24Genetics

Olivia, this is your
oral microbiota test

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1. Introduction

The microbial world has populated the earth since almost its origins and is part of the human body and that of other animals and plants. If you are currently reading this report on a screen, it probably has bacteria on its surface. And if you have printed it out, the pages will also be colonised by microorganisms.

A microorganism is an organism that can only be seen under a microscope. Microorganisms include bacteria, protozoa, algae and fungi. Although viruses are not considered living organisms, they are sometimes classified as microorganisms.

In your body, bacteria, fungi and viruses form communities called microbiotas, which are found in different parts of the body and have bacteria in common with each other and specific bacteria found only in one part of the body. Humans live in harmony with bacteria, which provide us with a wide range of immunological, metabolic and other benefits.

The mouth is by far the part of the body most exposed to pathogens and changes. The acidity of food, hygiene or alcohol have a direct impact on the concentrations of the different bacterial communities that live in our mouth. Stress, sleep deprivation or infectious processes will also directly influence the bacterial balance in your mouth. The different bacterial communities can change their structure, sometimes some bacteria decrease and others increase to a greater or lesser extent and break their natural balance. This balance between the different types of bacteria in our oral microbiota is important, as it can be directly related to poor oral health and, indirectly, to other types of pathologies. Knowing these imbalances and their possible implications is the value of this test.

Depending on the relationship between different microorganisms and human cells, microorganisms can be classified as mutualistic, commensal and pathogenic. Mutualistic bacteria are those that obtain a benefit from our cells, and at the same time provide us with a benefit. On the other hand, commensal bacteria do not provide any benefit, but they do not cause any harm either.

Finally, pathogenic bacteria are those that possess the genetic, biochemical and structural characteristics that allow them to cause harm to the host, and are classified into primary pathogens, which always cause harm, and opportunistic pathogens. Opportunistic pathogenic bacteria are those that, under healthy conditions, do not cause harm to the body, but will act as pathogens if the body's immune system is compromised.

Generally speaking, it is more common to hear microbiome than microbiota, and the two terms are often used synonymously. However, microbiome and microbiota are two different concepts, and it should be noted that the microbiome, in addition to the study of microorganisms, includes the study of their genes and metabolites. This report looks exclusively at bacteria; it will tell you about your microbiota, specifically your oral microbiota.

In recent decades we have been learning more and more about how oral bacterial populations are directly or indirectly related to different inflammatory processes. One of the most documented currently affects mainly the gums. We are talking about periodontitis, which produces dental deterioration that can lead to the loss of teeth, or even seriously damage the bone. Prevention in oral health, based on correct daily oral and dental hygiene, allows us to keep our gums, teeth, tongue and mouth clean and healthy. In this way our teeth can fulfil their function and we will also avoid other types of complications and diseases.

More recently, a large number of studies have focused on the relationship between changes in the

microbiome and other pathologies. For example, in recent years, the number of studies on the relationship between microorganisms and cancer has increased enormously. While it has been shown that bacteria alone are not capable of inducing cancer, since independent mutations in oncogenic signalling pathways are required, they have clearly established themselves as a further risk factor to be taken into account. The mechanisms by which bacteria (and other microorganisms) can induce cancer are classified into three pathways: chronic inflammation, direct manipulation of host cells, and alteration of tissue cell homeostasis. In the specific case of the oral microbiota and cancer, the most studied pathway is that of chronic inflammation, which is responsible for 25% of human cancers and is one of the main characteristics of these pathologies.

Unlike genetics, whose variation throughout life is practically nil, the microbiota evolves and changes constantly. Therefore, the results of this report will also differ depending on when it is carried out.

The fact that the result varies over time should not be seen as a disadvantage, but rather as a way of knowing the state of our bacteria at a specific time, and having several analyses at different times allows us to see the evolution of these bacteria and, as a consequence, the evolution of certain areas of our health. We can compare it to a blood test, which we are all more than used to. It varies every time we do it and that is its value as a diagnostic tool.

In addition, advances in scientific research may change the results over time. New bacteria and correlations are continually being discovered, which can change the results and conclusions of studies. At 24Genetics we make a great effort to apply new consolidated scientific discoveries to our reports.

In any case, we remind you that any change you want to make regarding your health must be supervised by your clinical reference service.

1.1. Methodology

The analysis of your oral microbiota is carried out through an in-depth study of the bacteria in your mouth.

Bacteria, like so many other elements of biology, need to be ordered and classified. This ordering is called taxonomy, which is the science that deals with the principles, aims and methods for the hierarchical and systematic arrangement of organisms into groups based on shared characteristics or evolutionary kinship. Taxonomy is essential in order to classify families of bacteria into different larger groups (genera) and smaller groups (species).

The taxonomic order of bacteria is as follows:

- Domain
- Phylum
- Class
- Order
- Family
- Genus
- Species
- Strain

In the 24Genetics microbiota report, we will go to the genus or species level.

In our mouth we find hundreds of different species, the results you will find in your report are based on the identification and quantification of the microbial DNA sequences of each of them. To do this, metagenomics studies are used, which consist of the analysis of the genetic material obtained from an

environmental sample, in this case, the oral cavity. Within metagenomics there are different methods, the one we carry out in this report is based on the sequencing of the DNA that codes for 16S ribosomal RNA. This method focuses on the study of a specific region of the bacterial genetic material that allows the classification of bacteria by genus and species.

As for the process we follow to produce our report, the first thing we obtain is a picture of how your oral microbiota is in general terms and what is the proportion of the total bacteria that make up your mouth, i.e. your phylogenetic diversity, which is analysed based on standardised population indices and which allows us to infer how healthy or unhealthy your oral health status is.

We then evaluate these bacteria, identifying which and how many of them are detrimental to your oral health, but rather than analysing your bacteria individually or independently, we study the percentages of the different genera and species present in your microbiota, which lead us to conclude what their status is, which can be one of two:

- Eubiosis, or microbiota balance.
- Dysbiosis, or microbiota imbalance.

And finally, we apply bioinformatics algorithms through which we are able to connect the data obtained from your sample with the results of multiple publications validated by the scientific community at an international level. This is how we obtain the results that we reflect in your personalised report, to let you know the impact of each of the bacteria we analyse.

As a result, your result will indicate the estimated proportion of each bacterium with its consequent direct influence on your oral health and indirectly on some other pathologies.

It is important to note that correlations do not imply causation or predict the occurrence of disease. The report is not valid for clinical or diagnostic use.

1.2. Structure of this report

Your 24Genetics microbiota report is classified in 2 main sections:

- Pathologies section. We have included the impact of certain bacterial communities on certain pathologies, for which there is the most scientific evidence, and we describe this correlation in more detail, informing you of your personal risk level.

- Bacteria section. Although we incorporate several hundred bacteria in our algorithm, we have selected the ones we consider most relevant and describe them in more detail. Some bacteria have an impact on their own in certain diseases, although it is usually the interaction of several of them that generates a greater propensity to suffer certain pathologies.

Throughout the report you will find different genera and species of bacteria that live in your mouth.

When we talk about the percentage of concentration in the different sections of the report, we are referring to the amount of bacteria of that species or genus out of the total bacteria in your microbiota, so that we tell you whether they are within or outside the range considered normal for health.

2. Frequently asked questions

Is the microbiome the same as the microbiota?

The microbiome is the set of microorganisms, genes and metabolites of an organism. It is a broader and more general concept, while the microbiota corresponds to the set of microorganisms that live in our body, either in a specific part or in the whole.

However, outside the scientific field, both terms are used interchangeably and are often considered synonyms.

Is oral microbiota the same as gut microbiota?

Oral microbiota is found in the mouth and gut microbiota in the gut. But the location, which gives them their name, is not the only difference between the two, but also the species and genera of bacteria that populate them. Some bacteria can be found in both areas of the body, but others are exclusive to one area.

Is having bacteria bad?

It depends on which bacteria. As mentioned above, we can have harmful bacteria, some of which inevitably result in the development of disease, but there are also bacteria called commensals, with which the body has a symbiotic relationship and which are harmless or even beneficial to us. However, an imbalance of these same commensal bacteria (dysbiosis) can be detrimental to health.

The human microbiome is made up of 100 billion microorganisms, many of which benefit from us and we from them.

How reliable are my results?

Our methodology ensures that the result of your report closely matches the reality of your microbiota, and the number of scientifically validated studies we apply in our algorithm allows us to ensure that the 24Genetics microbiota test is as reliable as current science allows.

Furthermore, we take care of the quality of our microbiota test in every detail of the process, from the sample collection kits to the way we write our reports to make them easy to understand. Only by providing adequate and accurate information will we fulfil our purpose as a company: to help you take advantage of the knowledge of your microbiota to make the best decisions in managing your health and well-being.

Is it possible that I will get different results in my microbiota report than in my genetic health report?

Yes, the reason is simple: your microbiota analysis is based on the study of the bacteria that live in your mouth, while in your genetic health report we analyse the DNA of your own cells. In other words, the two analyses study different components and are complementary. Having both reports can help you to have a more complete picture of your state of health and well-being.

Do my results change throughout my life?

Unlike genetic tests, in oral microbiota the idea of testing at different times does make sense, as it would provide different results, which would allow us to track the evolution and flow of the bacterial

communities that live in our mouths and, consequently, the evolution of certain areas of our health.

Based on the results of my microbiota analysis, should I make important changes to my diet on my own?

Our microbiota study will give you information about your propensities to certain pathologies. You should not make significant changes to your treatments or health and wellness habits without validation from your referring physician, who will have access to much more of your health history data.

Does my microbiota test replace my dental consultation?

The microbiota report provides an analysis of oral bacteria for preventive purposes for certain pathologies, including periodontitis. In no case does this test replace consultations with health professionals or diagnostic tests.

Can I be diagnosed with any nutritional alteration with this microbiota test?

The 24Genetics microbiota test is not valid for clinical or diagnostic use. If your healthcare professionals observe any relevant pathology in our reports, they may prescribe a second test with clinical validity to confirm the pathology.

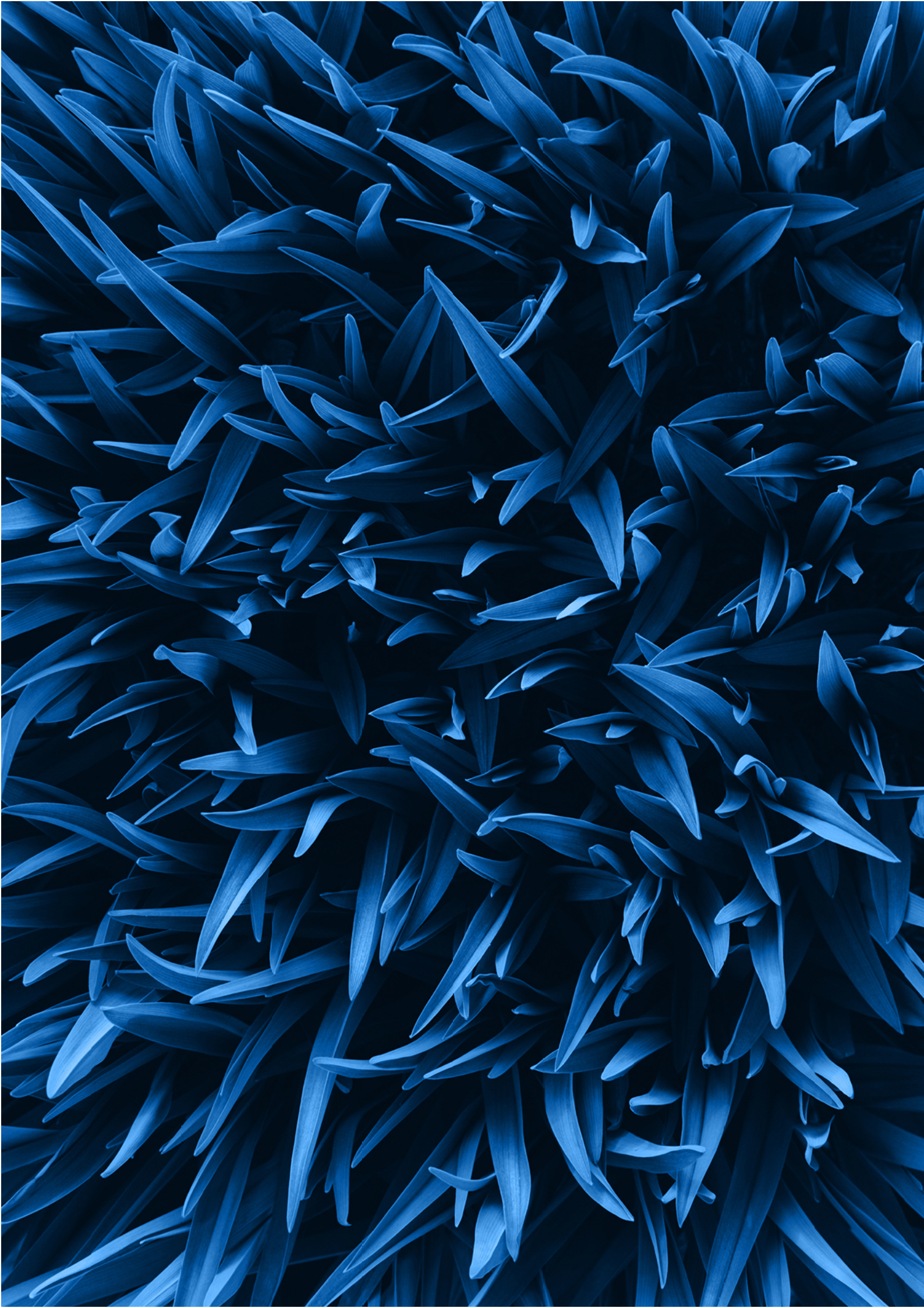### Is this microbiota test valid for clinical or diagnostic use?

No, this microbiota test is not valid for clinical or diagnostic use. In the event that your dentist or doctor considers that any bacteria reflected in our report is relevant to your health, he or she may prescribe a clinically valid test to confirm the bacteria in question. 24Genetics tests are preventative and their main purpose is to bring to light genetic issues that are often overlooked.

If my report says I have a high tendency to suffer from a certain pathology, does that mean I will suffer from it?

We are our microbiome, our genetics and our experiences. Apart from your bacteria, there are many other environmental and internal factors that influence the development or not of a disease, so you can have high levels of a particular bacterium that makes you prone to a pathology and never develop it due to environmental issues, health habits, lifestyle... But you can also have no predisposition and suffer from a certain disease at a certain time in your life. Furthermore, depending on the pathology, bacteria can have a greater or lesser influence on the appearance or development of a disease. Knowledge of our oral microbiota by means of a microbiota test allows health professionals to carry out their work with much more information. It also allows them to design prevention plans that can make a difference.

Some of the studies on which our microbiota test is based.

• https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5762296/

• https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7321711/

• https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7758303/

• https://pubmed.ncbi.nlm.nih.gov/25758458/

3. Summary

3.1. Your profile

Smoker

3.2. Pathologies

Pathologie	Results
Caries	🟢
Periodontitis	🔴
Oral cancers (squamous cell carcinoma of the head and neck)	🟢
Lung cancer	🟢
Pancreatic cancer	🟢

3.3. Bacteria

Bacteria	Results
Prevotella	
Streptococcus	
Veillonella	
Neisseria	
Haemophilus	
Porphyromonas	
Rothia	

Actinomyces

Fusobacterium

Gemella

Campylobacter

Oribacterium

Selenomonas

Capnocytophaga

Tannerella forsythia

Porphyromonas gingivalis
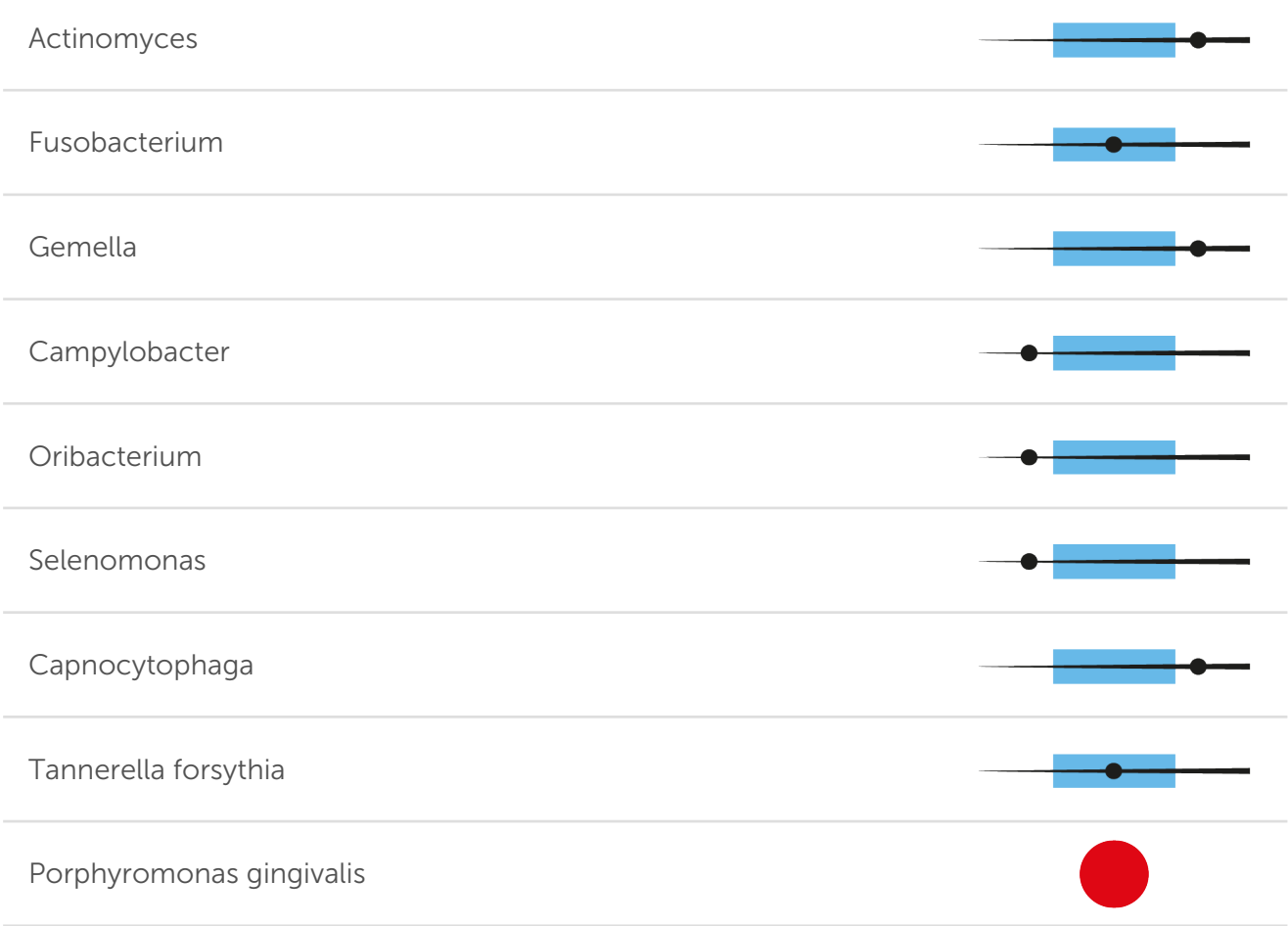
3.4. Other bacteria

Bacteria	Results
Streptococcus	35,87 %
Actinomyces	13,88 %
Prevotella	13,44 %
Prevotellaceae	3,62 %
Prevotella melaninogenica	3,57 %
Lachnoanaerobaculum	3,25 %
Lancefieldella	2,85 %
Rothia mucilaginosa	2,41 %
Segatella salivae	2,38 %
Granulicatella adiacens	2,14 %
Gemella	1,82 %
Leptotrichia	1,68 %
Actinomycetaceae	1,45 %
Haemophilus	1,12 %
Prevotella pallens	0,96 %
Fusobacterium	0,95 %
Lachnospiraceae	0,82 %
Mogibacterium	0,58 %
Eubacterium	0,52 %

Bacteria	Results
Oribacterium	0,48 %
Peptostreptococcus	0,47 %
Porphyromonas	0,43 %
Campylobacter	0,34 %
Neisseria	0,29 %
Rothia	0,28 %
Neisseriaceae	0,27 %
Prevotella nigrescens	0,25 %
Veillonella	0,2 %
Segatella	0,18 %
Streptococcaceae	0,17 %
Segatella oris	0,17 %
Abiotrophia defectiva	0,17 %
Dialister invisus	0,14 %
Capnocytophaga	0,14 %
Olsenella	0,14 %
Cryptobacterium curtum	0,12 %
Granulicatella	0,12 %
Alloprevotella rava	0,11 %
Alloprevotella tannerae	0,11 %

Bacteria	Results
Hoylesella	0,11 %
Peptoniphilaceae	0,1 %
Parvimonas	0,1 %
Streptococcus mutans	0,09 %
Actinomyces gerencseriae	0,09 %
Corynebacterium durum	0,09 %
Schaalia	0,08 %
Lautropia mirabilis	0,08 %
Segatella oulorum	0,08 %
Catonella morbi	0,07 %
Oscillospiraceae	0,07 %
Micrococcaceae	0,07 %
Syntrophococcus	0,05 %
Megasphaera micronuciformis	0,05 %
Capnocytophaga leadbetteri	0,05 %
Gemellaceae	0,05 %
Atopobiaceae	0,05 %
Tannerella serpentiformis	0,04 %
Granulicatella elegans	0,04 %
Bifidobacterium dentium	0,04 %

Bacteria	Results
Porphyromonas gingivalis	0,04 %
Enterococcus	0,04 %
Actinobaculum	0,03 %
Aggregatibacter	0,03 %
Selenomonas	0,03 %
Enterococcaceae	0,03 %
Parvimonas micra	0,02 %
Campylobacter gracilis	0,02 %
Porphyromonadaceae	0,02 %
Leptotrichiaceae	0,02 %
Moryella	0,02 %
Actinomyces dentalis	0,02 %
Corynebacterium	0,02 %
Spodiobacter	0,02 %
Slackia exigua	0,02 %
Lactobacillus	0,01 %
Veillonellaceae	0,01 %
Porphyromonas endodontalis	0,01 %
Dialister pneumosintes	0,01 %
Pasteurellaceae	0,01 %

Bacteria	Results
Alloprevotella	0,01 %
Solobacterium moorei	0,01 %
Thermotaleaceae	0,01 %
Peptostreptococcaceae	0,01 %
Abiotrophia	0,01 %
Eubacteriaceae	<0,01 %
Cellulomonadaceae	<0,01 %
Corynebacterium matruchotii	<0,01 %
Pseudoramibacter	<0,01 %
Carnobacteriaceae	<0,01 %
Staphylococcus	<0,01 %
Eubacterium brachy	<0,01 %
Neisseria oralis	<0,01 %
Prevotella koreensis	<0,01 %
Flavobacteriaceae	<0,01 %
Anaerovoracaceae	<0,01 %
Peptococcus	<0,01 %
Fusobacteriaceae	<0,01 %
Segatella maculosa	<0,01 %
Parascardovia denticolens	<0,01 %

Bacteria	Results
Aggregatibacter aphrophilus	<0,01 %
Pseudoleptotrichia goodfellowii	<0,01 %
Hoylesella saccharolytica	<0,01 %
Capnocytophaga sputigena	<0,01 %
Catonella	<0,01 %
Pseudonocardiaceae	<0,01 %
Pseudoleptotrichia	<0,01 %
Dialister	<0,01 %
Campylobacter curvus	<0,01 %
Megasphaera	<0,01 %
Segatella baroniae	<0,01 %
Peptidiphaga gingivicola	<0,01 %
Paludibacteraceae	<0,01 %
Tannerella forsythia	<0,01 %
Tannerella	<0,01 %
Eikenella	<0,01 %
Kingella oralis	<0,01 %
Treponema	<0,01 %
Aerococcaceae	<0,01 %
Pseudescherichia	<0,01 %

Bacteria	Results
Peptoniphilus	<0,01 %
Mobiluncus	<0,01 %
Microbacteriaceae	<0,01 %
Selenomonadaceae	<0,01 %
Slackia	<0,01 %
Corynebacteriaceae	<0,01 %
Cryptobacterium	<0,01 %
Campylobacteraceae	<0,01 %
Cardiobacterium	<0,01 %
Cardiobacterium hominis	<0,01 %
Cardiobacterium valvarum	<0,01 %
Bacillaceae	<0,01 %
Solobacterium	<0,01 %

4. Results

4.1. What do the results show?

Group

Pathology
or bacteria
analyzed

A summary
and how
it affects

A summary
and how
it affects

More
information

4.3. Pathologies

Caries

Caries consist of damage to the tooth surface or enamel. The cause of this pathology is the colonization of the mouth by acidogenic bacteria, i.e., bacteria that produce acid due to their metabolism. Risk factors for the growth of these bacteria, and thus for the development of caries, are the consumption of highly sugary drinks and foods, frequent drinking or eating, poor toothbrushing, dry mouth, and age and eating disorders.
Symptoms include toothache, sensitivity, and holes or stains on the tooth surface.
Two types of invading bacteria are involved in the formation of caries. Primary invading bacteria can directly influence the development of the pathology, but they also create the necessary environment for secondary invaders to act.
Bacteria of the genus Lactobacillus are secondary (opportunistic) invaders that only grow in an acidic and anaerobic (i.e., without oxygen) environment created by the primary invaders. Therefore, the presence of Lactobacillus in the saliva is used as a marker for caries.

Result of analysis:

NEGATIVE

We have not detected the presence of bacteria of the genus Lactobacillus in the oral microbiota analysis. Therefore, according to this analysis, you do not have caries markers. However, other bacteria may be involved in this pathology. In any case, in addition to your daily dental hygiene (brushing at least twice a day and daily flossing), it is advisable to have your teeth professionally cleaned regularly, ideally once a year.

Bibliography and references:

https://pubmed.ncbi.nlm.nih.gov/25758458/

4.2. Profile

Smoker

Smoking, together with other environmental factors, favors the growth of anaerobic bacteria, i.e., those that grow in the absence of oxygen, and reduces oxygen-requiring bacteria (aerobic bacteria), negatively affecting the balance of the oral microbiome. Among the bacteria that decrease by tocacco consumption are bacteria of is the genus *Neisseria*, which are part of the healthy oral microbiota.

Result of your analysis:

NON-SMOKER

According to our analysis, the bacterial composition of your oral microbiota does not match the profile of a smoker. Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://www.nature.com/articles/ismej201637

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Here is some information about your risk of pathologies

4.3. Pathologies

Caries

Caries consist of damage to the tooth surface or enamel. The cause of this pathology is the colonization of the mouth by acidogenic bacteria, i.e., bacteria that produce acid due to their metabolism. Risk factors for the growth of these bacteria, and thus for the development of caries, are the consumption of highly sugary drinks and foods, frequent drinking or eating, poor toothbrushing, dry mouth, age, and eating disorders.

Symptoms include toothache, sensitivity, and holes or stains on the tooth surface.

Two types of invader bacteria are involved in the formation of caries. Primary invader bacteria can directly influence the development of the pathology, but they also create the necessary environment for secondary invaders to act.

Bacteria of the genus *Lactobacillus* are secondary invaders (opportunistic) that only grow in an acidic and anaerobic (i.e., without oxygen) environment created by the primary invaders. Therefore, the presence of *Lactobacillus* in saliva is used as a marker for caries.

Result of your analysis:

NEGATIVE

We have not detected the presence of bacteria of the genus Lactobacillus in the oral microbiota analysis. Therefore, according to this analysis, you do not have caries markers. However, other bacteria may be involved in this pathology. In any case, in addition to your daily dental hygiene (brushing at least twice a day and daily flossing), it is advisable to have your teeth professionally cleaned regularly, ideally once a year.

Bibliography and references:

https://pubmed.ncbi.nlm.nih.gov/25758458/

4.3. Pathologies

Periodontitis

Periodontitis, also known as gum disease, which are the tissues that surround and support the teeth, is one of the most common bacterial infections in humans. The most severe forms of the infection can lead to teeth falling out. The World Health Organisation estimates that periodontal diseases affect around 14% of the adult population, accounting for over 1 billion cases worldwide.

The leading causes are poor oral hygiene and smoking. Still, other risk factors include genetics, inadequate nutrition with vitamin C deficiency, certain diseases such as diabetes, and hormonal changes.

Multiple studies link periodontitis to other systemic diseases, such as atherosclerosis, mainly because it creates a pro-inflammatory environment in the body.

The bacterium *Porphyromonas gingivalis* is a critical pathogen in the development of periodontitis by altering the immune response. However, other types of imbalance in the oral microbiota may influence the development of the disease.

Result of your analysis:

VERY UNFAVOURABLE

According to our analysis, the bacteria in your oral microbiota indicate a high risk for periodontitis. Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7321711/
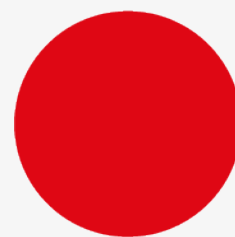
4.3. Pathologies

Oral cancers (squamous cell carcinoma of the head and neck)

Squamous cell carcinoma of the head and neck is a group of related tumors that grow in the oral cavity, oropharynx, hypopharynx, and larynx, also known as "oral cancers," and is the sixth most common cancer globally.

Around 50-70% of this type of cancer occurs in smokers men aged 60-70. Although the number of cases is decreasing worldwide, recent epidemiological studies show an increase in incidence in patients under 45 years of age, both men and women, whether or not related to smoking.

The main risk factors are tobacco and alcohol consumption, poor diet, and poor oral health.

Changes in the microbiota can lead to chronic inflammation and thus increase cancer risk. For example, patients with oral cancers have been found to have increased levels of *Prevotella* melaninogenica. In contrast, bacteria of the genus *Haemophilus*, for example, are found to be decreased.

Result of your analysis:

NO ASSOCIATION

According to our analysis, the bacteria in your oral microbiota do not indicate a predisposition to oral cancer.
Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5762296/

4.3. Pathologies

Lung cancer

Lung cancer is the second most common cancer globally, with more than 2 million new cases per year and almost 1.8 million deaths per year. Smoking is the major risk factor for developing lung cancer; it is estimated that around 80% of lung cancer deaths are due to smoking. However, other risk factors include exposure to carcinogens such as arsenic, environmental pollution, and lung infections such as pneumonia and tuberculosis.

There is growing evidence that oral microbiota may increase the risk of lung cancer. Several studies have found associations between the abundance of various bacteria in saliva and lung cancer in smokers. For example, an increased percentage of *Streptococcus* bacteria, together with other changes in the microbiota, is associated with an increased risk of lung cancer. In addition, smoking modifies the oral microbiome, which could be one of the pathways for its influence on lung cancer risk.

Result of your analysis:

NO ASSOCIATION

According to our analysis, the bacteria in your oral microbiota show no particular association with lung cancer. Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://pubmed.ncbi.nlm.nih.gov/35929779/

4.3. Pathologies

Pancreatic cancer

Pancreatic cancer kills more than 400,000 people annually and is the sixth leading cause of cancer deaths worldwide. It is estimated that by 2030 rates will double, making it the second leading cause of cancer mortality. Because there are usually no symptoms in the early stages, around 90% of pancreatic cancers are incurable at the time of diagnosis due to the advanced stage of the disease. In addition, early relapses are very common.

Risk factors include genetics, ethnicity, socio-economic status, smoking, alcohol consumption, age (more common in people over 50), and other diseases such as chronic pancreatitis, obesity, and diabetes.

Several studies have shown differences in the oral microbiota composition between pancreatic cancer patients and healthy people, although these have not been shown to cause the disease. Among the changes observed is a decrease in bacteria of the genera *Veillonella* and *Neisseria* and an increase in *Leptotrichia*.

Result of your analysis:

NO ASSOCIATION

Based on our analysis, your oral microbiota shows no particular association with pancreatic cancer. Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7789059/

24Genetics

And now, your bacteria

4.4. Bacteria

Prevotella

The *Prevotella* genus of bacteria has a tubular shape and is usually found in the gingival sulcus of your mouth, which is the space between the teeth and gums. However, it also occupies an important place in the vaginal and intestinal flora, which is why it can cause gynecological, urogenital, and soft tissue infections, among others. Specifically in the oral microbiome, 12% is the maximum concentration of this genus of bacteria that cannot be considered pathogenic, always depending on the balance with the rest of the microorganisms in your microbiome.

Prevotella is more common in non-Westernised populations consuming a plant-rich diet and is resistant to penicillin and clindamycin.

Result of your analysis:

EQUAL TO THE AVERAGE

The percentage of this bacterium in your oral microbiota is within normal parameters.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=838&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Streptococcus

Streptococcus, is a genus of lactic acid-producing, coccus-like bacteria that grow in chains or pairs. Most streptococci have more complex nutritional requirements than other bacteria. However, they find all the nutrients they need to grow in the mouth, especially without oxygen. For this reason, it is one of the predominant genera in healthy oral microbiota, with an average abundance of about 21%. In addition, it is also part of the healthy microbiota of the skin, intestine, and upper respiratory tract of humans. However, this genus includes important pathogenic bacteria such as *Streptococcus* pneumoniae, which causes bacterial pneumonia.

Result of your analysis:

ABOVE AVERAGE

The percentage of this bacterium in your oral microbiota is above the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1301&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Veillonella

Bacteria of the genus *Veillonella* occur as cocci arranged in pairs (diplococci) and are part of the healthy oral microbiota in the oral cavity, colon, and vagina. These bacteria can ferment lactic acid, produced by the fermentation of carbohydrates by other bacteria such as *Streptococcus* or *Lactobacillus*. This lactic acid fermentation neutralizes the acidity of dental plaque, which is why these bacteria are considered an indicator of good oral health. However, elevated bacteria levels can behave as opportunistic pathogens under certain circumstances and are accompanied by dysbiosis.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=29465&lvl=3&p=has_linkout&p=blast_url&p=genome_blast&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Neisseria

Neisseria is a genus of bacteria, commonly spherical, found naturally in the microbiota of the human body, mainly the oral cavity and nasopharynx. As a genus of bacteria, *Neisseria* groups several species of bacteria with differences between them, including *Neisseria* gonorrhoeae, which will be described elsewhere in this report if found in your oral microbiota, and which is pathogenic regardless of its concentration. However, the genus *Neisseria* also contains many commensal species, most of which are harmless upper respiratory and alimentary tract inhabitants.

  It is considered that a concentration of less than 2% of *Neisseria* bacteria could be associated with pancreatic cancer, depending on the balance with the other microorganisms in your microbiome.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=482&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Haemophilus

The *Haemophilus* genus of bacteria is rod-shaped and grows mainly in dental plaque and saliva, although it can also be found in other body mucous membranes. The average population usually has percentages between 3 and 12%; however, only rates lower than 3% can be associated with some pathologies and always depend on the balance of microorganisms in your microbiota. The treatment of an infection caused by *Haemophilus* is based on the use of antibiotics, of one type or another, depending on the organ affected and the severity of the disease.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=724&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Porphyromonas

The bacterial genus *Porphyromonas* is composed of pleomorphic bacteria, i.e., they can alter their shape, are obligate anaerobes (able to grow only in the absence of oxygen), and are non-motile. This genus is involved in pathological processes in the oral cavity, respiratory and gastrointestinal tracts. However, the role played by this genus is unclear, as studies suggest that they act as benign bacteria for the organism, while in other cases, they are pathological. The latter is the case of *Porphyromonas gingivalis*, a pathological agent of periodontitis, which will be described elsewhere in this report, should it be found in your oral microbiota.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=836&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Rothia

Rothia is a genus of bacteria with varied morphology, generally requiring oxygen for growth (i.e., aerobic) and without movement capacity. It is common to find several species of *Rothia* in the oral cavity and pharynx. Their virulence or pathogenicity is low, although they have been described as causing opportunistic infections in immunocompromised individuals. For example, it can cause illness in patients with that same pathology. However, in cases where the disease does not develop, it may have an anti-inflammatory effect in patients with lung cancer.

Result of your analysis:

EQUAL TO THE AVERAGE

The percentage of this bacteria in your oral microbiota is within normal parameters.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=508215&lvl=3&p=has_linkout&p=blast_url&p=genome_blast&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Actinomyces

The *Actinomyces* genus of bacteria consists of rod-shaped, facultative anaerobic bacteria, i. e., they grow preferentially without oxygen. This group of bacteria is part of the normal microbiota of the oral cavity, pharynx, intestine, genitourinary tract, and skin. However, under certain circumstances, they can behave as pathogens (opportunistic pathogens). For example, within this genus is *Actinomyces israelii*, which generally does not cause infections, but can cause actinomycosis, a suppurative granulomatous disease most commonly caused by dental abscesses or oral surgery.

Result of your analysis:

ABOVE AVERAGE

The percentage of this bacterium in your oral microbiota is above the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1654&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Fusobacterium

Fusobacterium is a genus of obligate anaerobic (requires the absence of oxygen to grow) rod-shaped bacteria with pointed ends. Most species belonging to this genus are part of the healthy microbiota in the oral cavity and the intestine, respiratory tract, and female genital tract. Despite this, many anaerobic bacterial infections in the oral cavity are caused by species belonging to the genus *Fusobacterium*. In addition, elevated levels of this genus and other changes in the oral microbiome have been associated with oral cancers.

Result of your analysis:

EQUAL TO THE AVERAGE

The percentage of this bacterium in your oral microbiota is within normal parameters.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=848&lvl=3&p=has_linkout&p=blast_url&p=genome_blast&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Gemella

Bacteria of the genus *Gemella* grow preferentially in environments with high carbon dioxide pressures and absence of oxygen (facultative anaerobes) and are mainly found in the mucous membranes of humans and other animals, with a preference for the oral cavity and upper digestive tract. They have been shown to have a hemolytic capacity, i.e., they can destroy red blood cells, resulting in the release of hemoglobin. It has been found that the levels of these bacteria in subgingival plaque are usually lower in people with periodontitis than in healthy people. However, a strong relationship between the stories of these bacteria in saliva and periodontal disease has not yet been demonstrated.

Result of your analysis:

ABOVE AVERAGE

The percentage of this bacterium in your oral microbiota is above the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1378&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Campylobacter

Campylobacter is a bacillus-shaped, motile bacteria within which pathogenic species are found. For example, *Campylobacter* food poisoning is the leading cause of diarrhea worldwide. In general, infection by this genus of bacteria develops with mild symptoms. However, its presence in the oral cavity is part of the normal microbiota and is widespread in the healthy population. In recent years, the relationship between *Campylobacter* species in the oral cavity and inflammatory bowel disease has been studied, although insufficient evidence exists.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=194&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Oribacterium

The genus *Oribacterium* is composed of rod-shaped, motile, obligate anaerobic bacteria, i.e., they require an absence of oxygen to grow and are usually part of the healthy oral microbiota. Within this genus, three species have been described: *Oribacterium saccharolytic*, *Oribacterium parvum*, and *Oribacterium sinus*; they are found in the oral cavity and, although frequently found in saliva, are more prevalent in subgingival plaque.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=265975&lvl=3&p=has_linkout&p=blast_url&p=genome_blast&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Selenomonas

Selenomonas is a genus of motile, crescent-shaped bacteria. This genus is part of the healthy oral microbiota, although it is usually more abundant in people with gingivitis or periodontitis. Despite this, the bacteria of this genus alone cannot trigger these pathologies.

Result of your analysis:

BELOW AVERAGE

The percentage of this bacterium in your oral microbiota is below the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=970&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Capnocytophaga

This genus of bacteria, shaped like a bent filament or rod, is found in the oral cavity and saliva and is responsible for generating dental plaque, which requires CO_2 for its formation (hence the name of this genus of bacteria). Concentrations of less than 1.2% *Capnocytophaga* are considered harmless. The above 1.2% will depend on the balance with the other microorganisms in your microbiome.

Result of your analysis:

ABOVE AVERAGE

The percentage of this bacterium in your oral microbiota is above the normal range.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1016&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Tannerella forsythia

Tannerella forsythia bacteria are tubular and occur naturally in the mouth, intestinal tract, and vagina. Regarding oral microbiota, it responds well to mechanical treatment (oral hygiene), but if it prevails after treatment, it indicates a worse prognosis of periodontal pathology. The bacteria, as well as the substances that are generated in their presence in the periodontal pockets, can spread systemically through the bloodstream and can cause various pathologies. It is considered that 0.04% of this bacterium is the maximum concentration percentage at an oral level, below which it is not considered pathogenic. Concentrations above this percentage are directly related to periodontal disease, always depending on the balance with the rest of the microorganisms in your microbiome.

Result of your analysis:

EQUAL TO THE AVERAGE

The percentage of this bacterium in your oral microbiota is within normal parameters.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=28112&lvl=3&lin=f&keep=1&srchmode=1&unlock

4.4. Bacteria

Porphyromonas gingivalis

Porphyromonas gingivalis is a rod-shaped bacterium with diverse clinical implications. It invades the gingival epithelial cells, i.e., the gum surface or the oral biofilm on the surface of your teeth. It is a bacterium that reproduces quickly under certain conditions and remains active for long periods. Being free of these bacteria is healthy, but only concentrations above 0.1% are considered pathogenic.

High concentration levels of this bacterium are directly related to periodontal disease.

Result of your analysis:

POSITIVE

The percentage of this bacteria in your oral microbiota is above normal parameters, which may indicate periodontal disease. Other genetic, clinical, and environmental factors may play a role.

Bibliography and references:

https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=837&lvl=3&lin=f&keep=1&srchmode=1&unlock

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