Report Panta Germ Test

Tank Name: XXXXXXX

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Table of Contents

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Executive Summary – Key Findings at a Glance

Summary of your results:

- The **total bacterial count** in the water sample is within **the moderate range (10^4–10^6 germs/ml)**
- The **water sample** shows **high species richness** combined with **very high diversity** and **evenness**
- **The biofilm** exhibits **low species richness** but **high diversity** and **complexity**
- **No primary fish-pathogenic bacteria** were detected
- **Several facultative pathogenic bacterial** species were detected
- **Cyanobacteria were detected** mainly in the **biofilm sample**

Overall assessment:

Both the water and biofilm samples exhibit **diverse** and **functionally stable microbial communities**. The **water microbiome** is characterized by **very high diversity** and an **exceptionally balanced distribution** of bacterial species, while the **biofilm shows lower species richness** but maintains **high diversity** and **structural stability**. **No primary fish pathogens** were detected; however, the **occurrence of facultative pathogens** and **cyanobacteria** should be monitored as part of routine system management.

PGS: 74

PantaGermScore[1]

Predominant bacterial species in water: *Thalassotalea euphylliae*
Predominant bacterial species in biofilm: *Litoreibacter ponti*

[1]**Definition Panta Germ Score (PGS):** The Panta Germ Score (PGS) is an easy-to-understand overall measure for assessing microbial diversity in aquatic systems. It combines the parameters species richness, Shannon diversity index, Simpson diversity index, and evenness into a weighted score. The PGS enables a clear, qualitative assessment of the microbiome and makes the ecological condition of a system understandable even to readers without a scientific background. The score is presented on a scale from 0 to 100 and additionally visualized using a five-level color scale. The exact numerical value of the calculated score is displayed in the color corresponding to the assessment: 0–20 (Red) = Urgent need for action: severely limited microbial diversity, high risk of instability; 21–40 (Orange) = Need for action: significantly unbalanced microbiome, targeted measures required; 41–60 (Yellow) = Optimizing conditions is advisable: stable foundation present, potential for improvement exists; 61–80 (Light Green) = Good conditions for the microbiome: balanced and resilient microbial community; 81–100 (Green) = Optimal microbiological composition and stability: very high diversity and balance.

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Water Sample Analysis

Bacterial abundance in water

The **total bacterial count** ranges between **10^4 and 10^6 germs per milliliter**, indicating a moderate microbial density. This range is typical for biologically active aquatic systems and does not represent a critical finding on its own.

Important note:

It is not the absolute number of bacteria that determines system health, but rather their composition and balance.

Bacterial diversity in the water

The analysis shows:

- **Species Richness:** high number of species
- **Simpson‘s Diversity Index:** very high diversity
- **Shannon Diversity Index:** very high complexity
- **Evenness:** very high evenness of distribution

This means:

- Broad functional diversity
- Very high microbial diversity and complexity
- Evenly distributed bacterial community

Overall, the **water microbiome** can be described as a **highly diverse** and **balanced** bacterial community that is **functionally resilient.**

Composition of the bacterial community in the water

The most abundant bacterial species detected were:

- *Thalassotalea euphylliae (3.55%)*
- *Alkalimarinus sediminis (3.28%)*
- *Aliikangiella marina (3.21%)*
- *Thalassotalea montiporae (3.14%)*
- *Cognatishimia maritima (2.46%)*

Assessment

No pronounced dominance of individual bacterial species was observed. The community shows a very even distribution and broad functional diversity. Although the PGBI highlights moderate deviations for some taxa, the overall bacterial community remains highly balanced and microbiologically stable.

Bacterial diversity in the biofilm

The analysis shows:

- **Species Richness:** very low number of species
- **Simpson‘s Diversity Index:** very high diversity
- **Shannon Diversity Index:** high complexity

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- **Evenness:** high evenness of distribution

This means:

- Low number of species present
- High functional diversity and complexity
- Evenly distributed bacterial community

Overall, the **biofilm** represents a **stable and structured microbial community.**

Composition of the bacterial community in the biofilm

The most abundant bacterial species detected in the biofilm were:

- *Litoreibacter ponti (10.98%)*
- *Marinicella sediminis (9.35%)*
- *Granulosicoccus marinus (8.94%)*
- *Odorella benthonica (6.50%)*
- *Fluctibacter halophilus (4.27%)*

Assessment

Several species occur at elevated relative abundances, while the overall distribution remains balanced. The biofilm exhibits high diversity and a broad functional spectrum, resulting in a stable and resilient microbial community.

Detection of pathogenic bacteria

Primary fish pathogens

No primary fish-pathogenic bacterial species were **detected** in either the water or biofilm samples.

Assessment:

- No indication of an acute bacterial disease risk
- Microbiologically unremarkable findings

Facultative pathogenic bacteria

The following facultative pathogenic bacterial species were detected in the water sample:

- *Vibrio fortis, Vibrio parahaemolyticus, Vibrio alginolyticus, Vibrio harveyi, Vibrio proteolyticus*

Assessment

These bacteria are common members of marine microbial communities and are generally harmless under stable environmental conditions. If present, they may act as opportunistic pathogens under stress or deteriorating water quality and should therefore be considered during routine monitoring.

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Detection of Cyanobacteria

The following cyanobacterial species (>0.1%) were detected:

Acaryochloris marina, Cymatolege isodiametrica, Odorella benthonica, Pleurocapsa fuliginosa, Waterburya agarophytonicola.

Significance

- Indication of cyanobacterial presence within the system
- May reflect environmental conditions that support cyanobacterial growth
- Should be evaluated in the context of nutrient availability and overall microbial balance

Recommended Actions

- Regularly monitor animal behavior (feeding, respiration, activity)
- Maintain stable water parameters & Check nutrient levels (e.g., nitrate, phosphate)
- Optimize flow and lighting conditions if necessary
- Avoid sudden system changes

The **goal** is to **achieve a balanced** and **resilient microbiome** in the long term.

Overall Conclusion

Strengths

- Very high diversity and complexity in the water sample
- Exceptionally high evenness and balanced bacterial distribution
- Stable and diverse biofilm community
- Absence of primary fish pathogens

Notable Findings:

- Facultative pathogenic Vibrio species detected
- Cyanobacteria detected in the biofilm sample

Final Assessment:

The investigated system exhibits a highly diverse and functionally balanced microbiome in both the water column and the biofilm. High diversity indices and excellent evenness values indicate a resilient microbial community with strong ecological stability. While facultative pathogens and cyanobacteria are present, no primary fish pathogens were detected. Overall, the system can be classified as microbiologically stable and well balanced.

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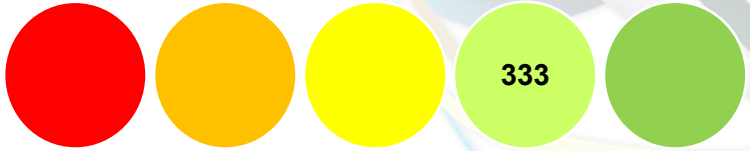
Your test results: Water sample

The **total bacterial count** in your water sample ranges between **10^4 and 10^6 germs per ml** and indicates a **moderate microbial density**.

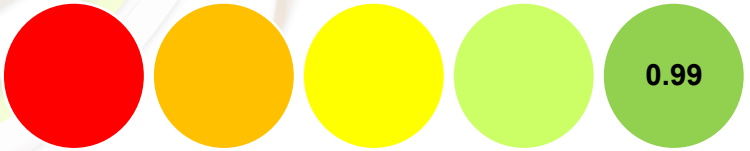
Gesamtkeimzahl pro ml / total bacterial count per ml

The analysis of the diversity of the bacterial community in the submitted water sample showed that a high number of different bacterial species was present and therefore a **high species richness** was observed. Two diversity indices were evaluated. In your water sample, the **Simpson diversity index** ranged between 0.80 and 1, indicating **very high bacterial diversity**. The **Shannon diversity index** is above 4.00 and indicates **very high diversity and complexity** of the microbial community in the water. The value for the **evenness of bacterial distribution** in your water sample ranged between 0.80 and 1 and is therefore classified as **very high**.

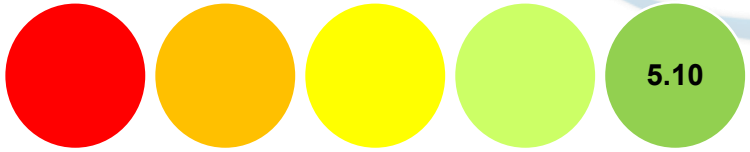
Species Richness



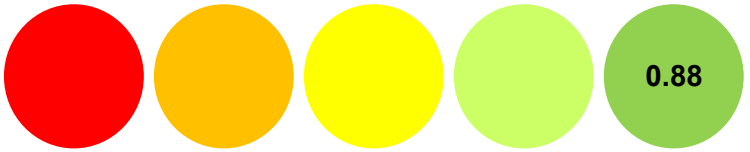
Simpson's Diversity Index



Shannon Diversity Index



Evenness



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Bacterial composition in your water sample:

Table 1: The ten most detected bacterial families and their representatives by genus/species

Bakterienfamilie / bacterial family	Bakteriengattung / bacterial genus	Bakterienspezies / bacterial species	Prozentualer Anteil [%] mit PGBI-Bewertung / percentage [%] with PGBI-rating
Colwelliaceae	*Thalassotalea*	Sonstige/Others	11.612%
		Thalassotalea euphylliae	**3.552%**
		Thalassotalea montiporae	**3.142%**
	Thalassomonas	*Thalassomonas actiniarum*	**0.273%**
		Thalassomonas viridans	**0.205%**
		Thalassomonas haliotis	**0.068%**
	Sonstige/Others	Sonstige/Others	0.478%
Roseobacteraceae	Sonstige/Others	Sonstige/Others	8.197%
	Ruegeria	Sonstige/Others	2.322%
		Ruegeria conchae	**1.298%**
		Ruegeria arenilitoris	**1.093%**
	Shimia	*Shimia marina*	**0.956%**
		Sonstige/Others	0.410%
		Shimia isoporae	**0.410%**
Alteromonadaceae	Sonstige/Others	Sonstige/Others	3.484%
	Alkalimarinus	*Alkalimarinus sediminis*	**3.279%**
	Fluctibacter	*Fluctibacter halophilus*	**1.981%**
Paracoccaceae	Sonstige/Others	Sonstige/Others	3.893%
	Cognatishimia	*Cognatishimia maritima*	**2.459%**
	Pikeienuella	*Pikeienuella piscinae*	**0.478%**
Vibrionaceae	*Vibrio*	Sonstige/Others	2.254%
		Vibrio fortis	**1.571%**
		Vibrio tubiashii	**0.410%**
Hyphomicrobiaceae	*Methyloceanibacter*	*Methyloceanibacter caenitepidi*	**1.776%**
	Filomicrobium	*Filomicrobium fusiforme*	**0.683%**

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		Filomicrobium insigne	**0.478%**
	Hyphomicrobium	*Hyphomicrobium nitrativorans*	**0.683%**
Pleioneaceae	*Aliikangiella*	*Aliikangiella marina*	**3.210%**
	Pleionea	*Pleionea mediterranea*	**0.205%**
Erythrobacteraceae	*Pontixanthobacter*	*Pontixanthobacter luteolus*	**1.366%**
		Pontixanthobacter aquaemixtae	**0.137%**
	Erythrobacter	*Erythrobacter rubeus*	**0.205%**
		Erythrobacter longus	**0.137%**
	Qipengyuania	*Qipengyuania xiamenensis*	**0.137%**
		Qipengyuania vesicularis	**0.068%**
		Qipengyuania psychrotolerans	**0.068%**
Kordiimonadaceae	*Kordiimonas*	Sonstige/Others	0.751%
		Kordiimonas pumila	**0.615%**
		Kordiimonas lacus	**0.546%**
Terasakiellaceae	*Terasakiella*	*Terasakiella brassicae*	**1.434%**
		Terasakiella pusilla	**0.478%**
Sonstige/Others	Sonstige/Others	Sonstige/Others	33.197%

[2]**Panta Germ Balance Index (PGBI):** The Panta Germ Balance Index (PGBI) is an assessment tool designed to visually represent the distribution of microbial species in aquatic systems. Green indicates a balanced presence, yellow indicates moderate deviations, and red indicates significant imbalances. In this way, the PGBI highlights both over- and under-representations of individual species and enables a quick, intuitive assessment of the microbiome's balance.

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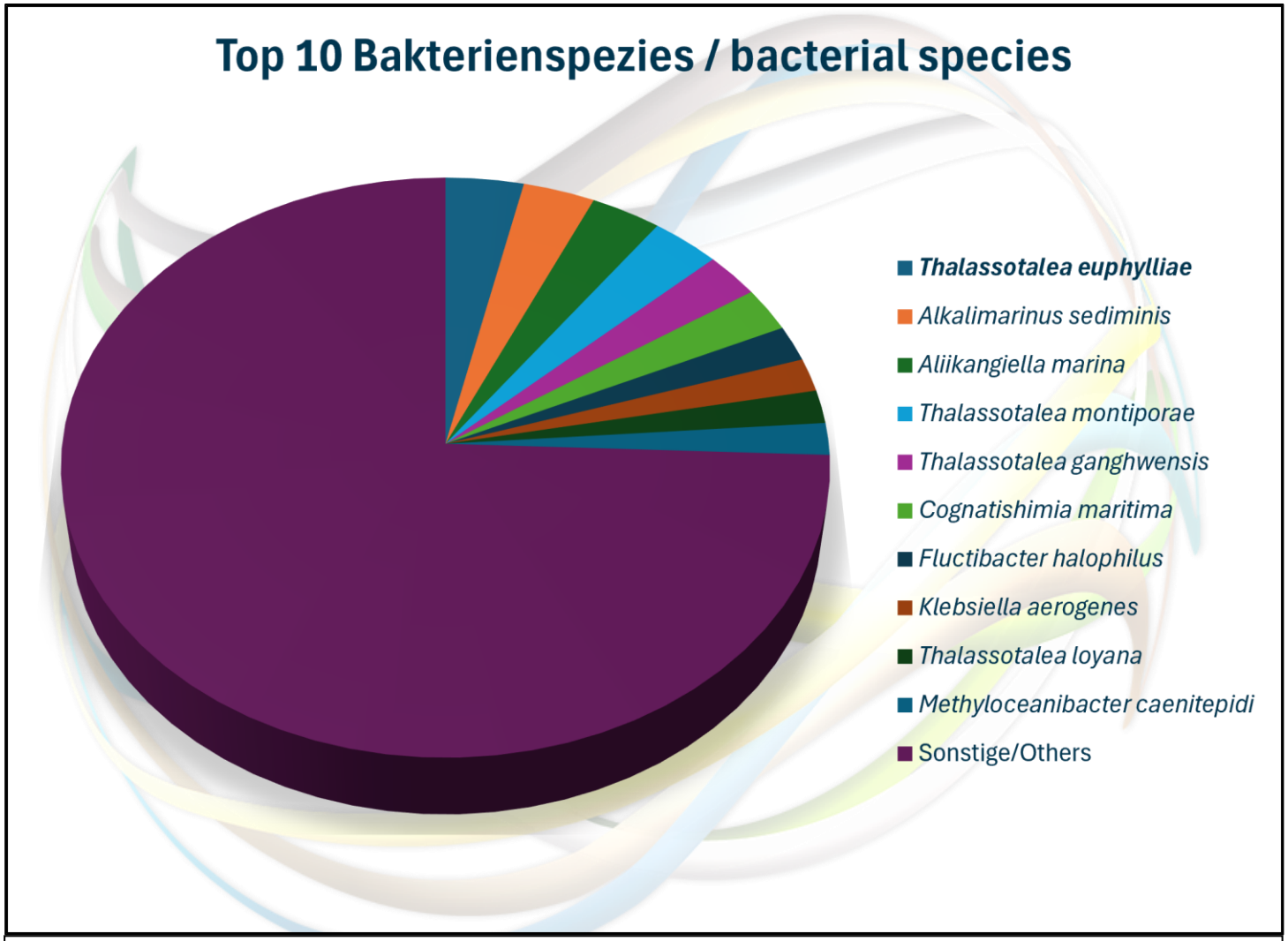

Pie chart showing the ten most detected bacterial species in the water sample.

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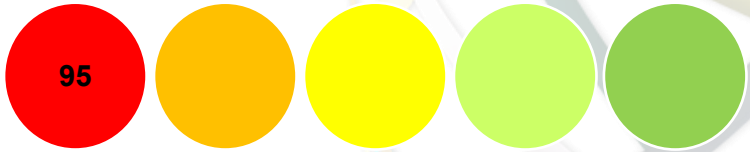
Your test results: Biofilm sample

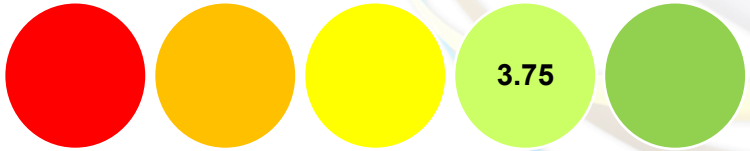
The analysis of the diversity of the bacterial community in the submitted biofilm sample showed that a very low number of different bacterial species was present and therefore a **very low species richness** was observed. Two diversity indices were evaluated. In your biofilm sample, the **Simpson diversity index** ranged between 0.80 and 1, indicating **very high bacterial diversity**. The **Shannon diversity index** ranges between 3.00 and 3.99 and indicates **high diversity and complexity** of the microbial community in the biofilm. The value for the **evenness of bacterial distribution** in your biofilm sample ranged between 0.80 and 1 and is therefore classified as **very high**.

Species Richness

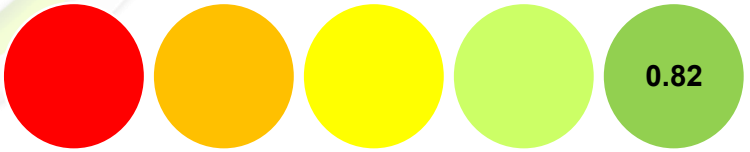


Simpson's Diversity Index

Shannon Diversity Index



Evenness



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Bacterial composition in your biofilm sample:

Table 2: The ten most detected bacterial families and their representatives by genus/species

Bakterienfamilie / bacterial family	Bakteriengattung / bacterial genus	Bakterienspezies / bacterial species	Prozentualer Anteil [%] mit PGBI-Bewertung / percentage [%] with PGBI-rating
Roseobacteraceae	*Litoreibacter*	***Litoreibacter ponti***	10.976%
		Litoreibacter roseus	1.423%
	Sonstige/Others	Sonstige/Others	4.675%
	Sulfitobacter	*Sulfitobacter alexandrii*	2.236%
		Sonstige/Others	0.610%
		Sulfitobacter noctilucicola	0.610%
Alteromonadaceae	Sonstige/Others	Sonstige/Others	4.472%
	Alteromonas	*Alteromonas facilis*	1.829%
		Alteromonas aestuariivivens	1.423%
		Sonstige/Others	1.220%
	Fluctibacter	*Fluctibacter halophilus*	4.268%
Granulosicoccaceae	*Granulosicoccus*	*Granulosicoccus marinus*	8.943%
		Granulosicoccus coccoides	4.268%
Alcanivoracaceae	*Marinicella*	*Marinicella sediminis*	9.350%
		Marinicella litoralis	0.203%
Paracoccaceae	Sonstige/Others	Sonstige/Others	4.878%
	Tritonibacter	*Tritonibacter aquimaris*	0.813%
		Tritonibacter litoralis	0.203%
	Cognatiyoonia	*Cognatiyoonia koreensis*	0.813%
Pleurocapsales_Incertae_sedis	*Odorella*	*Odorella benthonica*	6.504%
Arenicellaceae	*Perspicuibacter*	*Perspicuibacter marinus*	2.846%
	Arenicella	*Arenicella chitinivorans*	2.439%
		Arenicella xantha	0.203%
Flavobacteriaceae	*Aquimarina*	*Aquimarina agarilytica*	0.813%
		Aquimarina penaei	0.610%

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		Sonstige/Others	0.610%
	Sonstige/Others	Sonstige/Others	1.423%
	Hyunsoonleella	*Hyunsoonleella ulvae*	**0.407%**
Hyellaceae	*Pleurocapsa*	*Pleurocapsa fuliginosa*	**2.236%**
	Waterburya	*Waterburya agarophytonicola*	**1.220%**
Ahrensiaceae	*Pseudahrensia*	*Pseudahrensia aquimaris*	**1.016%**
		Pseudahrensia todarodis	**0.610%**
	Ahrensia	*Ahrensia marina*	**0.813%**
Sonstige/Others	Sonstige/Others	Sonstige/Others	15.041%

[2]**Panta Germ Balance Index (PGBI):** The Panta Germ Balance Index (PGBI) is an assessment tool designed to visually represent the distribution of microbial species in aquatic systems. Green indicates a balanced presence, yellow indicates moderate deviations, and red indicates significant imbalances. In this way, the PGBI highlights both over- and under-representations of individual species and enables a quick, intuitive assessment of the microbiome's balance.

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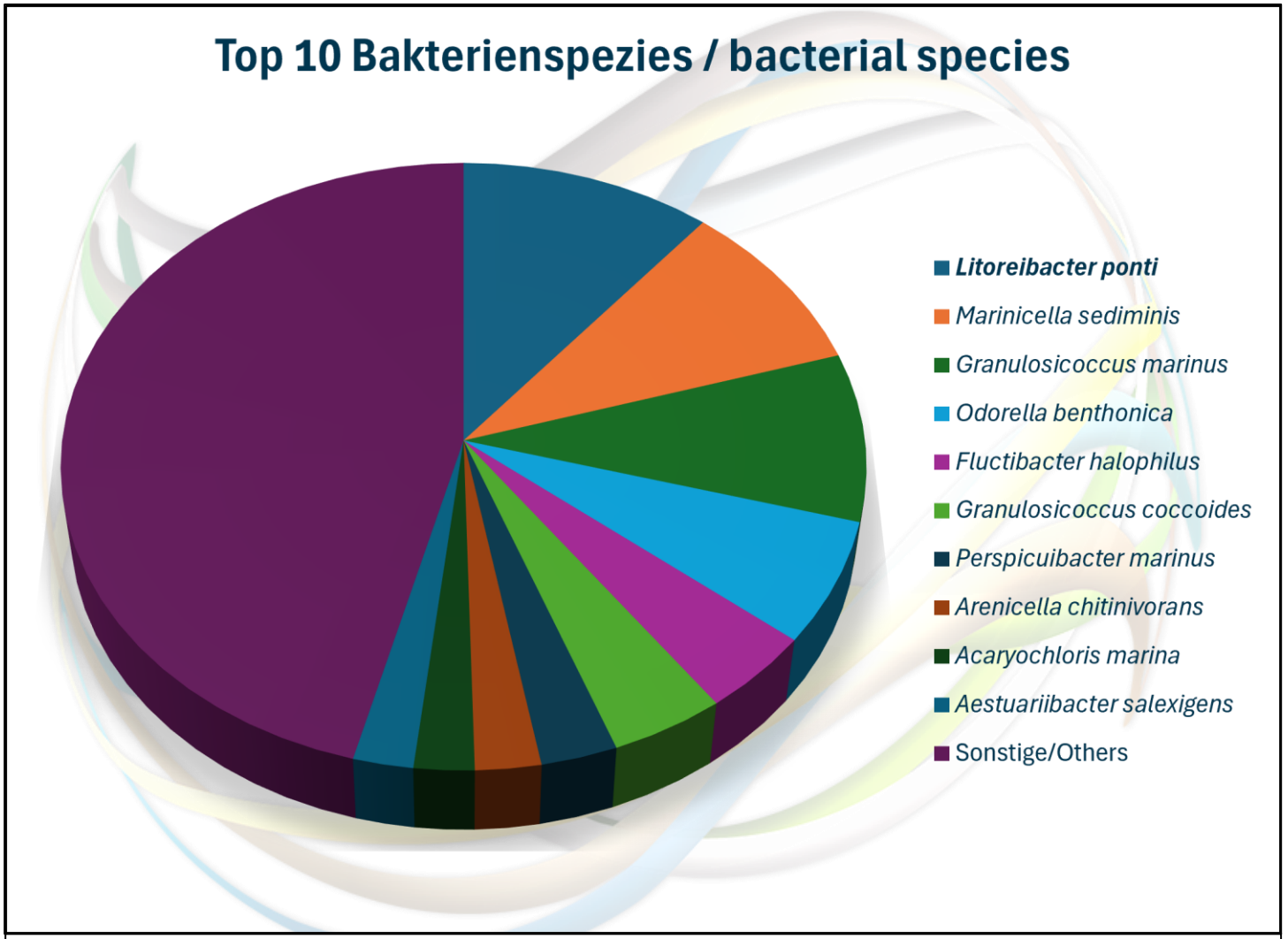

Pie chart showing the ten most detected bacterial species in the biofilm sample.

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Detection of fish-pathogenic bacteria:

None of the primary pathogenic bacterial species listed in Table 3 were detected in the samples.

Table 3: List of primary bacterial pathogens of fish tested in this analysis

Primary pathogenic bacterial species	Relative abundance in analyzed water sample (%)	Relative abundance in analyzed biofilm sample (%)
Aeromonas salmonicida	0	0
Moritella viscosa	0	0
Nocardia asteroides	0	0
Nocardia crassostreae	0	0
Nocardia salmonicida	0	0
Nocardia seriolae	0	0
Photobacterium damselae	0	0
Piscirickettsia salmonis	0	0
Renibacterium salmoninarum	0	0
Tenacibaculum maritimum	0	0
Yersinia ruckeri	0	0

The following **facultative pathogenic bacterial species** were detected in the water sample: *Vibrio fortis, Vibrio parahaemolyticus, Vibrio alginolyticus, Vibrio harveyi, Vibrio proteolyticus.*

Detection of cyanobacteria:

The following **Cyanobacteria (>0.1%)** were detected in the samples: *Acaryochloris marina, Cymatolege isodiametrica, Odorella benthonica, Pleurocapsa fuliginosa, Waterburya agarophytonicola.*

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Appendix:

List of facultative fish pathogens analyzed

Note: This list is regularly reviewed and updated in accordance with the current state of scientific knowledge.

Acinetobacter baumannii, Acinetobacter haemolyticus, Acinetobacter iwoffii, Acinetobacter johnsonii, Acinetobacter junii, Acinetobacter pittii, Aeromonas allosaccharophila, Aeromonas caviae, Aeromonas hydrophila, Aeromonas schubertii, Aeromonas jandaei, Aeromonas piscicola, Aeromonas sobria, Aeromonas veronii, Aliivibrio fischeri, Aliivibrio salmonicida, Aquaspirillum sp., Arthromitus, Branchiomonas cysticola, Chryseobacterium balustinum, Chryseobacterium oncorhynchi, Chryseobacterium piscicola, Chryseobacterium scophtalmum, Chryseobacterium shigense, Citrobacter freundii, Clavochlamydia salmonicola, Edwardsiella anguillarum, Edwardsiella ictaluri, Edwardsiella tarda, Edwardsiella piscicida, Flavobacterium araucananum, Flavobacterium branchiophilum, Flavobacterium chilense, Flavobacterium columnare, Flavobacterium johnsoniae, Flavobacterium psychrophilum, Francisella asiatica, Francisella philomiragia, Francisella piscicida, Hafnia alvei, Halomonas aquamarina, Halomonas cupida, Hepatobacterium penaei, Janthinobacterium lividum, Lactococcus garviae, Moraxella sp., Moritella marina, Mycobacterium abscessus, Mycobacterium chelonae, Mycobacterium chesapeaki, Mycobacterium fortuitum, Mycobacterium gordonae, Mycobacterium interjectum, Mycobacterium marinum, Mycobacterium montefiorense, Mycobacterium neoaurum, Mycobacterium palustre, Mycobacterium peregrinum, Mycobacterium poriferi, Mycobacterium pseudoshottsii, Mycobacterium salmoniphilum, Mycobacterium simiae, Mycobacterium scrofulaceum, Mycobacterium shottsii, Mycobacterium smegmatis, Mycobacterium stomapetiae, Mycobacterium szulgai, Mycobacterium triplex, Mycobacterium triviale, Mycobacterium ulcerans, Mycoplasma mobile, Pasteurella multocida, Pasteurella skyensis, Piscichlamydia salmonis, Proteus vulgaris, Pseudoalteromonas piscicida, Pseudomonas aeruginosa, Pseudomonas anguilliseptica, Pseudomonas fluorescens, Renichlamydia lutjani, Serratia liquefaciens, Serratia marcescens, Serratia plymuthica, Shewanella putrefaciens, Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus ictaluri, Streptococcus iniae, Streptococcus maltophilia, Streptococcus milleri, Streptococcus parauberis, Streptococcus uberis, Streptomyces hiroshimensis, Tenacibaculum aiptasiae, Tenacibaculum discolour, Tenacibaculum ovolyticum, Tenacibaculum solea, Vagococcus salmoninarum, Vibrio alginolyticus, Vibrio anguillarum, Vibrio campbelli, Vibrio cholera, Vibrio corallilyticus, Vibrio fluvialis, Vibrio harveyi, Vibrio jasicida, Vibrio mimicus, Vibrio ovensium, Vibrio owensii, Vibrio ordalli, Vibrio parahaemolyticus, Vibrio penaeicida, Vibrio proteolyticus, Vibrio splendidus, Vibrio vulnificus.

[1]Panta Germ Score (PGS): The Panta Germ Score (PGS) is an easy-to-understand overall measure for assessing microbial diversity in aquatic systems. It combines the parameters species richness, Shannon diversity index, Simpson diversity index, and evenness into a weighted score. The PGS enables a clear, qualitative assessment of the microbiome and makes the ecological condition of a system understandable even to readers without a scientific background. The score is presented on a scale from 0 to 100 and additionally visualized using a five-level color scale. The exact numerical value of the calculated score is displayed in the color corresponding to the assessment: 0–20 (**Red**) = Urgent need for action: severely limited microbial diversity, high risk of instability; 21–40 (**Orange**) = Need for action: significantly unbalanced microbiome, targeted measures required; 41–60 (Yellow) = Optimizing conditions is advisable: stable foundation present, potential for improvement exists; 61–80 (**Light Green**) = Good conditions for the microbiome: balanced and resilient microbial community; 81–100 (**Green**) = Optimal microbiological composition and stability: very high diversity and balance.

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Fundamentals of Microbial Diversity Analysis

Species Richness – How many different microorganisms are present?

Species richness describes the **number of different species** of microorganisms detected in your sample. Therefore, it provides a basic overview of the **breadth of the microbial community**, regardless of how frequently individual species occur.

A **high species richness** indicates that many different microorganisms are present in the system. This suggests a biologically **diverse microbiome with broad functional potential**.

Conversely, **low species richness** means that only a few different microorganisms are present. In such cases, the **microbiome is less diverse** and **may be more susceptible to change**.

However, **species richness alone does not indicate the balance of individual microorganisms**. For this reason, it is considered alongside diversity indices in the report, which also take into account the distribution and dominance of individual species.

Evenness – How evenly are the microorganisms distributed?

Evenness describes **how evenly the different types of microorganism are distributed in your sample**. It shows whether many species are present in similar proportions, or if certain microorganisms account for a significantly larger proportion than the rest. This distribution is illustrated by theder PGBI[2].

A **high degree of evenness** means that the microorganisms present **coexist in a balanced manner**. Such microbiomes are considered **stable** and **resilient**, as no single species dominates the system.

Low diversity means that a small number of microorganisms dominate the community. This makes the microbiome **more susceptible to disturbances or undesirable shifts**.

Evenness complements species richness:

- **Species richness** indicates how many different microorganisms are present.
- **Evenness** indicates how evenly distributed these microorganisms are within the system (PGBI[2]).

Simpson's Diversity Index – How diverse is your microbiome?

The Simpson diversity index indicates **how balanced the composition of the microbial community** in your sample is. It counts not only how many different microorganisms are present, but also **considers how evenly they are distributed**.

A **high value** indicates that the system is supported by many different microorganisms, with no single species dominating. **Such microbiomes are considered stable, resilient and well-regulated.**

A **low value** suggests that only a few microorganisms make up the majority of the community. In this case, the **microbiome is less stable**

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and may be more susceptible to disturbances, such as fluctuations in nutrients or environmental changes.

Shannon Diversity Index – How Complex Is Your Microbiome?

The Shannon diversity index measures the **diversity and complexity of the microbial community** in your sample. It **considers both** the **variety of microorganisms present** and their **distribution**.

A **high value** indicates that many different microorganisms are interacting in a **balanced manner**. This suggests a **complex, adaptable and functionally diverse microbiome** that can reliably support biological processes.

A **low value** suggests that either only a few microorganisms are present, or individual species are predominant. In such cases, the **microbiome is less complex** and may be more susceptible to change.

Comparison of the Shannon and Simpson Diversity Indices – Two Perspectives on Your Microbiome

Two complementary metrics are used to assess the diversity of your microbiome: the **Shannon diversity index** and **the Simpson diversity index**. Both describe the diversity of microorganisms, but they emphasize different aspects.

The **Shannon diversity index** primarily assesses the **overall diversity and complexity of the microbiome**. It is sensitive to the number of different microorganisms present and how evenly they are distributed. A high Shannon value indicates **a multifaceted microbiome with a broad functional range**.

The **Simpson diversity index** places greater emphasis on the **dominance of individual microorganisms**. It shows whether the system is supported by many species collectively or whether a few microorganisms account for a disproportionately large share. **A high Simpson value indicates a balanced and stable microbiome.**

Taken together, **these two indices** provide a **more complete picture**:

- The **Shannon diversity index** describes the **complexity** and **species richness of the microbiome**.
- The **Simpson diversity index** shows how **balanced** and **stable this diversity is**.

A microbiome with **high values on both indices** is considered **particularly robust, adaptable and biologically stable**.

The importance of considering multiple metrics collectively

A microbiome is a **complex ecosystem** whose condition cannot be fully described by a single metric. For this reason, the report considers four complementary parameters: **species richness, evenness, the Shannon diversity index and the Simpson diversity index**. The PGS[1] score is derived from the interaction of these four parameters. This score provides a comprehensive measure of microbial diversity in aquatic systems.

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A **reliable assessment** is only possible by **considering all four metrics** together:

- **Species richness** describes the basis.
- **Evenness** indicates balance.
- **Shannon diversity index** measures complexity.
- **Simpson diversity index** assesses stability and dominance relationships.

In summary:

A **comprehensive picture** of the microbiome emerges only when all four parameters are considered together, from biodiversity and distribution to stability and resilience.

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Practical measures to promote microbial diversity

The biodiversity of an aquatic system can be enhanced by considering it from both a chemical and an ecological perspective. The aim is to create more **ecological niches** to **provide stable living conditions** for **various microorganisms**.

1. Increase structural diversity (create habitats)

Microorganisms need **surfaces** and **hiding places** to colonize an area. Having diverse surfaces prevents individual species from becoming dominant.

The following are particularly effective:

- Different substrates, such as sand, gravel and porous materials
- Textured surfaces, such as stones, wood and ceramics
- Filter media with a large surface area
- Areas with varying flow rates

➔ **More structrue = more habitats= more species**

2. Ensure a balanced nutrient supply

A microbiome **thrives on organic matter**, but only in the **right quantities**.

Factors that promote diversity:

- Regular, moderate input of organic matter (nitrogen (N), carbon (C), sulphur (S) and phosphorus (P))
- Varied and consistent feeding/nutrient supply (different carbon sources)

Problematic factors:

- Sharp spikes in nutrient levels
- Persistently extremely nutrient-poor conditions

➔ **Diversity arises from balance, not extremes**

3. Ensure chemical stability

Many microorganisms are sensitive to sudden changes.

Important factors for biodiversity:

- Stable temperature
- Constant pH levels and salinity/conductivity
- Consistent oxygen supply throughout the entire system
- Avoidance of frequent, large water changes
- Careful use/avoidance of disinfectants (e.g. ozone, UV-C, hydrogen peroxide, etc.)

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➔ **Stable environmental conditions enable specialisation and diversity**

4. Using flow and oxygen strategically

Different microorganisms prefer different conditions.

Diversity increases when:

- There are zones with strong and weak water flow
- Oxygen-rich and oxygen-poor areas coexist within the overall system
- Not all areas are completely 'flushed through'

➔ **Heterogeneity yields maximum performance**

5. Protect the microbial balance

Excessive hygiene reduces biodiversity.

Avoid:

- Frequent, complete cleaning of filters
- Simultaneous replacement of all biological media
- Aggressive chemical cleaning agents (e.g. hydrogen peroxide or peracetic acid)

Better:

- Perform maintenance in stages
- Preserve biofilms selectively
- Clean systematically, not forcefully

➔ **Allow for a certain amount of 'biological growth'**

6. Promoting biodiversity within the system

Plants and animals significantly impact the microbiome.

The following are beneficial:

- Aquatic plants or macroalgae
- Invertebrates (e.g. snails and shrimp)
- Microfauna (e.g. copepods)
- Diverse stocking structures

➔ **More biological interactions lead to greater microbial diversity**

7. Be patient. Allow time for things to develop

A common mistake is trying to **force diversity**.

- Diversity develops over weeks or months
- Young ecosystems are almost always species-poor
- Well-maintained, stable, mature ecosystems exhibit greater diversity

➔ **Time is a crucial factor for diversity**

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