore, research on the identification and inventory of bacterial types from peat water has not yet been explored, so there is minimal data on the types of bacteria found in peat water. Based on the background discussed, there was no previous research that examined the microbiological parameters of peat water in the Sebangau River Pier area, Palangka Raya City, especially the types of bacteria, the researchers were interested in conducting research on the identification of bacteria found in the peat water of the Sebangau River Pier, Palangka Raya City.

METHODS

Time and Place Research

This research was carried out in November 2021. Meanwhile, the research location was at the Sebangau River Pier Base, Palangka Raya City, and sample testing was carried

out at the Palangka Raya Fisheries Quarantine and Quality Control (SKIPM) Station Laboratory.

Tools and Materials

The tools and materials used in the research were boats, GPS, label paper, dropper pipettes, petri dishes, tube needles, Bunsen lamps, glass objects, cover glasses, sample bottles, microscopes, 70% alcohol, peat water, distilled water, crystal violet, iodine solution, safranin and Tryptic Soy Agar (TSA) Media.

Research Methods and Stages

The method used in this research is descriptive observation in the waters of the Sebangau River, Palangka Raya City, Central Kalimantan Province. Descriptive observation is an observation that aims to obtain data about a problem so that an understanding is obtained as a means of proving the information or information obtained.

Research Procedure

a. Location Determination

The location of the observation station was determined using the "purposive sampling" method using a GPS device. The sampling locations are 3 (three) stations, namely:

1. Station I at coordinates 03°01' 39.09" S and 112°59'22, 26" E, this sampling location. It is relatively far located upstream of Kereng Bengkirai Pier and residential areas. In this section the water is not too polluted by household waste and the water is reddish black.
2. Station II at coordinates 02°17' 50.96" S and 113°54'18.46" E, this location is located in the middle of the river and is relatively close to Kereng Bengkirai Pier and also close to residential areas. In this section the water has been polluted by domestic waste, the color of the water is slightly brownish black due to population activities and community tourism activities.
3. Station III at coordinates 02°17' 51.60" S and 113°54'21.79" E, this location is located downstream, relatively far from Kereng Bengkirai Pier and quite close to residential areas but not too much activity. At this location the color of the water is reddish black.

b. Water Sampling

The method for taking samples is that the sample is taken using a bottle where the end of the bottle is tied using a rope then dip the end of the bottle until it sinks vertically. Next, the bottle for taking the water sample is covered using black material so that the sample is not exposed to direct sunlight which causes the bacteria to be damaged. Taking water depends on the condition of the water itself, if you take samples in flowing river water, the bottle is sunk at an angle with the tip of the bottle against the flow of river water (Safitri et al., 2010). then taken to the UPT Laboratory, Fish Quarantine Station, Quality Control and Safety of Class I Fishery Products, Palangka Raya, Central Kalimantan to observe and identify bacteria.

c. Bacterial Observation Work Procedures

1. Sterilization of Tools

Sterilization of equipment is carried out by cleaning all equipment that will be used in bacterial identification activities. Equipment is sterilized using two types of sterilization, namely wet sterilization and dry sterilization. The sterilization process is adjusted to the type of equipment used. Equipment that has been used is then cleaned again and stored in a rack or place that has been sterilized and free from contamination.

2. Bacterial purification
   The colonies that grow are then purified until a pure isolate is obtained. One colony of bacterial isolates was taken from a petri dish aseptically and inoculated onto the surface of Agar medium using the streak plate method and incubated in an incubator at a temperature of 35 – 37^{o}C for 24 hours or 48 hours. A bacterial colony can be said to be pure if the colonies at the end of the streak have the same shape. If there are still different colonies at the end of the streak, it is necessary to repeat the streak on each of the different colonies until a pure colony is obtained.
3. Macroscopic observations
   Macroscopic observation is observing the form of growth of bacterial colonies that grow on the surface. Macroscopic observations include the shape of bacterial colonies in the form of dots, round, threaded, irregular, root-like, coil-like; the surface of the colony is flat, flat, curved, hilly, similar to a crater; the edge of the colony is intact, wavy, serrated, threaded; Colony color is whitish, gray, yellowish or almost clear.
4. Identify bacteria
   Bacterial identification includes morphological characteristics and biochemical tests. The guidebook used in bacterial identification refers to Bergey's Manual of Determinative Bacteriology 9th ed. The identification stage begins with gram staining with the aim of determining the form of bacteria (bacillus or cocci or spirals), gram positive or negative when observed in a microscope.

RESULT AND DISCUSSION

Based on research in Hulu Sungai Sebangau, to find out the type of bacteria present in Tapah fish, bacterial isolation was carried out, namely in the first stage of preparing tools and materials for initial isolation for bacterial growth, namely by 2 isolation methods, namely:

1. Isolate retail 10-8 with distilled water
   At a dilution of 10-8, no bacterial growth was found on TSA media within a period of 1x24 hours with an incubation temperature of 28^{o}C.
2. Isolate directly to TSA media
   Bacterial growth was found in the TSA median which had been assigned station codes of ST1A, ST2A, ST1B, ST2B, ST3A and ST3B within a period of 1x24 hours with an incubation temperature of 28^{o}C. This isolation uses general agar media, namely Tryptic Soy Agar (TSA) because this media is good for bacterial growth (Kismiyati et al., 2009). The results of observing cell morphology and cell colony morphology can be seen in the Table 1.

Cell Morphology

Table 1. Cell morphology observations

No	Sample Code	Cell Form and Gram test	Color Cell
1	ST1A	1 Coccus (Positive), 2 Bacillus (Positive and negative)	2 purple and 1 red
2	ST1B	3 Coccus (Positive)	3 pueple
3	ST2A	4 Bacillus (Negative)	4 red
4	ST2B	1 Coccus (Positive) 2 Bacillus (Negatif)	1 purple and 2 red
5	ST3A	3 Bacillus (2 Negative and 1 Positive)	1 Purple and 2 red
6	ST3B	1 Coccus (Positive) and 2 Bacillus (Negative)	1 Purple and 2 red

Colony Morphology

Tabel 2. Colony Morphology

No	Sample Code	Colony Form	Colony Color
1	ST1A	Circular	Beige
2	ST1A	Circular	Beige
3	ST1A	Circular	Beige
4	ST1B	Circular	Beige
5	ST1B	Circular	Beige
6	ST1B	Circular	Beige
7	ST2A	Circular	Beige
8	ST2A	Circular	Beige
9	ST2A	Circular	Beige
10	ST2A	Circular	Beige
11	ST2B	Circular	Beige
12	ST2B	Circular	Beige
13	ST2B	Circular	Beige
14	ST3A	Circular	Beige
15	ST3A	Circular	Beige
16	ST3A	Circular	Beige
17	ST3B	Circular	Beige
18	ST3B	Circular	Beige
19	ST3B	Circular	Beige

Description: ST; Station code A-B; Sample codes 1-4; Bacterial growth in the media

Based on the results of the research carried out, it was found that there were 12 (twelve) types of bacteria, shown in table 3.

Table 3. Types of Bacteria

No	Nama Bakteri
1	*Aeromonas hydrophila*
2	*Aeromonas sobria*
3	*Aeromonas caviae*
4	*Citrobacter freundii*
5	*Edwardseilla tarda*
6	*Escherichia coli*
7	*Staphylococcus aureus*
8	*Staphylococcus epidermidis*
9	*Plesiomonas shigelloides*
10	*Bacillus subtilis*
11	*Listeria* sp
12	*Enterobacter cloacae*

From Table 1, the gram-positive and gram-negative test results showed that there were 19 bacterial isolates from both ST1A (2 gram-positive and 1 gram-negative), ST1B (3 gram-positive), ST2A (4 gram-negative), ST2B (1 gram -positive and 2 gram-negative), ST3A (1 gram-positive and 2 gram-negative) and ST3B (1 gram-positive and 2 gram-negative). It is known that gram negatives will produce mucus and gram positives will not produce mucus when dripped with 3% KOH liquid. According to Suwanda (2008), the suspension turns slimy, sticky, and is lifted like a thread with the loop needle, meaning

gram negative bacteria (-). If the suspension remains runny, it is not lifted with the loop needle, it means gram positive bacteria (+).

Observation of gram staining showed that only 9 bacterial isolates were gram positive and 10 isolates were gram negative, with coccus and bacillus cells. Of the 19 bacterial isolates, most were found to be in the form of coccus. This is in accordance with research (Suryanto & Munir, 2006), that there are more gram-negative bacteria in the form of bacillus cells and gram-positive coccus. According to (Rostinawati, 2008) gram staining is used to determine the morphology of bacterial cells and differentiate gram-positive and gram-negative bacteria.

(Barrow & Feltham (1993), stated that gram-positive bacteria are purple in gram staining because the crystal violet-iodine dye complex is retained even though they are given an alcoholic acetone bleaching solution, while gram-negative bacteria are red because the complex dissolves when the acetone bleaching solution is applied. alcohol so it takes on the red color of safranin.

The difference in color between gram-positive and gram-negative bacteria indicates that there are differences in the cell wall structure between the two types of bacteria. Gram-positive bacteria have a cell wall structure with a thick peptidolecan content, while gram-negative bacteria have a cell wall structure with a high lipid content (Fitri & Yasmin, 2011).

Based on the results of table 2. above, it shows that the shape of the bacterial colonies starting from stations ST1A, ST1B, ST2A, ST2B, ST3A and ST3B, has a circular shape. In the table you can also see the color of the colony, namely cream. The colony morphology of bacterial isolates found in this study is in accordance with the statement (Budiharjo et al., 2013), that in general the shape of bacterial colonies is circular, irregular, filamentous and rhizoid.

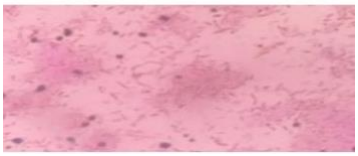
Observations regarding the morphological characteristics of bacterial colonies need to be carried out, in order to facilitate the process of identifying bacterial types. This is in accordance with the statement (Lay, 1994), that based on the morphological characteristics of bacterial colonies and pure cultures, the process of identifying types of bacterial microorganisms can be carried out. According to Budiharjo, (2013) stated that morphological characterization aims to observe both colony morphology and bacterial cell morphology in bacterial isolates that have passed selection. Microorganisms grown in various media will show different macroscopic appearances during their growth.

From table 3, 13 types of bacteria were found, namely *Aeromonas hydrophila, Aeromonas sobria, Aeromonas caviae, Bacillus subtilis, Citrobacter freundii, Citrobacter diversus, Edwardseilla tarda, Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis, Plesiomonas shigelloides, Enterobacter cloacae* and *Listeria* sp. The following is the classification and description of the types of bacteria in the water found at the Pier Base on the Sebangau River:

1. *Aeromonas hydrophila*

   The classification of *Aeromonas hydrophila* bacteria according to (Endari, 2009) is as follows:

   Phylum : Protopyhta
   Class : Schizomycetes
   OrdO : Pseudanodeles
   Family : Vibrionaceae
   Genus : *Aeromonas*
   Species : *Aeromonas hydrophila*



Gambar 1. *Aeromonas hydrophila*

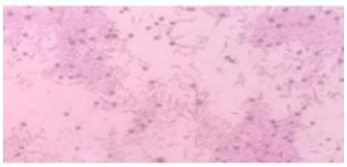
Aeromonas hydrophila was first discovered in 1962, by Hoshina when observing the cause of a disease that attacks fish and eels called red fin. Aeromonas hydrophila has been linked to several diseases in fish, including tail lesions, gill damage and septicemic hemorrhage (Galuh, 2016).

Aeromonas hydrophila is a bacteria that is often found in freshwater environments, especially in environments rich in organic matter. The optimal temperature for the growth of this bacteria is 20-37^{o}C (Pathol et al., 2009). *Aeromonas* sp. bacteria could potentially become a pathogen, depending on the level of prevalence and intensity of disease attacks on fish (Suraya et al., 2011).

2. *Aeromonas sobria*

The classification of *Aeromonas sobria* bacteria according to Kreig & Holt (1984) is as follows:

Phylum : Proteobacteria
Class : Gammaproteobacteria
Ordo : Aeromondales
Family : Aeromonadaceae
Genus : *Aeromonas*
Species : *Aeromonas sobria*



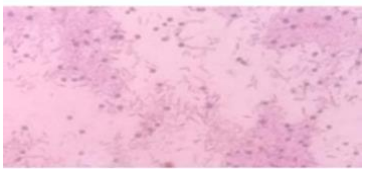
Gambar 2. *Aeromonas sobria*

Aeromonas sobria is a bacteria that produces enzymes and toxins as an ECP product or Extra Cellular product in which homolysis and protease activity occurs which are dangerous or pathogenic to fish. *Aeromonas sobria* can basically be isolated from various environments where bacteria are common. The habitats of these bacteria include water, fish, food, livestock, invertebrate species, birds, ticks, insects and soil. *Aeromonas sobria* has been recognized as a bacterial pathogen in fish since 1987 and was first discovered in the gizzard of wild shad (*Dorosoma cepedianum*) in the United States. Furthermore, the number of cases throughout the world continues to increase, for example in Turkey, *A. sobria* was found in the intestines of Atlantic salmon (*Salmo salar*). This pathogen was also detected in rainbow trout (*Oncorhychus mykiss*), goldfish (*Carassius auratus*), green terror fish (*Andinocara rivulatus*), ika dorade (*Sparus aurata*) and sea bass (*Dicentrarchus labrax*) in Turkey (Nursabrina, 2021).

3. *Aeromonas caviae*

The classification of *Aeromonas caviae* bacteria according to Kreig & Holt (1984) is as follows:

Phylum : Proteobacteria
Class : Gammaproteobacteria
Ordo : Aeromondales
Family : Aeromonadaceae
Genus : *Aeromonas*
Species : *Aeromonas caviae*



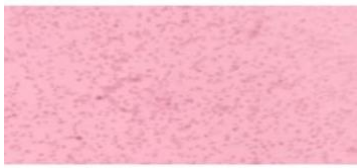
Gambar 3. *Aeromonas caviae*

Aeromonas caviae is an acoustic microorganism that lives in marine and fresh waters. *Aeromonas* species are gram-negative, facultative anaerobic bacteria belonging to the Aeromonadaceae family. Members of the genus *Aeromonas* are straight rods with rounded cell ends that are close to spherical in shape, 0.3-1.0 µm in diameter and 1.0-3.5 µm in length. Cells are found in unicellular form or in groups. The Aeromonas genus grows at optimal temperatures ranging from 22-28 oC and many members of the species grow well at temperatures of 37^{o}C (Olga et al., 2020).

4. *Citrobacter freundii*

According to Sabir (2021) the taxonomy of *Citrobacter freundii* bacteria is as follows:

Phylum : Proteobacteria
Class : Gammaproteobacteria
Ordo : Enterobacteriales
Family : Enterobacteriacae
Genus : *Citrobacter*
Speies : *Citrobacter freundii*



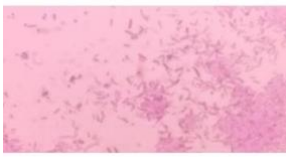
Gambar 4. *Citrobacter freundii*

Citrobacter sp. has the characteristic morphology of round colonies with flat edges, white colonies with convex surfaces. Citrobacter genus bacteria have rod-shaped characteristics with a diameter of between 2-6 µm. This bacterium is also a gram-negative bacterium which is motile, facultative anaerobic and can grow at an optimal temperature of 37^{o}C and can grow at pH 5-9. *Citrobacter* sp. and *Shigella* sp. bacteria are indicator bacteria in water, food, etc. which are classified as gram-negative bacteria. Since it is known that these bacteria spread to all individuals, bacteriological analysis has had positive results for *Citrobacter* sp. and *Shigella* sp. bacteria in total. Certain types can be used as indicators of the presence of pathogenic bacteria in water (Sabir, 2021).

5. *Edwardsiella tarda*

According to Park et al., (2012), the classification of *Edwardsiella tarda* is as follows:

Phylum : Bacteria
Class : Gammaproteobacteria
Ordo : Enterobacteriales
Family : Enterobacteriacae
Genus : *Edwardsiella*
Species : *Edwardsiella tarda*



Gambar 5. *Edwardsiella tarda*

This bacteria can be found in freshwater and seawater environments, with an optimal temperature for growth of around 35 oC. At temperatures below 10^{o}C or above 45^{o}C it cannot grow. This bakery can survive 0-4% sodium chloride, pH 4.0-10.0 and temperature 14-45^{o}C (Park et al., 2012).

According to Narwiyani & Kurniansih, (2011) *Edwardsiella tarda* has spread to several countries including Europe, Japan, Taiwan, Thailand, the United States, Singapore and Malaysia. In Indonesia, *Edwardsiella tarda* has been found in Java, Sumatra and Kalimantan. Edwardsiella tarda can be identified through clinical symptoms, isolation and molecular DNA. *Edwardsiella tarda* is the cause of septicemia with serious wounds on the skin, attacking internal organs such as: liver, kidneys, spleen and muscles. These bacteria attack the host's defense mechanisms, therefore the proliferation process of these bacteria is very fast in the host and causes death. Differences in the pathogenesis of Edwardsiella tarda in various types of fish, especially freshwater fish in Indonesia, have never been reported in detail.

6. *Escherichia coli*

According to Nurtsani (2018) classification of *Escherichia coli* is as follows:

Phylum : Proteobacteria
Class : Gammaproteobacteria
Ordo : Enterobacteriales
Family : Enterobacteriacae
Genus : *Escherichia*
Species : *Escherichia coli*

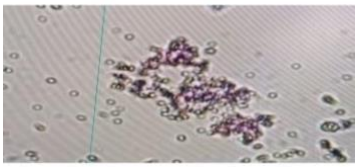
Gambar 6. *Escherichia coli*

Escherichia coli bacteria commonly live in the digestive tract of humans or animals. Physiologically, *Escherichia coli* has the ability to survive in difficult environmental conditions. *Escherichia coli* grows well in fresh water, sea water, or ground water. In these conditions, Escherichia coli is exposed to the abiotic and biotic environment. Diseases caused by *Escherichia coli* are caused by its ability to adapt and survive in different environments. There are several types of environmental conditions that are not favorable for *Escherichia coli* to survive, for example acidic environments (low pH) such as in the human tract, changes in temperature and osmotic pressure (Rahayu et al., 2018).

7. *Staphylococcus aureus*

According to Saraswati (2015) classification of *Staphylococcus aureus* is as follows:

Phylum : Proteobacteria
Class : Gammaproteobacteria
Ordo : Enterobacteriales
Family : Micrococaceae
Genus : *Staphylococcus*
Species : *Staphylococcus aureus*



Gambar 7. *Staphylococcus aureus*

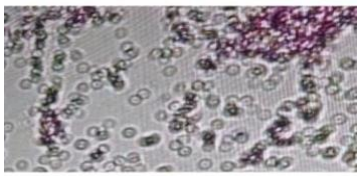
According to Rahmaningsih et al., (2017) *Staphlococcus aureus* has a round cell shape and is nonmotile. Biochemical characteristics are gram-positive reactions, producing oxidase, producing indole, negative use of carbon from citrate, positive catalase, hydrolyzing glatin and fermenting mannitol.

Staphylococcus aureus is a gram-positive bacterium, a member of the Micrococcus family, which is round, clusters like the arrangement of grapes, the colonies are gray to dark colored, cougulase positive and is a commensal bacterium in the human body whose numbers are balanced with other normal flora. S. aureus in humans is found in the nose, skin, throat, etc. Saraswati (2015).

8. *Staphylococcus epidermidis*

According to Saraswati (2015) classification of *Staphylococcus epidermidis* is as follows:

Phylum : Firmincutes
Class : Bacilli
Ordo : Bacillales
Family : Stapyhlococcaceae
Genus : *Staphylococcus*
Species : *S. epidermidis*



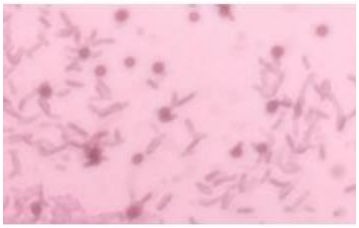
Gambar 8. *Staphylococcus epidermidis*

Staphylococcus epidermidis is a bacteria that is often found as normal flora on human skin and mucous membranes. Staphylococcus epidermidis is a round-shaped gram-positive bacteria, usually arranged in irregular series like grapes and is a facultative anaerobe. This bacteria causes mild skin infections accompanied by abscesses (Saraswati, 2015).

9. *Plesiomonas shigelloides*

According to Mindar et al., (2017) classification of *Plesiomonas shigelloides* is as follows:

Phylum : Protobacteria
Class : Gammaprotobacteria
Ordo : Enterobacterales
Family : Vibriomaceae
Genus : *Plesiomonas*
Species : *P. shingelloides*



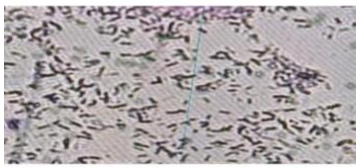
Gambar 9. *Plesiomonas shigelloides*

Plesiomonas shigelloides is a bacterium that is often found in the surrounding environment but is most often found in water, both in fresh water and sea water. This is in accordance with the statement by Mindar et al., (2017), that *Plesiomonas shigelloides* is an environmental organism but is mostly associated with water, both fresh water and sea water. Plesiomonas shigelloides bacteria are bacteria in the same family as Vibrionaceae. And *Plesiomonas shigelloides* is a water and soil sediment bacterium that has proteolytic abilities and is a pathogenic bacteria that is detrimental to organisms (Rizaldi et al., 2018).

10. *Bacillus subtilis*

According to Nirma (2018) classification of *Bacillus subtilis* is as follows:

Phylum : Firmicutes
Class : Bacilli
Ordo : Bacillales
Family : Bacillaceae
Genus : *Bacillus*
Species : *Bacillus subtilis*



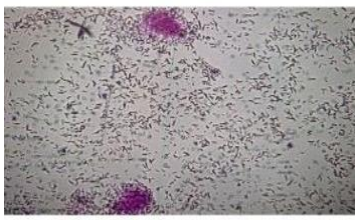
Gambar 10. *Bacillus subtilis*

Bacillus subtilis, also known as hay bacillus or grass bacillus, is found in the soil and digestive tract of ruminants and humans. *Bacillus subtilis* is usually rod-shaped, and is approximately 4-10 micrometers long and 0.25-1.0 micrometers in diameter. Like other members of the genus *Bacillus*, it can form endospores to survive extreme environmental conditions of temperature and desiccation. *Bacillus subtilis* is a facultative anaerobe and was considered an obligate aerobe until 1998. Bacillus subtilis is highly flagellated, which gives it the ability to move quickly in fluids. Bacillus subtilis has been proven to manipulate genetics and has been widely adopted as a model organism for laboratory research, especially of sporulation which is a simple example of cellular differentiation (Nirma, 2018).

11. *Listeria* sp.

According to Putra (2021)classification of *Listeria* sp. is as follows:

Phylum : Firmicutes
Class : Bacilli
Ordo : Bacillales
Family : Listeriaceae
Genus : *Listeria*
Species : *Listera* sp.



Gambar 11. *Listeria* sp.

Listeria sp. The genus Listeria contains a number of species including *L. Monocytogenes, L. Innocua, L. welshimeri, L. Seeligeri, L. Ivanovii, L. Marthii, and L. Grayi, which are considered pathogenic. L. Monocytogenes* is an important human foodborne pathogen and the third leading cause of microbial foodborne deaths in the United States. Initially the microorganism isolated from this case was named Bacterium monocytogenes because the infection that occurred showed typical symptoms in the form of monocytosis. Isolated similar bacteria from the liver of an infected gerbile (a type of laboratory animal) and named it *Lesteria hepatolytica* in 1940 (Putra, 2021).

12. *Enterobacter cloaceae*

According to Garrity et al., (2004) classification of *Enterobacter cloaceae* is as follows:

Phylum : Protobacteria
Clasa : Gammaprotobacteria

Ordo : Enterobacteriales
Family : Enterobacteriaceae
Genus : *Enterobacter*
Species : *Enterobacter cloaceae*


Gambar 12. *Enterobacter cloaceae*

Enterobacter cloacae bacteria are the only bacteria that are not pathogenic to fish because they do not produce exotoxine and endoxitoxin but produce enzyme *ß*-galatoksidase which can break down lactose into glucose and galactose which are easily digested in the fish intestines. *E. cloacae* produces ß-gallatoxidase, arginine dihydrolase and ornithine decarboxylase (Mahendra, 2016).

Grimont & Grimont (2006) explained the original habitat of *Enterobacter* sp. unknown until now, but *Enterobacter* sp. Widely distributed in the environment, food, water, soil and vegetables. *Enterobacter* sp. It reproduces well in the intestines of all warm-blooded animals and is usually absent in the intestines of fish and cold-blooded animals. And Keller et al., (1998) added that organs that often become breeding grounds for Enterobacter sp. in the body of cold-blooded animals is the intestines and then spreads to other organs such as the kidneys and liver.

CONCLUSSION AND SUGGESTION

Based on the results of research conducted at the Sebangau River Pier Base, Palangka Raya City, it was found that there were 12 (thirteen) types of bacteria, namely: *Aeromonas hydrophila, Aeromonas sobria, Aeromonas caviae, Citrobacter freundii, Edwardseilla tarda, Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis, Plesiomonas shigeloides, Bacillus subtilis, Listeria sp, and Enterobacter cloacae.*

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