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(57) Abrégé/Abstract:
The present invention discloses different specific bacterial strains isolated from individuals without caries which are characterised in that they present inhibitory activity against cariogenic organisms. The invention also discloses a process for isolating said strains, as well as bioactive peptides, such as anti-microbial peptides of human and bacterial origin, which also show anti-cariogenic activity. Moreover, the present invention also discloses pharmaceutical and/or probiotic/prebiotic compositions, functional foods, mouthwashes, toothpaste, chewing gum, etc., that comprise at least one of the strains and/or at least one of the bioactive peptides described in the invention, or a combination thereof, which are useful in the treatment and/or prevention of infectious diseases of the buccal cavity, preferably caries.

ABSTRACT

ANTI-CARIES COMPOSITIONS AND PROBIOTICS/PREBIOTICS

The present invention discloses different specific bacterial strains isolated from individuals without caries which are characterised in that they present inhibitory activity against cariogenic organisms. The invention also discloses a process for isolating said strains, as well as bioactive peptides, such as anti-microbial peptides of human and bacterial origin, which also show anti-cariogenic activity. Moreover, the present invention also discloses pharmaceutical and/or probiotic/prebiotic compositions, functional foods, mouthwashes, toothpaste, chewing gum, etc., that comprise at least one of the strains and/or at least one of the bioactive peptides described in the invention, or a combination thereof, which are useful in the treatment and/or prevention of infectious diseases of the buccal cavity, preferably caries.

ANTI-CARIES COMPOSITIONS AND PROBIOTICS/PREBIOTICS

FIELD OF THE INVENTION

The present invention belongs to the field of human health; more specifically, the field of bucco-dental health.

BACKGROUND

The human oral cavity is inhabited by hundreds of bacterial species, most of which are commensal species, necessary to maintain equilibrium in the oral ecosystem. However, some of them play a key role in the development of oral diseases, primarily dental caries and periodontal disease (1). Oral diseases begin with the growth of dental plaque, a biofilm formed by the accumulation of bacteria jointly with glycoproteins from human saliva and polysaccharides secreted by microbes (2). The subgingival plaque, located in the neutral or alkaline subgingival pocket, is typically inhabited by Gram-negative anaerobes and is responsible for the development of gingivitis and periodontitis. The supragingival dental plaque is formed on the surface of the tooth and includes acidogenic and acidophilic bacteria, which, upon fermenting the sugars ingested in the diet, produce acid and lower the pH. When the pH is too acidic (generally with a value less than 5.5), the tooth enamel is de-mineralised and destroyed, and, therefore, these bacteria are responsible for dental caries, which are considered to be the most widespread infectious disease in the world, affecting over 80% of the human population (3). A bad oral health may be associated with other pathologies, such as, for example, stomach ulcers, stomach cancer or cardiovascular diseases, amongst others.

One of the main reasons why, as of today, oral pathogens have still not been eradicated is the difficulty involved in studying microbial communities that inhabit the oral cavity, since, on the one hand, the complexity of the ecosystem (several hundreds of species have been detected, with numerous levels of interaction) makes it difficult to detect the potential pathogenic species (4); moreover, no single etiological agent may be identified, as in classic diseases, following Koch's postulates. This fact has been clearly demonstrated in periodontal disease, where there are at least 3 bacterial species belonging to very different taxonomic groups (the so-called "red complex" of periodontal pathogens) which have been associated with the development and progression of periodontal disease (5). On the other hand, a large proportion of oral bacteria cannot be cultured (6) and, therefore, traditional microbiological methods give an incomplete image of the natural communities that inhabit dental plaque. However, the current development of metagenomic techniques and Next-Generation Sequencing technologies allows for the study of the bacterial community as a whole, by analysing the total DNA of complex microbial samples (Metagenome)

without the need to culture the bacteria themselves.

In this regard, pioneering studies in metagenomics have focused on the intestinal ecosystem primarily through a shot-gun approach, wherein the DNA is cloned in small-size plasmids, followed by traditional Sanger-type sequencing (7, 8). More recent approaches include sequencing of the ends of large-size fosmids (9) and use of the "Illumina" sequencing technology, which provides a high coverage of short sequences (10). Studies of the microbiota of the oral cavity, as well as of other human body habitats, such as the skin, the vagina or the respiratory tract, have focused on the sequencing of ribosomal RNA amplicons (11, 12). These studies have provided a substantial improvement of our knowledge about these bacterial communities as compared to prior research based on cultures, but estimates of microbial diversity are hindered by the biases in PCR amplification (i.e. PCR only detects the bacteria that are most similar to those already known, and on the basis of which the amplification primers are used, giving an incomplete image of the diversity present), the cloning bias (a large number of genes are not cloned because they are toxic for the host bacteria and, therefore, this method does not allow for the study of the entire genetic reservoir of the sample) and a low sequence length (the sequences in the Illumina technology have only between 35-70 nucleotides, which in most cases makes a reliable taxonomic or functional assignment impossible), together with the fact that, as mentioned above, a large proportion of oral bacteria cannot be cultured.

In order to resolve the aforementioned problems, the present invention discloses the obtainment of the metagenome of dental plaque by the direct sequencing of metagenomic DNA, using 454-pyrosequencing, thereby eliminating the potential biases imposed by cloning and PCR techniques, and, furthermore, providing access to the entire genetic repertoire of the oral bacterial community under different health conditions, as well as the possibility to analyse which bacterial species amongst those found in the metagenome obtained may be associated with a good oral health, since those individuals who had never suffered from caries exhibit a different bacterial flora than those individuals who had suffered or currently suffer from it. By means of the oral metagenome obtained in the present invention, it is possible to direct the isolation, culture and identification of strains with anti-cariogenic activity from the conglomerate of bacteria in the buccal cavity sample; specifically, the supragingival plaque of individuals who have never suffered from caries, i.e. those strains capable of inhibiting the growth of cariogenic bacteria.

Another strategy disclosed in the present invention is the obtainment of a metagenomic library of fosmids (long DNA inserts, approximately 35-45 Kb) from the dental plaque of individuals who have never suffered from caries. By obtaining said fosmid library, it is possible to isolate and identify the bioactive anti-cariogenic peptides synthesised by the bacteria present in the oral cavity of

individuals who have never suffered from caries. In this regard, given that, in the state of the art, *Streptococcus mutans* has been shown to be the main causal agent of caries (13), it is not surprising that most strategies against this disease have been aimed against said microorganism. These strategies have included the development of vaccines using known surface antigens, passive immunisation strategies that may neutralise the bacteria, the co-aggregation of *S. mutans* with probiotic strains and the use of inhibitory proteins specific to *S. mutans*, amongst others (14).

Other different strategies have been those disclosed in different patent documents, which propose the use of different bacterial strains, preferably *S. mutans*, that produce a lower concentration of acid (15), or the use of the same resources, for example, the nutrients, by pathogenic strains and non-pathogenic strains, continuously supplying high concentrations of non-pathogenic bacteria, which results in the displacement of the pathogenic bacteria, provided that they share the same resource (16), or even a lower adherence of cariogenic bacterial strains to the tooth (17). On the contrary, the bioactive strains and peptides disclosed in the present invention have antibiotic activity, preferably anti-cariogenic activity, on their own, against caries-producing microorganisms. On the other hand, patent WO20040072093 (18) discloses a number of anti-microbial agents that are active primarily against Gram-negative microorganisms, but the main causal agents of caries, *S. mutans* and *S. sobrinus*, are Gram-positive microorganisms. Moreover, the *S. mitis* and *S. oralis* isolates that produce the anti-microbial peptides disclosed in WO20040072093 (18) have been isolated from the throat of patients with cystic fibrosis, not from the mouth of people without caries, as in the case of the peptides and/or strains of the invention. Similarly, the therapeutic use of said peptides is aimed at the treatment of respiratory tract diseases and not of caries, as in the case of the bioactive peptides disclosed in the present invention.

In this regard, the main technical characteristics that make the bacterial strains isolated and disclosed in the present invention different from the rest of strains disclosed in the state of the art are that they may be cultured by means of conventional microbiological techniques; that they present inhibitory activity against organisms that produce infectious diseases of the buccal cavity, preferably caries, without the need to be genetically modified; and that they have been isolated from individuals who have never suffered from caries. Consequently, both the anti-cariogenic bacteria themselves and the bioactive anti-cariogenic compounds, preferably peptides, disclosed in the present invention may be used as probiotic and/or prebiotic compositions as such, or as a part of different pharmaceutical compositions used for the treatment of infections of the buccal cavity, such as, for example, caries, periodontitis, etc., or even as functional foods. Moreover, the present invention also discloses a method for the prevention and/or treatment of infectious diseases of the buccal cavity, preferably caries, that comprises the administration of a pharmaceutically effective quantity of at least

one of the strains and/or at least one of the anti-microbial compounds, preferably peptides, described above, or of the probiotic or pharmaceutical composition or functional foods that comprise at least one of the strains and/or at least one of the compounds, preferably peptides, of the invention.

DESCRIPTION OF THE INVENTION

Brief description of the invention

The existing difficulty in the state of the art in identifying bacterial strains that directly inhibit the growth of pathogenic germs related to the onset of buccal cavity diseases is thus caused by the large quantity of bacterial species in said cavity; consequently, the difficulty involved in isolating, amongst all of them, strains that directly inhibit the growth of pathogenic species, many of which are non-culturable species, has made this problem hard to solve thus far.

The present invention resolves this problem by creating the metagenome of the buccal cavity of individuals who have never suffered from caries. The creation of said metagenome, using massive sequencing, preferably pyrosequencing, of the DNA present in the samples taken from the buccal cavity of said individuals who have never suffered from caries, makes it possible to identify the genera and species of the bacteria that are most frequent in the bacterial population present in the buccal cavity of said individuals. This quantification of the frequency of each bacteria in the sample had not been possible, thus far, using culture, cloning or PCR techniques, since these techniques only identify part of the bacteria and the proportions of those that are identified is biased due to the methodology itself (primarily due to the preferable culture, cloning or amplification of certain species, respectively).

In principle, the invention has been based on human beings, but could be applied to any superior mammal, especially pets or livestock, or even wild fauna. It would be sufficient to determine the characteristic metagenome of each species, in individuals who have never suffered from caries, as a representative disease of the typical buccal cavity diseases. Once the bacterial strains that are most frequent in the buccal cavity of healthy individuals have been identified from the data obtained from the metagenome, the following step of the present invention consists of culturing the samples obtained from the buccal cavity of these individuals, in the favourable culture media and under favourable conditions, such that the most frequent genera and species identified in the metagenome of the mammalian species under study may develop.

A second alternative to resolve the problem mentioned above consists of attempting to

isolate compounds, especially active peptides, secreted, amongst others, by the bacterial strains present in the buccal cavity of individuals who have never suffered from caries and which present direct inhibitory activity against the growth of cariogenic species. In the present invention, direct inhibitory capacity is defined as the capacity to completely inhibit growth, by creating inhibition haloes in lawn cultures of said pathogenic species, due to their antibiotic action, without ruling out the fact that, in addition to said inhibition caused by their antibiotic effect, the strains and compounds may exert their anti-microbial effect, preferably anti-cariogenic effect, by hindering the cariogenic action by other routes, such as modifying the optimal pH for the growth of said cariogenic strains, hindering their adherence to the teeth, etc.

To this end, the invention has started, once again, from buccal cavity samples taken from healthy individuals, but, in this alternative, it has not only focused on compounds of bacterial origin that may be secreted, amongst others, by the aforementioned isolated strains. Moreover, compounds secreted by other bacterial strains may exist which are not culturable and, therefore, cannot be isolated using the strategy proposed above. Finally, in addition to compounds of bacterial origin from the population of bacterial strains that inhabit the buccal cavity, said cavity also contains compounds secreted by the cells of the mammals themselves, particularly human beings, whereon the present invention is preferably based. Some of these compounds may have a direct inhibitory activity against the growth of cariogenic microorganisms. To this end, the samples obtained from the buccal cavity of healthy individuals were lysed, the DNA thereof was extracted, fosmids were constructed with said fragments and cloned in a host cell that may be cultured and assayed in cultures of cariogenic species, in order to observe whether inhibition haloes against the growth of the pathogenic cariogenic species are produced.

It must be noted that, although the isolated inhibitory strains and compounds have been obtained from samples of the buccal cavity and are active against pathogenic caries-producing (cariogenic) bacterial species, given their inhibitory capacity against the growth of pathogenic bacteria that preferably inhabit the buccal cavity, in principle the bacterial strains and compounds isolated could be found in other parts of the body and produce or be associated with other diseases. For this reason, an object of the present invention is the use of the strains and compounds isolated as medicaments, particularly as anti-microbial agents and, more specifically, as anti-bacterial agents.

Therefore, the present invention discloses the isolation of culturable bacterial strains and compounds, primarily bioactive peptides, with an inhibitory capacity against the growth of pathogenic microorganisms involved in the onset of buccal cavity diseases. Throughout the present invention, the onset of caries has been taken as a representative disease of diseases typical of the buccal cavity, but the invention may be applied to any infectious disease attributable to pathogenic

microorganisms of the buccal cavity. For this reason, the present invention preferably focuses on the isolation of bacterial strains and compounds, primarily bioactive peptides, with an inhibitory capacity against the growth of pathogenic microorganisms, particularly those involved in the onset of caries.

The process for isolating culturable bacterial strains with anti-cariogenic capacity is based on obtaining the oral metagenome of individuals who have never suffered from caries, in order to determine which type of bacteria said individuals present most frequently in their buccal cavity and analyse which of them are associated with a good oral health, by inhibiting the growth of cariogenic bacteria. Said process has made it possible to isolate, characterise, culture and deposit different strains with anti-cariogenic activity in the Spanish Type Culture Collection (CECT): CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775. By means of sequence homology analysis, it was concluded that four of the strains that present anti-cariogenic activity and which were deposited in the CECT, specifically strains CECT 7746, 7747, 7773 and 7775, belonged to the same bacterial genus: *Streptococcus*; therefore, in addition to their functionality (anti-cariogenic activity) and the process for the obtainment thereof, said strains share a structural and taxonomic similarity, since they belong, as previously mentioned, to the same bacterial genus, *Streptococcus*.

On the other hand, the process for isolating and characterising bioactive anti-cariogenic peptides is based on obtaining a fosmid metagenomic library from individuals who have never suffered from caries. Using said method, it is possible to characterise the peptides with anti-cariogenic capacity produced by the bacteria found in individuals who have never suffered from caries, including non-culturable bacteria, as well as by the anti-microbial compounds, for example, of the defensin type, synthesised by the individuals themselves. Said peptides are assayed in order to determine their inhibitory activity against the growth of cariogenic bacteria, such as, for example, *S. mutans* or *S. sobrinus*.

Another aspect of the present invention discloses different specific culturable bacterial strains, CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, isolated from individuals with an excellent oral health who have never suffered from caries, characterised in that they present inhibitory activity against organisms that produce infectious diseases of the buccal cavity, preferably against caries-producing microorganisms. From the metagenome of the bacteria present in the dental plaque of individuals who had never suffered from caries, the genera and species of the bacteria that appeared most frequently in healthy individuals who had never suffered from caries were identified by homology with the existing bacterial DNA libraries. The bacteria that appeared most frequently in individuals without caries and which appeared to be absent or with a very low frequency in individuals with caries belonged to one of the following genera: *Rothia, Globicatella, Johnsonella, Kingella, Cardiobacterium, Phocoenobacter, Mannheimia, Haemophilus, Neisseria, Streptococcus* and

Aggregatibacter, the genus *Streptococcus* being amongst the most abundant. In this regard, the preferred bacterial strains of the invention are strains CECT 7746, CECT 7747, CECT 7773 and CECT 7775, all of them belonging to the genus *Streptococcus*.

Another aspect disclosed in the present invention describes bioactive compounds, preferably peptides, which inhibit the growth of organisms that produce infectious diseases of the buccal cavity, preferably caries-producing microorganisms. Specifically, it describes peptides encoded by DNA sequences included in any of the following fosmid inserts with inhibitory activity against organisms that produce infectious diseases of the buccal cavity, preferably caries-producing microorganisms: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14.

More specifically, the peptides encoded by the DNA sequences included in the fosmid inserts with inhibitory activity against organisms that produce infectious diseases of the buccal cavity: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5, are characterised in that they are of bacterial origin and have characteristics similar to those of bacteriocins. Similarly, the peptides encoded by the DNA sequences included in the fosmid inserts with inhibitory activity against organisms that produce infectious diseases of the buccal cavity: SEQ ID NO: 1, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13 and SEQ ID NO: 14, are characterised in that they are of human origin and have characteristics similar to those defensins.

More specifically, the invention discloses 2 specific peptides: SEQ ID NO: 8, an anti-microbial peptide of human origin with characteristics similar to those defensins; SEQ ID NO: 9, a peptide of bacterial origin with characteristics similar to those of bacteriocins.

Moreover, the invention discloses solid, powdery (for direct intake or in solution) or pasty compositions for buccal hygiene, such as toothpaste, chewing gum, candy, bars, etc., or liquid mouthwash solutions, such as collutories, syrups, drinks, etc., or probiotic and/or prebiotic food compositions the composition whereof comprises either the strains and/or the compounds, preferably peptides, of the invention, with inhibitory activity against organisms that produce infectious diseases of the buccal cavity, preferably caries-producing microorganisms. In a preferred embodiment of the invention, the strains and/or peptides of the invention are added to compositions that present anti-microbial activity against the flora of the buccal cavity and which may be commercially found, such as collutories of the Listerine® type, said collutories showing an improved inhibitory effect against organisms that produce infectious diseases of the buccal cavity, preferably caries-producing microorganisms, when the strains and/or peptides of the invention are added to the composition thereof.

A preferred embodiment of the invention are probiotics/prebiotics or functional foods, the

composition whereof comprises the strains and/or the compounds, preferably peptides, of the invention, with inhibitory activity against organisms that produce infectious diseases of the buccal cavity, preferably caries-producing microorganisms. The concept of probiotics or functional foods includes, without being limited thereto: dairy products, such as yogurts, for example, juices, solid foods, such as sweets, for example, as well as teas, herbalist and parapharmacy products, such as vitamin complexes, with nutritional supplements, etc.

For purposes of the present invention, the following terms are explained:

Infectious disease of the buccal cavity: for purposes of the present invention, the infectious diseases of the buccal cavity are preferably caries, periodontitis, gingivitis and halitosis.

Probiotics: for purposes of the present invention, the term probiotic refers to the use of live microorganisms that are added to foods (milk, yogurts, etc.), dietary supplements (in the form of capsules, tablets, pills, powder, etc.) or others, which remain active and exert their physiological effects on the subject that ingests the food or similar product containing said probiotic. Ingested in sufficient quantities they have beneficial effects, in this case, on buccal health.

Prebiotics: for purposes of the present invention, the term prebiotic refers to the use of substances that are added to foods, chewing gum, dietary supplements or others, which exert an effect on the composition of the oral microbiota, favouring the establishment of bacteria that are beneficial for oral health and/or hindering the establishment of pathogenic bacteria.

Metagenome: represents the genomes of all the bacteria that are present in a sample, an individual or an ecosystem, etc.

Microbiome: is the set of microbes or bacteria that co-exist with human beings.

Bioactive anti-microbial compounds: are compounds such as biologically active peptides, proteins, antibiotics, pigments, etc. that are found in vertebrates and invertebrates and act as natural antibiotics, being a part of the innate immune response. Some of these compounds, for example peptides, are produced by human beings, such as, for example, defensins and cathelicidins, amongst others. They are active against bacteria, fungi and cloistered viruses.

Bacteriocins: are biologically active peptides secreted by bacteria that have bactericidal properties against other species that are closely related to the producing strain, or against strains that are phylogenetically distant from the producing strain.

Phosmids: circular DNA fragments that may be easily introduced into the host cells, generally bacterial cells, and transport bacterial or human DNA fragments.

Functional foods: are defined as those foods that are prepared not only for their nutritional characteristics, but also to fulfil a specific function, such as improving health or reducing the risk of contracting diseases. To this end, biologically active compounds, such as minerals, vitamins, fatty

acids, bacteria with beneficial effects, dietary fibre and antioxidants, etc., are added thereto.

Culturable bacterial strains: culturable bacterial strains are considered to be those that grow in pure culture and keep growing in a stable manner, in an artificial laboratory culture medium under standard aerobiosis or anaerobiosis conditions.

Description of the figures

Figure 1. A. Photograph of a Petri dish, which shows the initial screening of the clones of *E. coli* that contain the fosmids from DNA from the dental plaque of individuals without caries which produce inhibition haloes on a lawn culture of *S. mutans*. **B.** Photograph of a Petri dish, which shows the confirmation screening of the clones of *E. coli* that contain the fosmids from DNA from the dental plaque of individuals without caries that had produced inhibition haloes on a lawn culture of *S. mutans*.

Figure 2. Growth curves of the *S. mutans* cariogenic bacteria (positive control, without the addition of the inhibitor of cariogenesis, exemplified in the graph as a solid line) in BHI medium (brain-heart infusion), and in BHI medium enriched with 100 µl (dotted line), 150 µl (short-dash line), 200 µl (line with short dashes and dots), 300 µl (long-dash line) or 400 µl (line with long dashes and two dots) of the 3-10-kD fraction of the concentrated supernatant produced by, respectively, 1.5-, 2.25-, 3.0-, 4.5- and 6-ml cultures of cells carrying the S12E fosmid containing the bacteriocin-type anti-microbial peptide of bacterial origin of the invention. The data, taken every half-hour for 19 hours, show the mean of 3 experiments. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 3. Growth curves of the S. *mutans* cariogenic bacteria in BHI medium (solid line, positive control without the addition of the inhibitor of cariogenesis) and in BHI medium with 50 µl (dashed line) and 100 µl (dotted line) of the 0-3-kD fraction of the concentrated supernatant produced by, respectively, 2- and 4-ml cultures of cells carrying the T5A fosmid containing the defensin-type anti-microbial peptide of human origin of the invention. The data, taken every half-hour for 12 h, show the mean of 3 experiments. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 4. Growth curves of the *S. mutans* cariogenic bacteria in the presence of Listerine® and the S12E inhibitor of bacterial origin. The data were taken for 19 hours at a temperature of 37°C in BHI culture medium and represent the mean of 3 experiments. The solid line represents the negative control, without bacteria. The short-dash line represents the positive control, growth of *S. mutans* in the absence of Listerine® and the S12E inhibitor. The long-dash line represents the growth of *S. mutans* in the presence of 100 µl of Listerine®. The dotted line represents the growth of *S.*

mutans in the presence of 100 µl of the S12E inhibitor. The line with short dashes and dots represents the growth of *S. mutans* in the presence of 100 µl of Listerine® + 100 µl of the S12E inhibitor. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 5. Growth curves of the S. *mutans* cariogenic bacteria in the presence of the S12E inhibitor (bacteriocin-type anti-microbial peptide of bacterial origin of the invention) chemically synthesised in the laboratory and re-suspended in 0.1% TCA. The data show the growth of *S. mutans*, measured as the absorbance at 600 nm, for 30 minutes, during 30 hours at a temperature of 37°C in 100 µl of BHI culture medium, of three independent experiments. The solid line represents the negative control, without bacteria. The line with black squares represents the growth of *S. mutans* in BHI culture medium. The dotted line represents the positive control, growth of *S. mutans* in BHI culture medium in the presence of 10 µl of 0.1% TCA. The line with short dashes and dots represents the growth of *S. mutans* in BHI culture medium in the presence of 0.3 mg of the S12E peptide re-suspended in 10 µl of 0.1% TCA. The short-dash line represents the growth of *S. mutans* in BHI culture medium in the presence of 0.03 mg of the S12E peptide re-suspended in 10 µl of 0.1% TCA. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 6. Growth curves of the *S. mutans* (**A**) and *S. sobrinus* (**B**) cariogenic bacteria in the presence of the S12E Inhibitor (bacteriocin-type anti-microbial peptide of bacterial origin of the invention) chemically synthesised in the laboratory and re-suspended in ultrapure water. The data show the growth of *S. mutans*, measured as the absorbance at 600 nm, for 30 minutes, during 48 hours, at a temperature of 37°C in 200 µl of BHI culture medium, being the mean of three independent experiments. In both graph A and graph B, the solid lines represent the negative control, without bacteria; the dotted lines represent the growth of *S. mutans* **(A)** or *S. sobrinus* **(B)** in BHI culture medium. The short-dash line represents the positive control, growth of *S. mutans* **(A)** or *S. sobrinus* **(B)** in BHI culture medium in the presence of water. The line with black squares represents the growth of *S. mutans* **(A)** or *S. sobrinus* **(B)** in BHI culture medium in the presence of 0.23 mg of the S12E peptide of the invention, re-suspended in ultrapure water. The line with black diamonds represents the growth of *S. mutans* **(A)** or *S. sobrinus* **(B)** in BHI culture medium in the presence of 0.047 mg of the S12E peptide of the invention, re-suspended in ultrapure water. The line with black triangles represents the growth of *S. mutans* **(A)** or *S. sobrinus* **(B)** in BHI culture medium in the presence of 0.094 mg of the S12E peptide of the invention, re-suspended in ultrapure water. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 7. Growth curves of the *S. mutans* cariogenic bacteria in the presence of 4 µg, 40 µg and 80 µg of the T5A inhibitor of the invention, chemically synthesised in the laboratory and re-suspended in ultrapure water. The data show the growth of *S. mutans*, measured as the absorbance at 600 nm, for 30 minutes, during 44 hours, at a temperature of 37°C in 200 µl of BHI culture medium, being the mean of three independent experiments. The solid line represents the negative control, without cells. The short-dash line represents the growth of *S. mutans* in BHI culture medium (positive control) with ultrapure water. The line with black squares represents the growth of *S. mutans* in BHI culture medium in the presence of 1 µl of the T5A peptide of the invention (defensin-type anti-microbial peptide of human origin). The line with black diamonds represents the growth of *S. mutans* in BHI culture medium in the presence of 10 µl of the T5A peptide of the invention. The line with black triangles represents the growth of *S. mutans* in BHI culture medium in the presence of 20 µl of the T5A peptide of the invention. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 8. Growth curves of the S. *mutans* cariogenic bacteria in liquid culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, produced by cultures of *E. coli* bacterial cells carrying the W4D fosmid that comprises polynucleotide sequence SEQ ID NO: 13, which encodes a defensin-type anti-microbial peptide of human origin of the invention. The data, taken every half-hour for 24 h, show the mean of 3 experiments. As a control, the graph shows the growth curve of *S. mutans* in the presence of the concentrated supernatant of an untransformed *E. coli* epi300 bacterial culture. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 9. Growth curves of the S. *mutans* cariogenic bacteria in liquid culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, produced by cultures of *E. coli* bacterial cells carrying the T5H fosmid that comprises polynucleotide sequence SEQ ID NO: 14, which encodes the defensin-type anti-microbial peptide of human origin of the invention. The data, taken every half-hour for 24 h, show the mean of 3 experiments. As a control, the graph shows the growth curve of *S. mutans* in the presence of the concentrated supernatant of an untransformed *E. coli* epi300 bacterial culture. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 10. Growth curves of the S. *mutans* cariogenic bacteria in liquid culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, produced by cultures of *E. coli* bacterial cells carrying the A5D11 fosmid that comprises

polynucleotide sequence SEQ ID NO: 6, which encodes the defensin-type anti-microbial peptide of human origin of the invention. The data, taken every half-hour for 24 h, show the mean of 3 experiments. As a control, the graph shows the growth curve of *S. mutans* in the presence of the concentrated supernatant of a culture of untransformed *E. coli* epi300 bacteria. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 11. Growth curves of the S. *mutans* cariogenic bacteria in liquid culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, produced by cultures of *E. coli* bacterial cells carrying the A4H11 fosmid that comprises polynucleotide sequence SEQ ID NO: 7, which encodes the defensin-type anti-microbial peptide of human origin of the invention. The data, taken every half-hour for 24 h, show the mean of 3 experiments. As a control, the graph shows the growth curve of *S. mutans* in the presence of the concentrated supernatant of a culture of untransformed *E. coli* epi300 bacteria. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 12. Photographs of Petri dishes that demonstrate the inhibition of the growth of lawn cultures of *S. mutans* in the presence of the isolates of the CECT 7746 (A), CECT 7747 (B), CECT 7773 (C), CECT 7774 (D) and CECT 7775 (E) strains disclosed in the invention.

Figure 13. Photographs of Petri dishes that demonstrate the inhibition of the growth of lawn cultures of *S. sobrinus* in the presence of the isolates of the CECT 7746 (A), CECT 7747 (B) and CECT 7775 (C) strains disclosed in the invention.

Figure 14. Growth curves of the S. *mutans* cariogenic bacteria in BHI culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, obtained from cultures of strains CECT 7746 (A) and CECT 7747 (B) in the stationary phase. The data, taken every 15 minutes for 20 h, show the mean of 4 experiments. The line marked as antb represents the treatment with the antibiotic chloramphenicol (positive control). The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 15. Growth curves of the S. *mutans* cariogenic bacteria in BHI culture medium in the presence of the supernatants, concentrated 10 times and isolated as a function of their molecular weight, obtained from cultures of strain CECT 7746 in the stationary phase (est) and the exponential phase (EXP). The data, taken every 15 minutes for 24 h, show the mean of 4 experiments. The line marked as clorf represents the treatment with the antibiotic chloramphenicol (positive control). The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD)

of the bacterial cultures.

Figure 16. Growth curves of the S. *mutans* cariogenic bacteria in BHI culture medium in the presence of the supernatant, concentrated 10 times and smaller than 3 kDa, obtained from cultures of strains CECT 7746 (A) and CECT 7747 (B), subjected to a treatment at 100°C for 10 minutes. The data, taken every 15 minutes for 24 h, show the mean of 4 experiments. The X-axis of the graph shows the time, expressed in hours, and the Y-axis shows the optical density (OD) of the bacterial cultures.

Figure 17. Photographs of Petri dishes that demonstrate the inhibition of the growth of lawn cultures of *S. mutans* in the presence of the supernatants of cultures of strains CECT 7746 (shown as 46 in the photograph) and CECT 7747 (shown as 47 in the photograph) under aerobiosis and anaerobiosis conditions.

Figure 18. Concentration of lactic acid, expressed in mM, produced by the biofilm from the culture of human saliva in an artificial tooth model under aerobiosis and anaerobiosis conditions, whereto bacterial strains CECT 7746 and CECT 7747, or their respective supernatants, have been added. For more details, see Example 15. The negative control used was strain C7.1, which is an isolate belonging to the species of the *Streptococcus mitis/oralis/infantis* group, obtained from an individual without caries, but which does not produce inhibition of the growth of cariogenic species.

Detailed description of the invention

An object of the present invention is a culturable anti-microbial bacterial strain selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775. In a preferred embodiment, the bacterial strains of the invention are characterised in that they belong to the genus *Streptococcus*, selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775. In another preferred embodiment, the anti-microbial bacterial strains disclosed in the invention present inhibitory activity against the growth of organisms that produce infectious diseases of the buccal cavity, preferably, caries-producing organisms. In a preferred embodiment, the strains of the invention are characterised in that, in addition to competitively growing to occupy the tooth, they are capable of producing inhibitory substances against the growth of cariogenic bacteria.

Another object of the present invention relates to the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, for use as a medicament. In a preferred embodiment, the anti-microbial bacterial strains disclosed in the invention are characterised in that they belong to the genus *Streptococcus* and are selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to the use of at least one of the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, in the manufacturing of a medicament. In a preferred embodiment, said use is characterised in that the bacterial strain belongs to the genus *Streptococcus*, selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to a culturable anti-microbial bacterial strain selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, for use as an anti-microbial agent, preferably an anti-bacterial agent. In a preferred embodiment, the anti-microbial bacterial strain is characterised in that it belongs to the genus *Streptococcus* and is selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to the use of at least one of the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, in the manufacturing of an anti-microbial composition, preferably an anti-bacterial composition. In a preferred embodiment, said use is characterised in that the bacterial strain belongs to the genus *Streptococcus* and is selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to a culturable anti-microbial bacterial strain selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, for use in the treatment of infectious diseases of the buccal cavity, preferably the treatment of caries. In a preferred embodiment, the bacterial strain of the invention is characterised in that it belongs to the genus *Streptococcus* and is selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to the use of at least one of the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, in the preparation of a composition designed for the treatment of infectious diseases of the buccal cavity, preferably the treatment of caries. In a preferred embodiment, the use of the strains of the invention is characterised in that the culturable bacterial strain belongs to the genus *Streptococcus* and is selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object of the present invention relates to the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, for use as a probiotic or functional food designed to improve buccal health, preferably to prevent caries. In a preferred embodiment, the strains of the invention are characterised in that they belong to the genus *Streptococcus*, selected from: CECT 7746, CECT

7747, CECT 7773 or CECT 7775.

Another object disclosed in the present invention relates to the use of at least one of the culturable anti-microbial bacterial strains selected from any of the following: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775, or a combination thereof, in the preparation of a probiotic or a functional food designed to improve buccal health, preferably to prevent caries. In a preferred embodiment, the use of at least one of the aforementioned bacterial strains is characterised in that said strains belong to the genus *Streptococcus* and are selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object disclosed in the present invention relates to a probiotic/prebiotic composition or functional food that comprises at least one culturable anti-microbial strain, as mentioned throughout the present invention, as well as the anti-cariogenic substances, compounds or molecules secreted by said strains.

Another object disclosed in the present invention relates to a medical-pharmaceutical composition or a composition designed for buccal health that comprises at least one culturable anti-microbial strain as described throughout the present invention or the anti-cariogenic substances, compounds or molecules secreted by said strains.

Another object disclosed in the present invention relates to an anti-microbial compound that comprises SEQ ID NO: 9 or an anti-microbial compound encoded by a DNA sequence that comprises any of the following sequences: SEQ ID NO: 1, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14.

Another object disclosed in the present invention relates to an anti-microbial compound that consists of SEQ ID NO: 9 or an anti-microbial compound encoded by a DNA sequence that consists of any of the following sequences: SEQ ID NO: 1, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14. In a preferred embodiment of the invention, the anti-microbial compounds described above present inhibitory activity against the growth of organisms that produce infectious diseases of the buccal cavity, preferably caries-producing organisms. In another preferred embodiment, said anti-microbial compounds are peptides.

Another object of the present invention relates to the anti-microbial compounds mentioned in the preceding paragraphs, or a combination thereof, for use as a medicament.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the manufacturing of a medicament.

Another object of the present invention relates to the anti-microbial compounds described above, or a combination thereof, for use in the manufacturing of an anti-microbial composition,

preferably an anti-bacterial composition.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the manufacturing of an anti-microbial composition, preferably an anti-bacterial composition.

Another object of the present invention relates to the anti-microbial compounds described above, or a combination thereof, for use in the treatment of infectious diseases of the buccal cavity, preferably the treatment of caries.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the preparation of a composition designed for the treatment of infectious diseases of the buccal cavity, preferably an anti-caries composition.

Another object of the present invention relates to the anti-microbial compounds mentioned above, in the present invention, for use as a prebiotic or a functional food designed to improve buccal health, preferably to prevent caries.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the preparation of a prebiotic or a functional food designed to improve buccal health, preferably to prevent caries.

Another object disclosed in the present invention relates to a probiotic/prebiotic composition or functional food that comprises at least one anti-microbial compound as described throughout the present invention.

Another object disclosed in the present invention relates to a medical-pharmaceutical composition or composition for buccal health that comprises at least one anti-microbial compound as described throughout the present invention.

Another object disclosed in the present invention relates to an anti-microbial compound that comprises sequence SEQ ID NO: 8 or an anti-microbial compound encoded by a DNA sequence that comprises any of the following sequences: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5.

Another object disclosed in the present invention relates to an anti-microbial compound that consists of sequence SEQ ID NO: 8 or an anti-microbial compound encoded by a DNA sequence that consists of any of the following sequences: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5. In a preferred embodiment, said anti-microbial compounds present inhibitory activity against the growth of organisms that produce infectious diseases of the buccal cavity, preferably, caries-producing organisms. In another preferred embodiment, the anti-microbial compounds described above are characterised in that they are peptides. In another preferred embodiment, the anti-

microbial compounds described above are characterised in that they inhibit the production of acid, preferably lactic acid, in the buccal cavity.

Another object disclosed in the present invention relates to an anti-microbial compound as described above, or a combination thereof, for use as a medicament.

Another object of the present invention relates to the use of at least one anti-microbial compound as described in the present invention, or a combination thereof, in the manufacturing of a medicament.

Another object of the present invention relates to an anti-microbial compound as mentioned above, or a combination thereof, for use in the manufacturing of an anti-microbial composition, preferably an anti-bacterial composition.

Another object of the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the manufacturing of an anti-microbial composition, preferably an anti-bacterial composition.

Another object disclosed in the present invention relates to an anti-microbial compound, as described above, or a combination thereof, for use in the treatment of infectious diseases of the buccal cavity, preferably the treatment of caries.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the preparation of a composition designed for the treatment of infectious diseases of the buccal cavity, preferably an anti-caries composition.

Another object of the present invention relates to the anti-microbial compounds as described above, or a combination thereof, for use as prebiotics or functional foods designed to improve buccal health, preferably to prevent caries.

Another object disclosed in the present invention relates to the use of at least one anti-microbial compound as described above, or a combination thereof, in the preparation of a prebiotic or a functional food designed to improve buccal health, preferably to prevent caries.

Another object disclosed in the present invention relates to a probiotic/prebiotic composition or functional food that comprises at least one anti-microbial compound as described in the present invention.

Another object disclosed in the present invention relates to a medical-pharmaceutical composition or a composition for buccal health that comprises at least one anti-microbial compound as described in the present invention.

Another object disclosed in the present invention relates to a process for isolating culturable anti-microbial bacterial strains, preferably with inhibitory activity against the growth of organisms that

produce infectious diseases of the buccal cavity and, more preferably, caries-producing organisms, characterised in that it comprises:

a) Obtaining samples from the supragingival dental plaque of individuals who have never suffered from caries.

b) Seeding the samples in the adequate media and under the adequate conditions so as to grow and isolate only those bacteria that are most frequent in individuals who have never suffered from caries, estimating the latter by means of pyrosequencing of the metagenome.

c) Culturing the isolated strains in a growth medium for cariogenic bacteria and selecting, after an appropriate culture time, those strains that present inhibition haloes against said growth.

In a preferred embodiment, the process described above is characterised in that, in step b), the bacteria that are most frequent in individuals who have never suffered from caries are estimated by means of pyrosequencing of the metagenome, a technique that makes it possible to estimate the proportions of each bacterial species. In another preferred embodiment, the process described above is characterised in that, in step c), bacteria belonging to the following genera are preferably selected: *Streptococcus, Rothia, Neisseria, Globicatella, Johnsonella, Haemophilus, Kingella, Cardiobacterium, Mannheimia, Phocoenobacter* and *Aggregatibacter.* Specifically, the following strains are selected: CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775. More specifically, bacteria belonging to the genus *Streptococcus* are selected, preferably those belonging to the following species: *S. sanguis, S. oralis, S. mitis, S. infantis* or new species that have not been described but belong to the *Streptococcus* subgroup that includes these four species. More specifically, at least one anti-microbial bacterial strain is selected from: CECT 7746, CECT 7747, CECT 7773 or CECT 7775.

Another object disclosed in the present invention relates to a method for the prevention and/or treatment of infectious diseases, preferably of the buccal cavity and, more preferably, caries, which comprises the administration of a quantity that is effective to inhibit the growth of the pathogenic microorganisms, preferably cariogenic microorganisms, habitually present in said cavity, of at least one of the culturable anti-microbial strains described in the present invention; or the probiotic/prebiotic composition or the functional foods described in the present invention which comprise said strains; or the medical-pharmaceutical composition or the composition for buccal health described in the present invention which comprise said strains.

Another object of the present invention relates to a process for obtaining anti-microbial compounds, preferably with inhibitory activity against the growth of organisms that produce infectious diseases of the buccal cavity and, more preferably, caries-producing organisms, characterised in that

it comprises:

a) Obtaining samples from the supragingival dental plaque of individuals who have never suffered from caries.

b) Lysing said samples and extracting intact genomic DNA therefrom.

c) From the remaining DNA extracted, preparing a metagenomic library of vectors, preferably plasmids or fosmids, capable of being inserted into, and expressing the extracted DNA that they carry, in a host cell.

d) Inserting the vectors into a host cell.

e) Seeding the clones of host cells that contain the vectors in a culture with caries-producing microorganisms and selecting, after an appropriate culture time, those clones that present growth inhibition haloes.

f) Sequencing the DNA of the vectors of the clones that exhibit inhibitory activity, synthesising and/or purifying the compound encoded by said DNA.

In a preferred embodiment, the process described above is characterised in that the concentration of the DNA extracted is at least 300 µg/ml. In another preferred embodiment, said process is characterised in that, following the DNA extraction process, fosmids are constructed that contain DNA with a size range of preferably between 35 and 45 kb. In another preferred embodiment, said fosmids contain DNA with a size smaller than 1 kb. In another preferred embodiment, said process is characterised in that the host cell wherein the fosmids are inserted is *E. coli.*

In another preferred embodiment, said process is characterised in that the culture of the microorganism whereon the clones with the DNA inserts contained in the fosmids are seeded is of a cariogenic bacteria, preferably *S. mutans* or *S. sobrinus.* In another preferred embodiment, said process is characterised in that the DNA sequence of the fosmids is selected from sequences that comprise: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14, or combinations thereof. In another preferred embodiment, said process is characterised in that the DNA sequence of the fosmids is selected from sequences that consist of: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14, or combinations thereof.

In another preferred embodiment, said process is characterised in that at least one anti-microbial peptide comprising a sequence selected from SEQ ID NO: 8 or SEQ ID NO: 9, or an anti-microbial compound encoded by a DNA sequence that comprises any of the following: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14, are obtained. In another preferred embodiment, said process is characterised in that at least one anti-microbial peptide consisting of a sequence selected from SEQ

ID NO: 8 or SEQ ID NO: 9, or an anti-microbial compound encoded by a DNA sequence that consists of any of the following: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13, SEQ ID NO: 14, are obtained.

In another preferred embodiment, the DNA sequences of fosmids SEQ ID NO: 1, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 13 and SEQ ID NO: 14, and the anti-microbial peptide with SEQ ID NO: 8 are of bacterial origin, preferably bacteriocins. In another preferred embodiment, the DNA sequences of fosmids SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5 are of human origin, preferably defensins/cathelicidins.

Another object disclosed in the present invention relates to a method for the prevention and/or treatment of infectious diseases, preferably of the buccal cavity and, more preferably, caries, which comprises the administration of a quantity that is effective to inhibit the growth of the pathogenic microorganisms habitually present in said cavity, of at least one anti-microbial compound as described throughout the present invention; or the probiotic/prebiotic composition or the functional foods which comprise at least one of the anti-microbial compounds described in the present invention, or the medical-pharmaceutical composition or the composition for buccal health which comprises at least one of the anti-microbial compounds described in the present invention.

Deposit of microorganisms in accordance with the Budapest treaty

The microorganisms used in the present invention were deposited in the Spanish Type Culture Collection (CECT), located in the Research Building of the University of Valencia, Campus Burjassot, Burjassot 46100 (Valencia, Spain), with deposit nos.:

- CECT 7746: bacterial strain of the genus *Streptococcus* deposited on 7 June 2010.
- CECT 7747: bacterial strain of the genus *Streptococcus* deposited on 7 June 2010.
- CECT 7773: bacterial strain of the genus *Streptococcus* deposited on 22 July 2010.
- CECT 7774: bacterial strain of the genus *Rothia* deposited on 22 July 2010.
- CECT 7775: bacterial strain of the genus *Streptococcus* deposited on 22 July 2010.

The purpose of the examples listed below is to illustrate the invention without limiting the scope thereof.

Example 1. Obtainment of the metagenome of supragingival dental plaque

In the first place, samples of the supragingival dental plaque were taken from volunteers who

have never suffered from caries, and, for comparative purposes, similar samples were taken from volunteers who had previously suffered from caries and volunteers who suffer from caries and, moreover, present lesions in said caries, after signing the informed consent. The sampling process was approved by the Clinical Research Ethics Committee of the General Directorate of Public Health of the Valencian Regional Government (GSP-CSISP). The buccal health condition of each volunteer was evaluated by a dentist following the recommendations and the nomenclature of the Studies in Buccal Health of the World Health Organisation (WHO), and the samples were taken using sterile probes. The volunteers were asked not to brush their teeth for 24 hours prior to the taking of samples.

In order to study the microbial diversity in the dental plaque and obtain the metagenome thereof, the material collected from the plaque of the surfaces of all the teeth of each individual was mixed in order to subsequently lyse it and obtain the total DNA of each dental plaque. The DNA was extracted using the MasterPure™ Complete DNA and RNA Purification Kit (Epicentre Biotechnologies), following the manufacturer's instructions and adding a treatment with lysozyme (1 mg/ml at 37°C for 30 minutes) during the lysis step. The DNA concentration was measured with NanoDrop (Thermo Scientific) and the samples chosen must preferably have a DNA concentration greater than 300 µg/ml and a total quantity of at least 5 µg (due to the sensitivity threshold of the equipment and the processes involved in the pyrosequencing). Moreover, the DNA samples were run through an agarose gel in order to verify the integrity of the genomic DNA extracted from the volunteers' dental plaques. Subsequently, the pyrosequencing of said extracted DNA was performed by means of the GS FLX-Titanium Chemistry sequencer (Roche). Pyrosequencing consists of the fragmentation of DNA into fragments of about 500-800 nucleotides by means of nitrogen under pressure, adding adapters at the ends which make it possible to anchor the DNA to spheres of less than one micrometre in diameter. The spheres are introduced into an specific oil that acts as a microreactor, in order to perform an emulsion PCR (emPCR), where the DNA integrated in each sphere is amplified.

Following an enrichment of the spheres that have amplified the DNA, the solution is placed on titanium plates in the GS FLX sequencer (Roche), where the pyrosequencing reaction takes place. This reaction consists of the transformation of each pyrophosphate molecule released by polymerase upon adding a nucleotide in a light beam, by means of a set of enzymes such as luciferase. This light beam is proportional to the number of nucleotides added and, in this manner, a high-sensitivity chamber translates the light pulses into the corresponding DNA sequence (19). The average length of said DNA was 425 pb. Those sequences artifactually replicated by means of the 454-pyrosequencing technique that appeared systematically were eliminated from the set of final

data through the "454 Replicar Filter" (20), such that the number of reads of a given sequence was related only to the frequency thereof in the sample.

The quantity of human DNA in the metagenomes ranged between 0.5%-40% in the samples from the supragingival dental plaque (Table 1) and were identified using the human genome database by means of Megablast (21) and eliminated from the set of final data.

Table 1. Characteristics of the pyrosequenced oral samples and the metagenome thereof.

Sample[1]	CAO Index[2]	No. of reads	% human DNA	Total Mbp	Contigs > 5kbp	Largest contig	16S reads[3]	Simpson Index[4]	Shannon Index[4]	Chao1 Index[4]
NOCA_01P	0	347927	40.59	77.54	13	12856	543	0.93	3.19	100 ± 24.6
NOCA_03P	0	347927	22.76	100.13	49	43857	374	0.91	2.94	92 ± 28.4
CA1_01P	8 (1)	494659	2.23	203.71	657	46856	1160	0.94	3.21	120 ± 24.8
CA1_02P	6 (4)	315892	2.74	129.85	154	15919	575	0.92	3.11	85.2 ± 9
CA_04P	25 (15)	402049	11.54	142.37	181	19835	663	0.89	2.89	74.4 ± 9.9
CA_06P	11 (8)	354192	10.83	123.27	47	51033	615	0.95	3.38	129.2 ± 41
CA_06_1.6	11 (8)	305820	66.97	37.52	0	3376	194	0.92	3.21	77 ± 13.3
CA_05_4.6	10 (7)	291162	74.99	27.67	2	29784	130	0.88	2.82	55.3 ± 8.3

[1] "P" indicates supragingival dental plaque samples. The samples with a number code indicate the tooth wherefrom samples from the caries cavity have been extracted.
[2] Number of dental pieces with caries (C), absent (A) and obstructed (O). The number in parenthesis indicates the number of exposed caries in the patient.
[3] Number of sequences of 16S rRNA detected in the metagenome and assigned by means of the RDP classifier.
[4] Simpson, Shannon, and Chao1 diversity indices, performed at the genus level.

Subsequently, a mean of 425 pbs allowed for the functional assignment in a significant fraction of the metagenome (Table 2). Moreover, the assembly of said reads produced 1103 assemblies ["contigs"] greater than 5 kpb and 354 greater than 10 kpb. We obtained a mean of 129.5 Mpb of high-quality filtered sequences (greater than 100 pb and where over 90% of the nucleotides had a 99.99% accuracy: The probability that the nucleotide read by the pyrosequencer is correct; i.e.,

a 99.99% accuracy means that only 0.01% of the nucleotides are incorrect (sequencing errors)) for each of the 6 oral samples. In the two samples with caries lesions, about 70% of the sequences pertained to human DNA, and in this case an average of 32.5 Mpb of high-quality filtered reads were obtained.

Table 2. Functional assignment of the samples present in the oral metagenome on the basis of different classification systems

Sample	Dental health[1]	Total reads	cdd (n) [a]	cd (%)	cog (n) [b]	cog (%)	Tfam (n) [c]	Tfam (%)	seed (n) [d]	seed (%)
NOCA_01P	h	204218	126729	62	108929	53	82457	40	111497	50
NOCA_03P	h	244881	116575	48	95327	39	74356	30	93391	38
CA1_01P	c	464594	321997	69	280652	60	214050	46	271868	59
CA1_02P	c	295072	182091	62	150966	51	118716	40	146161	55
CA_04P	ac	339503	192003	57	161384	48	126281	37	158887	48
CA_06P	ac	306740	182349	59	151524	49	119477	39	146032	47
CA_05_4.6	cav	70503	40999	58	31864	45	26245	37	29625	42
CA_06_1.6	cav	97722	54305	56	45440	46	35395	36	44552	46

[1] h: healthy individuals without caries; c: individuals with caries in the past; ac: individuals with active caries; cav: samples of caries lesions.
(n): absolute count.
(%): total percentage of reads in the sample that were assigned to a function.
[a]cdd : assignment to conserved domains analysed in the NCBI Conserved Domains database.
[b]cog: assignment to sets of orthologous groups.
[c]Tfam: assignment to Tigr Fams.
[d]seed : assignment to the Seed / MG-RAST subsystems.

Example 2. Construction of the fosmid metagenomic library of supragingival dental plaque

Using the samples of intact DNA extracted from the supragingival dental plaque of the healthy volunteers included in the study which had not been used for the pyrosequencing process, the metagenomic library of fosmids (inserts that have a length of preferably between 35-45 kb) of the dental plaque of said volunteers was performed, using, to this end, the EpiFOS™ Fosmid Library Production Kit (Epicentre Biotechnologies), following the instructions provided by the manufacturer.

Briefly, in a preferred alternative of the process for constructing the metagenomic library of the invention, the fosmids are inserted into a host, preferably *Escherichia coli*. The library is prepared, as explained above, using the EpiFOS™ Fosmid Library Production Kit (Epicentre), following the manufacturer's instructions with some modifications, such as increasing the ligation time (12 hours in a bath at 20°C), the use of the total DNA for the insertion, and not the DNA extracted from the pulse-field gel, slightly modifying the DNA extraction process such that the latter breaks as little as possible (use of cut pipette tips, avoiding the vortex, use of Centricom membranes (Millipore) to concentrate the DNA).

Insertion of the DNA into the *E. coli* host is performed by packaging the fosmids in lambda phage particles and subsequently infecting them in Epi300T1R strains of *E. coli*. During the packaging, the ligation product is placed in contact with the viruses for 3 hours at 30°C in 1 ml of phage buffer. The infection is performed at 37°C for 30 minutes, by placing the virus particles in contact with the *E. coli* strain. A prior titration is performed in order to select the optimal concentration of colonies in a plate (sufficiently distant so as to be able to seed a single colony with the aid of a sterile stick), by culturing different dilutions of the mixture in LB-agar medium with chloramphenicol.

Subsequently, each colony is inoculated in a 96-well Elisa plate in liquid LB medium with chloramphenicol, where they will be allowed to grow once again prior to being stored. The clones are stored in 96-well Elisa-type plates (Nunc) at a temperature of –80°C in 19% glycerol, in order to prevent the formation of ice crystals and maintain the integrity of the cells. The fosmids are frozen without being induced to multiple-copy in order to prevent recombination processes between them.

The different *E. coli* clones with the different fosmid inserts are then seeded in cultures of cariogenic bacteria, such as *Streptococcus mutans* or *Streptococcus sobrinus*. Those clones are selected which, in said cultures, present an inhibition halo around the seeding point (Figure 1). The clones obtained are identified by means of sequence homology of the DNA contained in each fosmid, on the basis of different available public sequence databases. In order to obtain the DNA sequence of each fosmid, the total DNA thereof is extracted by separating it from the vector DNA by means of midiprep kits from QIAGEN, and performing the direct pyrosequencing thereof. This is how the respective ORFs and, subsequently, the peptides encoded thereby, are obtained.

Example 3. Analysis of the diversity of the human oral Metagenome

Once the metagenome of the supragingival dental plaque from individuals with caries and from healthy individuals was obtained following the process described in the present invention, the diversity of said oral metagenome was analysed using three different techniques:

Taxonomic assignment by means of the analysis of the 16S rRNA: the 16S rRNA sequences were extracted from the reads obtained from each metagenome by means of similarity searches with BLASTN (26) against the RDP database (Ribosomal Database Project). The sequences with a size smaller than 200 pb were eliminated. The phylogenetic assignment of the sequences was performed using the RDP Classifier (27), with a confidence threshold of 80%.

Gene taxonomic assignment: the taxonomic assignment of all the ORFs was performed on the basis of the lowest common ancestor (LCA) algorithm, by means of the characteristics described in the MEGAN software (28). In order to obtain the LCA of each sequence, homology searches were performed using the BLASTx database against another customised database that includes non-eukaryotic sequences from the non-redundant NCBI database (NR). For each sequence read, only those results that showed a coincidence of at least 90% were considered in the obtainment of the LCA.

Taxonomic assignment of the reads (PhyMM): said taxonomic assignment is performed using PhymmBL (29), which combines the assignment of sequences by both homology and the composition of nucleotides; to this end, hidden Markov models are used. All the available complete genomes were obtained from the Human Oral Microbiome Database (HOMD) (30), as well as the NCBI database (RefSeq), which contain all the genomes of bacteria and archaea (March 2010), and were used to construct a local database designed to perform taxonomic construction models and homology searches by means of PhymmBL. In this analysis, we only used sequences greater than 200 pb to predict the taxonomic identification. Using said read length, the class-level accuracy of the search with PhymmBL has been estimated to be greater than 75%. All the taxonomic and functional results were analysed in a MySQL database for the subsequent analysis thereof.

The results obtained using these three methods show that a small number of 16S genes in directly sequenced metagenomes are sufficient to describe the main taxonomic groups present in the oral metagenome, without the biases associated with cloning or PCR techniques.

From the samples examined, interesting differences may be observed between healthy and ill individuals. The trend shown by the three methods was that the Bacilli and Gamma-proteobacteria taxonomic groups were the most common in healthy individuals, whereas typically anaerobic taxa, such as Clostridials and Bacteroidets, are more frequent in samples from ill subjects. The reads assigned to Beta-proteobacteria (primarily Neisserials) and phylum TM7 (as yet without a definite name and without any member having been cultured thus far) were present in a very low proportion in samples from ill individuals and, therefore, may be associated with healthy conditions.

Correspondence analysis between the metagenomes, based on the taxonomic assignment of the 16S rRNA reads, showed that the samples from individuals with bad oral health tended to

group together, whereas different bacterial consortia may be found in healthy individuals. By means of the present metagenomic study, the invention demonstrates that the genera *Streptococcus and Rothia*, more preferably, the genus *Streptococcus*, are prevalent genera in subjects without caries. For this reason, when we select, from the supragingival plaque samples of individuals who had never suffered from caries, those that could have anti-cariogenic activity, the selection was aimed at searching (culture media, culture parameters, microscope morphology of the bacteria, morphology of the colonies, etc.) species belonging to said genera, *Streptococcus* and *Rothia*, more preferably, the genus *Streptococcus*.

One of the powerful applications of the LCA and PhymmBL approaches is that most of the reads with significant coincidences may be assigned to a taxonomic origin and, moreover, to a possible function. By relating the taxonomy and the function, it has been possible to predict the ecological or metabolic role that each bacterial group may play. Using the COG (Cluster of Orthologous Groups) functional classification system, it may be observed that the categories are not evenly distributed, and that certain bacterial groups are especially suited to perform certain functions. For example, a large proportion of genes involved in defence mechanisms (e.g. restriction endonucleases and drug discharge pumps) are encoded by Bacilli, which, jointly with the greater presence of *Streptococci* in people without caries, allowed us to predict that those bacteria could be potential producers of natural inhibitors of human pathogens in a possible replacement therapy strategy for the treatment of buccal infectious diseases.

Example 4. Analysis of the microbial richness and abundance present in the human oral metagenome

Initial studies based on traditional culture techniques and pioneering molecular works, including amplification and cloning of the 16S rRNA gene, predicted a diversity of about 500 different species in the oral cavity (6). The use of last-generation technologies (Next Generation Sequencing, NGS) gave estimates of between 4000 and 19000 operational taxonomic units (OTUs). OTUs are estimates of the number of species on the basis of the DNA sequences, which take into consideration the fact that sequences of the 16S rRNA gene with a similarity lower than a given threshold belong to different species. The threshold used is the standard for the 16S rRNA gene, a 97% sequence identity; thus, if the similarity is greater than 97%, it is considered to be of the same species, but, if it is lower than 97%, it is probably a different species. Longer pyrosequencing reads (250 pbs) in three healthy subjects estimated about 600 OTUs per person, and a recent project attempted to sequence 11447 amplicons with almost the full length of 16S rRNA amplicons using Sanger-type sequencing

(22), reducing the estimates to less than 300 OTUs in 10 individuals.

Although our estimates of microbial diversity are closer to those obtained using Sanger-sequenced reads (6,22), the 16S rRNA reads extracted from our metagenomic data identified 186 new OTUs that had not been previously detected by PCR amplification. The rarefaction curves (the saturation in the number of species as the sampling stress increases) and different diversity indices, as described in Table 1 (specifically, the Shannon, Simpson, and Chao1 indices), based on 4254 rRNA reads, indicated an estimate of 73-120 genera for the dental plaque samples (Tables 1 and 2). Clear differences between the samples of volunteers with different health conditions were not observed in regards to the diversity, although the two samples with caries lesions tended to present a lower diversity.

An effective tool to quantify the presence of selected species in metagenomes is sequence recruitment. Those individual metagenomic reads with coincidences greater than a certain identity threshold against a reference bacterial genome are "recruited" to plot a graph that will vary in density depending on the abundance of that organism in the sample. If the mean nucleotide identity shown is greater than 94%, the recruitment has probably been performed against reads from the same species (23).

Upon comparing our metagenomes with the 1117 genomes available thus far, using the Nucmer and Promer v 3.06 algorithms, we have been able to estimate the abundance of these species in our samples. Surprisingly, bacteria related to *Aggregatibacter* and *Streptococcus sanguis* were amongst the most abundant in people without caries, which agrees with the greater PCR amplification frequency of these species in the oral cavity of healthy individuals. The genus *Neisseria* was also frequent in samples from healthy individuals. Moreover, the recruitment graphs indicate that a few taxa are normally dominant in each metagenome, which suggests that, although there is a great bacterial diversity in the oral cavity, a few taxa comprise most of the bacterial cells.

Example 5. Functional diversity in the oral ecosystem

In order to analyse the functional diversity of the organisms that are a part of the oral ecosystem of the individuals analysed in the present invention, all the metagenomic sequence reads obtained were compared to different databases: conserved domain database (CDD) (24), subsystem-based annotation system (SEED) and TigrFams profiles (25).

Correspondence analysis (CoA) of the samples on the basis of the functional assignment of the reads provided similar grouping patterns for the three functional classification systems (CDD, SEED and TigrFams). The samples from ill subjects (with caries) tended to group together, indicating

that a similar group of functions were encoded in their metagenomes, and the samples from individuals who had never suffered from caries, jointly with one of the individuals who presented a low number thereof, are separately grouped. When comparing the functional assignment of the oral metagenomes against the intestinal microbiome of adult persons (8), the oral samples are grouped together, indicating that the intestine and the mouth are two different ecosystems in terms of the relative frequencies of the encoded functions. The present invention demonstrates that there are blocks of functions that are over-represented in the intestinal microbiome, whereas others are over-represented in the oral samples.

In the oral samples, the individuals are grouped on the basis of their health condition. From an applied standpoint, it is interesting to note that many functional categories are over-represented in the samples from individuals without caries. These include DNA capture genes involved in competition in Gram-positive bacteria, others involved in the phospholipid metabolism, fructose and mannose-induced phosphotransferase systems, the *Streptococcus mga* regulon, proteins involved in mixed acid fermentation, quorum-sensing genes and bacteriocin-type anti-bacterial peptides. Said bioactive compounds, bacteriocins, are potential anti-caries agents and, therefore, the present invention demonstrates that the dental plaque of individuals who have never suffered from caries is a genetic reservoir of new anti-microbial and potentially anti-cariogenic substances.

Example 6. Inhibition assays of the clones obtained in the fosmid library of the invention on cariogenic *Streptococcus* cultures

Once the fosmid library of the supragingival dental plaque from individuals who had never suffered from caries was obtained, different clones of *E. coli*, with the different fosmid inserts, were seeded in cultures of cariogenic bacteria, such as *Streptococcus mutans* or *Streptococcus sobrinus*. A replica of the fosmid metagenomic libraries of those volunteers who had never suffered from caries was pinned on said plates, by means of a Nunc 96-pin replicator, such that each Petri dish may host the growth of the 96 clones of each plate in the library, previously induced to multiple copy by means of an inducer (Epicentre Technologies). Using this simple screening, a high-yield activity assay of thousands of clones may be performed during a limited time, selecting those clones that produce an inhibition halo on the cariogenic bacteria (Figure 1).

The DNA sequences or inserts of these fosmids, as explained in Example 2 of the present invention, are those that potentially produce excreted substances that spread in the agar and prevent the growth of those bacteria that cause dental caries. Subsequently, a second activity screening was performed with the positive clones in order to eliminate the false positives (Figure 1B). The clones

obtained are identified by means of sequence homology of the DNA contained in each fosmid, against different public databases of available sequences.

In order to obtain the DNA sequence of each fosmid, the total DNA thereof is extracted by separating it from the vector DNA by means of midiprep kits from QIAGEN, and performing direct sequencing. The ends of twenty fosmids were sequenced using the classic Sanger technology by means of Reverse (SEQ ID NO: 10 and SEQ ID NO: 11) and T7 (SEQ ID NO: 12) primers of commercial PCC1Fos vectors. Of the twenty fosmids sequenced, four sequences show homology with bacterial DNA (30%-98%) and five other sequences show 99%-100% homology with human DNA. Therefore, of the sequences of fosmid ends that present inhibitory capacity, four are of bacterial origin and five others are of human origin. In two of the cases (one bacterial and one human), the insert turned out to be of a very short length; for this reason, the sequence of the two ends overlapped, thus obtaining the full length of the insert. The insert of human origin completely sequenced using this process has 244 nucleotides (SEQ ID NO: 1) and the bacterial insert has 666 nucleotides (SEQ ID NO: 2).

The sequence of the other seven inserts was obtained by pyrosequencing, using groups of 2-5 fosmids, and combining their DNA in a 1/16 or 1/8 plate of the Genome Sequencer FLX pyrosequencer (Roche). The sequences obtained were assembled by means of the Newbler programme (Roche) using standard parameters, and the assemblies obtained were related to the corresponding fosmids on the basis of the previously-obtained insert end sequences. The characteristics of the nine inserts are shown in Table 3.

Table 3. Characteristics of the DNA inserts of the fosmids with inhibitory capacity against cariogenic bacteria

Name	Origin	Length of Insert (pb)	Sequence No.
T5A	Human	244	SEQ ID NO: 1
S12E	Bacterial	666	SEQ ID NO: 2
T1F	Bacterial	42797	SEQ ID NO: 3
T4H	Bacterial	28023	SEQ ID NO: 4
T9B	Bacterial	33804	SEQ ID NO: 5
A5D11	Human	45166	SEQ ID NO: 6
A4H11	Human	32692	SEQ ID NO: 7
W4D	Human	34079	SEQ ID NO: 13

T5H	Human	27661	SEQ ID NO: 14

Example 7. Identification of the anti-microbial peptides in the short S12E and T5A fosmids.

Once the sequences of the seven fosmids were obtained as described in Example 6, the DNA sequence of the two short-length DNA inserts was analysed, to obtain all the ORFs encoded in the 3'-5' and 5'-3' direction. Of these ORFs, we selected those that contained ribosome-binding sequences (with a 3'-end complementary sequence of 16S from *E. coli*) and, therefore, could be efficiently translated, and those that could be excreted, either by the presence of a signal peptide (identified using the SIGNAL-IP software) or by the non-classical secretory pathway (identified using the SECRETOME-P software). Using said methods, a candidate ORF was obtained in the fosmid of human origin (T5A), only 26 amino acids in length (SEQ ID NO: 8), and another candidate ORF was obtained in the fosmid of bacterial origin (S12E), 39 amino acids in length (SEQ ID NO: 9). Moreover, these genes showed an amino acid composition characteristic of anti-microbial peptides, and, furthermore, in the case of T5A, of human origin, the presence of two cysteines that may form a disulfide bridge was observed. This, together with their short length and their net positive charge, suggests that they are bioactive anti-microbial peptides.

Subsequently, said peptides were purified. To this end, they were separated from the rest of the products secreted on the basis of their molecular weight. Thus, 15 ml of each clone induced to multiple copy were cultured in Brain-Heart Infusion (BHI) medium, centrifuging the cells and collecting the supernatant, which was filtered through Millipore filters with a 0.2-micron pore size in order eliminate any bacterial residue. This supernatant, which contains the secreted products, was filtered once again through Amicon 10-kD Millipore filters and the filtrate was run, once again, through Amicon 3-kD Millipore filters, thereby obtaining the fraction between 3 and 10 kD to a volume of 1 ml. The fraction with a size smaller than 3 kD (0-3 kD fraction) was concentrated under cold conditions in a speed-vac to a volume of 1 ml.

Subsequently, 50-, 100- and 150-µl volumes of these two fractions, 3-10 kD and 0-3 kD, respectively, were added to a liquid culture of *S. mutans* and to a liquid culture of *S. sobrinus*, and the optical density was measured in a 48-well Fluostar luminometer every half-hour, with each treatment in triplicate, for 12-19 hours. As may be observed in Figures 2 and 3, the growth curves of the cariogenic bacteria show that, in the case of the defensin-type anti-microbial peptide of human origin (Figure 3), the fraction smaller than 3 kD has a dose-dependent inhibitory effect on the cariogenic bacteria, whereas, in the case of the bacteriocin-type anti-microbial peptide of bacterial origin, the 3-

10 kD fraction has the dose-dependent inhibitory effect on said cariogenic bacteria (Figure 2), which agrees with the molecular weights estimated on the basis of the amino acid sequence for each of the fosmids.

Example 8. Comparative assay of the inhibitory activity of the bioactive peptides of the invention against cariogenic bacteria.

In order to compare the inhibitory effect of bacteriocin to that of other competitive products available in the market, the same growth experiments of *S. mutans* in a liquid BHI medium were performed as those described in the preceding example, but now adding: a) 100 µl of one of the leading mouthwashes in the market (Listerine®, which is an anti-dental plaque agent and oral antiseptic), b) 100 µl of the concentrated supernatant (as explained in the preceding example) of the S12E clone containing bacteriocin (3-10-kDa fraction), and c) 100 µl of Listerine® + 100 µl of the supernatant of the S12E clone containing bacteriocin. The inhibitory effect of bacteriocin at this concentration, 100 µl, on the growth of *S. mutans* is greater than that of the commercialised product for this bacterial species (Figure 4) and, moreover, it may be observed, in said Figure 4, that the addition of bacteriocin to the commercialised product significantly improves the inhibitory activity of said product against *S. mutans.*

Example 9. Analysis of the cariogenic activity of the chemically-synthesised S12E and T5A peptides.

The chemical synthesis of the 2 inhibitory peptides isolated (SEQ ID NO: 8 and 9) was performed in accordance with the solid-phase synthesis method (32 and 33). Peptide synthesis by means of SPPS (Solid-Phase Peptide Synthesis) is the most common method used to synthetically create peptides and proteins in the laboratory, and allows for the synthesis of natural peptides that are difficult to express in bacteria, the incorporation of unnatural amino acids or peptide modification (for example, the formation de disulfide bridges).

In the case of the peptide of human origin, a protecting group, Fmoc-Cys(trt)-OH, was used to protect the –SH groups, which are quite reactive and were relatively frequent in this peptide. The peptides covalently bind to spheres, leaving the N-terminal amino group free, such that it may bind to a single N-protected amino acid. Following the binding, the latter is de-protected and washed. After repeated cycles of binding, washing, de-protection and washing, the peptide chains are constructed. When the peptide is complete, it is released by the addition of a reagent (in this case, anhydrous

hydrogen fluoride). The quality control, designed to verify that the peptide synthesised is the correct one and does not contain impurities, was performed by means of mass spectrometry and HPLC.

In order to corroborate that the peptides identified are those responsible for the inhibitory activity against cariogenic bacteria, the S12E (bacteriocins of bacterial origin) and T5A (peptide of human origin with a structure similar to that of defensins) peptides were chemically synthesised, obtaining approximately 4 mg of each of said peptides with a purity greater than 80%. They were totally re-suspended in 0.1% trichloroacetic acid (TCA) and the experiments designed to test the inhibition of liquid cultures of *S. mutans* by said chemically-synthesised compounds were performed.

In the case of the bacteriocin-type S12E peptide, of bacterial origin, the inhibitory activity against cultures of *S. mutans* was confirmed, especially at high concentrations (Figure 5). Subsequently, more S12E peptide was chemically synthesised, now with a purity greater than 95%, and said peptide was re-suspended in ultrapure water, in order to demonstrate that the previously obtained inhibitory effects were not due to TCA, but to the chemically-synthesised S12E peptide itself. Once again, it was observed that treatment of cultures of *S. mutans* and *S. sobrinus* with the chemically-synthesised S12E peptide at a high purity produced a dose-dependent inhibitory effect on both cariogenic bacteria, *S. mutans* (Figure 6A) and *S. sobrinus* (Figure 6B).

In the case of the T5A peptide (of human origin, defensin-type), at first no inhibitory effect was found. It occurs that this peptide has several reactive amino acids, including two cysteines, the presence whereof is typical in human anti-microbial peptides, and often a disulfide bridge between these two cysteines is necessary for the peptide to be active. For this reason, said peptide was synthesised once again, adding a disulfide bridge between cysteines 3 and 12, and protecting the reactive amino acids during the synthesis. Following these modifications, it was confirmed that this peptide is capable of inhibiting the growth of the cariogenic bacteria, *S. mutans*, at different concentrations, with total inhibition of the growth when the maximum peptide concentration, 80 µg, is added (Figure 7).

Example 10. Identification of the inhibitory genes in long fosmids.

As regards the rest of the potential anti-microbial compounds, DNA was isolated from all the fosmids that produced an inhibition halo, and their ends and the complete insert were sequenced (Table 3). This makes it possible to obtain a catalogue of bacteria that produce anti-microbial substances (not only anti-bacterial peptides), as well as the regions in the human genome which encode them. Inhibition experiments were performed on liquid cultures of *S. mutans*, by adding the concentrated supernatant (as indicated in the preceding examples) produced by the corresponding

clones, in fractions of 0-3 kDa, 3-10 kDa, 10-100 kDa and >100 kDa. These experiments reveal that the size fractions that cause inhibition are the 0-3 kDa fraction in the T9B and T4H bacterial fosmids and in the W4D (Figure 8), T5H (Figure 9), A5D11 (Figure 10) and A4H11 (Figure 11) human fosmids, and the 3-10 kDa fraction in the T1F bacterial fosmid. Therefore, these results once again show that inhibition is produced by small-size peptides, i.e. peptides with a size between 0-3 kDa or 3-10 kDa, which is consistent with the fact that they are anti-bacterial peptides of the bacteriocin type or human defensins/cathelicidins.

Similarly, a search of the ORFs that encode peptides with these sizes (i.e., 0-3 kDa or 3-10 kDa, as the case may be) was performed on the sequences of said fosmids, and the following genes were selected as possible candidates to be the inhibitor-encoding genes: those with a ribosome-binding sequence, the presence of signal peptides and a use of amino acids similar to that of the anti-bacterial peptides and/or with a sequence similar to that of other known anti-bacterial peptides, and/or with hydrophobicity and/or a net positive charge.

Example 11. Identification of anti-caries bacteria.

The existence of a small proportion of the adult human population that has never suffered from caries has led to suggest the presence of bacterial species with a potential antagonistic effect against cariogenic bacteria (23). Bacterial replacement of the pathogenic strains by innocuous isolates obtained from healthy individuals has satisfactorily proven to prevent pharyngeal infections and is the basis for probiotics designed to prevent infectious diseases in the intestine and other human ecosystems (31). Metagenomic recruitments of cariogenic bacteria against the oral microbiome of healthy subjects show a total absence of *S. mutans* and *S sobrinus*. Surprisingly, the lack of detection of cariogenic bacteria is accompanied by an intense recruitment of other species of *Streptococcus* (primarily those similar to *S. sanguis*), *Aggregatibacter* and *Neisseria*, which are the most abundant genera in these individuals.

Given the possibility that isolates of these dominant genera may be involved in antagonistic interactions with cariogenic bacteria, fresh samples of dental plaque were taken from 10 healthy individuals (including the 2 healthy individuals wherefrom the metagenomic sequences were obtained) and used to culture, under optimal growth conditions, species of *Neisseria, Rothia and Streptococcus* (specifically, in blood agar, chocolate agar, brucella agar and TSA culture media, under aerobiosis conditions and in anaerobic jars). Following a microscopic examination, diplococci and streptococci were selected (in order to maximise the possibility of finding species of *Streptococcus, Rothia and Neisseria*), and a set of 249 isolates was obtained.

Those that were able to grow in the same medium as *S. mutans and S. sobrinus* were transferred to lawn cultures in the presence of said cariogenic bacteria. This simple screening identified 16 strains with inhibition haloes (Figures 12 and 13). Using PCR techniques and sequencing of the 16S rRNA, most of said strains were identified as belonging to species of *Streptococcus*, showing a 96%-99% sequence identity with the *S. oralis*, *S. mitis* and *S. sanguis* species or other related species, and also with *Rothia* species, with a 100% sequence identity with the *R. mucilaginosa* species in the 16S gene. The strains that showed inhibition haloes against *S. mutans* and/or *S. sobrinus* were deposited in the CECT, being assigned numbers CECT 7746, CECT 7747, CECT 7773, CECT 7774 and CECT 7775. As previously discussed, strains CECT 7746, CECT 7747, CECT 7773 and CECT 7775 belong to the same bacterial genus *Streptococcus* and, therefore, in addition to the method for obtaining them, share a structural and taxonomic similarity, since they belong to the same bacterial genus.

Specifically, on the basis of the 16S ribosomal gene sequence, said strains, which belong to the bacterial genus *Streptococcus*, are similar to the *S. mitis* (CECT 7746 and CECT 7775) and *S. oralis* (CECT 7747 and CECT 7779) species. Sequencing of the complete genome of strains CECT 7746 and 7747 reveals that they are new species of the genus *Streptococcus* (see Example 12), that they are sister strains despite coming from different individuals and, moreover, belong to the *S. mitis/oralis/infantis* cluster of species. The other bacterial strain deposited in the CECT, with number CECT 7774, belongs to the genus *Rothia* and, more specifically, to the *R. mucilaginosa* species. The inhibition haloes against cultures of cariogenic species, *S. mutans* or *S. sobrinus*, of said strains deposited in the CECT may be observed in Figures 12 and 13, respectively.

Example 12. Characterisation of bacterial strains CECT 7746 and CECT 7747.

Characterisation of bacterial strains CECT 7746 and CECT 7747 was performed by means of different techniques. In the first place, the complete genome of these two strains was obtained by means of shot-gun (7, 8) and pair-ends pyrosequencing; the latter consists of breaking the DNA into fragments of about 3000 nucleotides and the sequencing of approximately 200 nucleotides from each end, such that the known distance between these two ends helps in the assembly of the sequences.

In order to obtain the complete genome for each of strains CECT 7746 and CECT 7747, we started from samples collected from each of the cultures of said strains; specifically, a one-fourth culture plate was used for the pyrosequencing experiments by means of the shot-gun system (7, 8), using the GS-FLX pyrosequencer from Roche (Titanium Chemistry), and another one-fourth culture plate was used for the pyrosequencing experiments using the pair-ends system. The sequence

quantity obtained for each of the strains using both systems was:

Strain 7746

Shot-gun type: 441.549 reads, with a total of 165,105,921 nucleotides

Pair-ends type: 187.530 reads, with a total of 32,721,622 nucleotides

Strain 7747

Shot-gun type: 28.021 reads, with a total of 5,711,998 nucleotides

Pair-ends type: 305.826 reads, with a total of 51,501,510 nucleotides

The expected genome size for each of the strains was about 2.1 Mb. For strain CECT 7746, the size of the assemblies greater than 500 pb is 2,122,087 pb. In the case of strain CECT 7747, the size of the contigs greater than 500 pb is 1,953,989 pb.

The sequences were filtered and assembled using the Newbler software (Roche), adapted by the inventors with standard parameters, to obtain a total of 109 assemblies > 500 pb for strain CECT 7746 and of 51 contigs for strain CECT 7747. Subsequently, said genomes were automatically annotated, to obtain the complete sequence of the genome of said strains CECT 7746 and CECT 7747.

Once the complete genome of strains CECT 7746 and CECT 7747 was obtained, said isolates were taxonomically assigned on the basis of the phylogenetic trees obtained on the basis of the complete sequence of the 16S and 23S rRNA genes, which are the most widespread when preparing bacterial phylogenetic trees.

By linking together the sequences of the 16S and 23S rRNA genes, a single fragment greater than 4,000 nucleotides was obtained, which was aligned with the same fragment of the *Streptococci* species sequenced thus far. The sequences were aligned using the MAFFT free computer software, by aligning the 16S and 23S genes separately, and subsequently linking the alignment together. Afterward, the alignment is purified using the GBlocks free computer software in order to select the conserved informative positions. The tree is obtained using the RAxML programme, by the maximum verisimilitude method, with 500 repeats. The phylogenetic tree obtained showed that both strains are sister strains despite coming from different individuals and, moreover, belong to the *S. mitis/oralis/infantis* cluster of species, and the topology of the tree suggests that they are strains that belong to a new, non-described species.

In order to determine whether said strains belong to different species, the ANI (average nucleotide identity) was used. When the genomes of the sequenced strains are compared, the mean similarity between the homologous genes of the same species at the nucleotide level is greater than 95% (34, 35). In fact, taxonomists accept this 95% ANI value as the limit to separate bacterial

isolates belonging to different species and as an alternative to the classic 70% threshold in the DNA-DNA hybridisation value (36). Using the J-species free computer software to determine the ANI values between the two sequenced strains of the invention, CECT 7746 and CECT 7747, and the rest of the *Streptococci* sequenced, it was demonstrated that they are two strains belonging to a new species that has not been described as yet. In the case of the bacterial strain of the invention CECT 7746, there is no strain with a similarity above the 95% threshold and, in the case of the bacterial strain of the invention CECT 7747, only another strain of those sequenced, *Streptococcus M143*, exceeds said threshold. Said strain *M143* is a strain that, despite having a draft genome sequence, has not been taxonomically described as a species. The results used to calculate the ANIs were obtained by means of two different methodologies: Mummer and Blast (36), and both methodologies showed almost identical results.

Example 13. Inhibition assays of cariogenic bacteria, *S. mutans*, in the presence of the supernatants obtained from the cultures of the CECT 7746 and CECT 7747 strains disclosed in the invention.

The two strains of the invention, CECT 7746 and 7747, were grown in BHI culture medium at a temperature of 37°C. Subsequently, the supernatants of the cultures were collected, in the exponential phase and the stationary phase, being filtered through a 0.2-micron filter, in order to eliminate any bacterial residue. Subsequently, said supernatants were filtered once again by means of centrifugation, using membranes with a pore size of 100, 10 and 3 kDa (Amicon, Millipore), as described in the previous examples shown in the present invention.

The fraction of the supernatants obtained from each of strains CECT 7746 and 7747, collected in the stationary phase of growth, which produced inhibition of the growth of bacterial cultures of *S. mutans,* was concentrated in the size fraction smaller than 3 kDa for both tested strains, CECT 7746 (Figure 14 A) and CECT 7747 (Figure 14 B). Said results show that the inhibitory substance synthesised by said strains, which presents specific bactericidal effect against cariogenic species, must be of a small size, preferably <3 kDa, as in the case of bacteriocins.

On the contrary, when the same experiment was performed with samples of the supernatants of cultures of the strains of the invention CECT 7746 and 7747, collected in the exponential phase of growth, no inhibition of the growth of bacterial cultures of *S. mutans* (Figure 15) was observed, which indicates that the inhibitory agent is only produced in the stationary phase of bacterial growth of the strains of the invention.

When the samples of the concentrated supernatant obtained in the stationary phase, and

smaller than 3 kDa, were subjected to a temperature of 100°C for 10 minutes, it was verified that the inhibitory activity of said supernatant on cultures of *S. mutans* was maintained and even increased (Figure 16). These results are consistent with the fact that the inhibitory agent is a bacteriocin and not another type of peptide, since small-size bacteriocins are extremely thermostable and even increase their anti-microbial effect, since they are better eluted in the medium after their aggregates are dissolved through thermal shock.

Subsequently, inhibition assays against cultures of *S. mutans* were performed with the supernatants obtained from the cultures of the bacterial strains of the invention CECT 7746 and CECT 7747, but changing the seeding order and the growth temperature of the cultures of said cariogenic bacteria, in order to verify whether said modifications had any effect on the inhibitory activity of the supernatants of the strains of the invention.

In the first place, culture plates were seeded with the *S. mutans* cariogenic bacteria and, after 24 h had elapsed, the strains of the invention were seeded in the same culture plate. After a time had elapsed, no inhibition haloes were observed. On the contrary, when culture plates were seeded with both strains at the same time, inhibition of the growth of *S. mutans* was observed, as we had previously shown. The greatest inhibition of the growth of cultures of *S. mutans* was observed when the strains of the invention, CECT 7746 and 7747, were seeded first and, 24 h later, the strains of *S. mutans* were seeded, which indicates that there is a greater concentration of the inhibitory agent or substance prior to the growth of the cariogenic bacteria, and that, moreover, the presence of said bacteria is not necessary to activate the production of the inhibitory agent by the strains of the invention.

Subsequently, inhibition experiments against the growth of cariogenic bacteria were performed in a solid medium, by first seeding the strains of the invention with a drop of the culture in a liquid medium in the stationary phase, followed by a tapestry culture of *S. mutans* at different temperatures: 30°C, 33°C and 36°C. No inhibition of the growth of *S. mutans* was observed at a temperature of 30°C, but inhibition was observed at 33°C, being in fact greater than that obtained at 36°C.

Example 14. Inhibition assays against cariogenic bacteria, *S. mutans*, cultured in the presence of the supernatants obtained from the cultures of the bacterial strains of the invention CECT 7746 and CECT 7747, under aerobiosis and anaerobiosis conditions.

In order to determine whether the inhibitory action of the strains of the invention against the growth of cariogenic bacteria was modified by an aerobic or anaerobic environment, inhibition

experiments were performed in a solid BHI medium, by first seeding the strains of the invention with a drop of the culture in a liquid medium, in the stationary phase, in an anaerobic jar for 12 h, followed by a tapestry culture of *S. mutans* at 37°C, or followed by seeding with one drop of the culture of *S. mutans* at 37°C.

The results of both experiments showed that inhibition of the growth of *S. mutans* is much lower under anaerobic conditions, especially for strain CECT 7746 (Figure 17). Therefore, the results demonstrate that, for the strains of the invention, the inhibition exerted on cariogenic bacteria is more effective during the aerobic step of formation of the dental plaque, i.e. during the period of adherence and initial formation of the biofilm on the tooth.

Example 15. Anti-cariogenic effect of bacterial strains CECT 7746 and CECT 7747 and the supernatants thereof on the biofilm in an artificial tooth model.

In order to demonstrate the anti-cariogenic effect of the bacterial strains disclosed in the present invention, inhibition assays against the production of acid were performed with strains CECT 7746 and CECT 7747 on a biofilm in an artificial tooth model. Said experiments were performed on the Active Attachment biofilm model of the Academic Center for Dentistry Amsterdam (ACTA, Amsterdam). Said biofilm model was described by Exterkate RA *et al.* (37). Briefly, hydroxyapatite or glass discs are inoculated with human saliva from a volunteer with a high percentage of *S. mutans* (greater than 4%), with or without the presence of the probiotic strain, or the supernatant thereof. In the present assays, strains CECT 7746 and 7747, disclosed in the present invention, were tested, as was strain C7.1, an isolate belonging to species of the *Streptococcus mitis/oralis/infantis* group, obtained from an individual without caries, but which does not produce inhibition of the growth of cariogenic species and, therefore, acts as a negative control.

The human saliva is stored at -80 °C. Probiotic strainsCECT 7746 and 7747 and control strain C7.1 are grown in BHI culture medium with sucrose for 12 hours, until a culture density of approximately 4 x 10^8 cfu (Colony-Forming Units) is obtained. Subsequently, the saliva sample is mixed at 50% with the inoculum of the probiotic strains of the invention (CECT 7746 or 7747) or the inoculum of the control strain (C7.1), and applied onto the glass disc.

The biofilms are formed for 48 hours in modified artificial saliva medium (38) under aerobiosis and anaerobiosis, and, once formed, are incubated for 3 hours at a temperature of 37°C in cysteine peptone water (Sigma-Aldrich, St Louis, USA) containing 0.2% glucose, in order to measure the production of acid. During this incubation period, the strains will produce acid, which is measured by means of a colorimetric reaction: Said biofilm is transferred to an Eppendorf tube and incubated at a

temperature of 80°C for 5 min in order to stop the bacterial metabolism. The quantity of L-lactic acid is enzymatically determined by means of a colorimetric assay using the Spectra Max M2 spectrophotometer (Molecular Devices, USA), following the protocol described by Pham LC *et al.* (38).

In order to analyse the inhibition of the production of acid by the supernatants, of the strains of the invention (CECT 7746 and 7747) as well as the control strain (C7.1), in the first place, the supernatants of the cultures of said bacterial strains were obtained. To this end, cultures of said strains were grown in BHI medium for 12 hours. Subsequently, the bacterial cells were eliminated by centrifugation and subsequent filtering through pores with a size of 0.2 microns. The medium is filtered through Amicon 100-, 10- and 3-kDa Ultra membranes (Millipore). The fraction smaller than 3 kDa is concentrated to half of its volume in a rotavapor and mixed at 50% with the saliva sample; subsequently, as in the case of the probiotics, the biofilm is formed for 48 hours and incubated for 3 hours in a Buffered Peptone Water culture medium (38) containing 0.2% glucose, so as to be able to measure the production of acid.

Each treatment is repeated in quadruplicate under aerobiosis and anaerobiosis conditions. The experimental groups analysed were:

1. Biofilms formed with saliva inoculum.
2. Biofilms formed with saliva inoculum + CECT 7746.
3. Biofilms formed with strain CECT 7746.
4. Biofilms formed with saliva inoculum + CECT 7747.
5. Biofilms formed with strain CECT 7747.
6. Biofilms formed with saliva inoculum + non-inhibitory *Streptococcus* strain (strain C7.1).
7. Biofilms formed with saliva inoculum + supernatant of strain CECT 7746, which contains the active inhibitory substance.
8. Biofilms formed with saliva inoculum + supernatant of strain CECT 7747, which contains the active inhibitory substance.
9. Biofilms formed with saliva inoculum + supernatant of the non-inhibitory strain (strain C7.1).
10. Biofilms formed with the non-inhibitory *Streptococcus* strain (strain C7.1).

The results are shown in Figure 18, and indicate that the monospecific biofilm formed solely by strains CECT 7746 (experimental group 3) or CECT 7747 (experimental group 5) produce a quantity of acid that is significantly lower than that of saliva (experimental group 1). Taking human saliva as the reference value (experimental group 1), the supernatants of strain CECT 7747 (experimental group 8) significantly reduced the production of acid, under both aerobiosis and

anaerobiosis, whereas the supernatant of strain CECT 7746 (experimental group 7) reduced the quantity of acid produced by the biofilm only under anaerobiosis conditions. The addition of strain CECT 7747 to the biofilm reduced the production of acid under both aerobiosis and anaerobiosis, whereas the addition of strain CECT 7746 to the biofilm caused a reduction only under aerobiosis.

The reduction of acid, particularly in the case of strain CECT 7747 and the supernatants thereof, is very relevant for the treatment and prevention of dental caries, since the latter is formed due to the production of acid by microorganisms when these ferment the sugars ingested in the diet. Acid pH is precisely what de-mineralises the enamel and produces caries, and, therefore, any acidogenic species, and not only *Streptococci* from the *mutans* group, could be potentially cariogenic (2). Therefore, the reduction in the production of acid is an indicator that the overall effect of treatment with the probiotic strain or the supernatant thereof is the reduction of acid and, consequently, a lower probability of developing caries.

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CLAIMS

1. Culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775.

2. Culturable anti-bacterial strain according to claim 1, which presents inhibitory activity against growth of bacteria of the buccal cavity that produce an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

3. Culturable anti-bacterial strain according to claim 2, wherein the infectious disease of the buccal cavity is caries.

4. Culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for use as a medicament for treatment or for prevention of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

5. Use of at least one culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, in manufacturing of a medicament for treatment or for prevention of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis, wherein said strain is a bacterial strain.

6. Culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for use as an anti-bacterial agent.

7. Use of at least one of culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, in manufacturing of an anti-bacterial composition.

8. Use of at least one of culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, as an anti-bacterial agent.

9. Use of at least one of a culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, in the preparation of a composition for treatment of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

10. The use according to claim 9, wherein the infectious disease of the buccal cavity is caries.

11. Use of at least one of a culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for treatment of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

12. The use according to claim 11, wherein the infectious disease of the buccal cavity is caries.

13. Culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for use as a probiotic or functional food for prevention of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

14. The culturable anti-bacterial strain according to claim 13, wherein the infectious disease of the buccal cavity is caries.

15. Use of at least one of a culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for preparation of a probiotic, or a functional food, for prevention of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis, wherein said strain is a bacterial strain.

16. The use according to claim 15, wherein the infectious disease of the buccal cavity is caries.

17. Use of at least one of a culturable anti-bacterial strain selected from any one of the following bacterial strains: CECT 7746, CECT 7747, CECT 7773 and CECT 7775, or a combination thereof, for prevention of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

18. The use according to claim 17, wherein the infectious disease of the buccal cavity is caries.

19. Probiotic, or prebiotic composition, or functional food, that comprises at least one anti-bacterial strain according to any one of claims 1 to 3 and a suitable carrier.

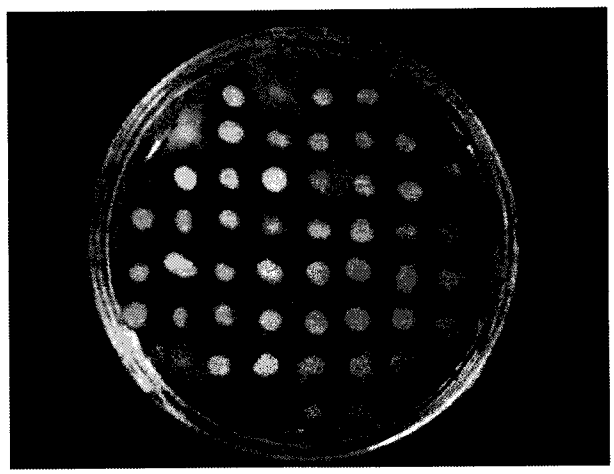
20. Pharmaceutical composition, or composition for buccal health, that comprises at least one culturable anti-bacterial strain according to any one of claims 1 to 3 and a suitable pharmaceutical carrier.

21. Use of at least one of the culturable anti-bacterial strain of claims 1 to 3; or the probiotic, or the prebiotic composition, or the functional food of claim 19; or the pharmaceutical composition, or the composition for buccal health, of claim 20; for prevention and/or treatment of an infectious disease of the buccal cavity selected from the group consisting of caries, periodontitis, gingivitis and halitosis.

22. The use according to claim 21, wherein the infectious disease of the buccal cavity is caries.

FIGURE 1

A



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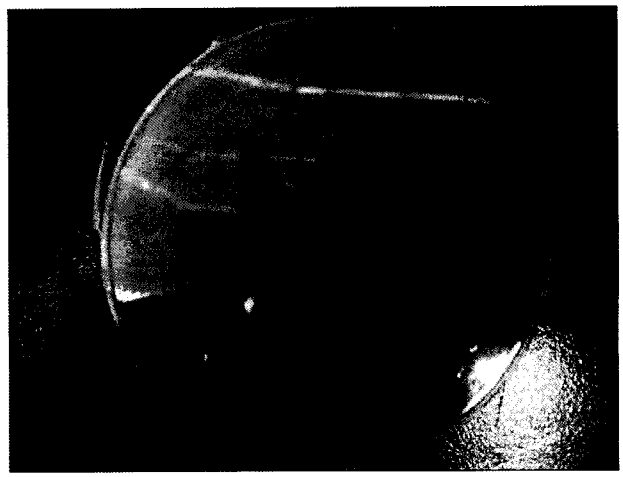

FIGURE 2

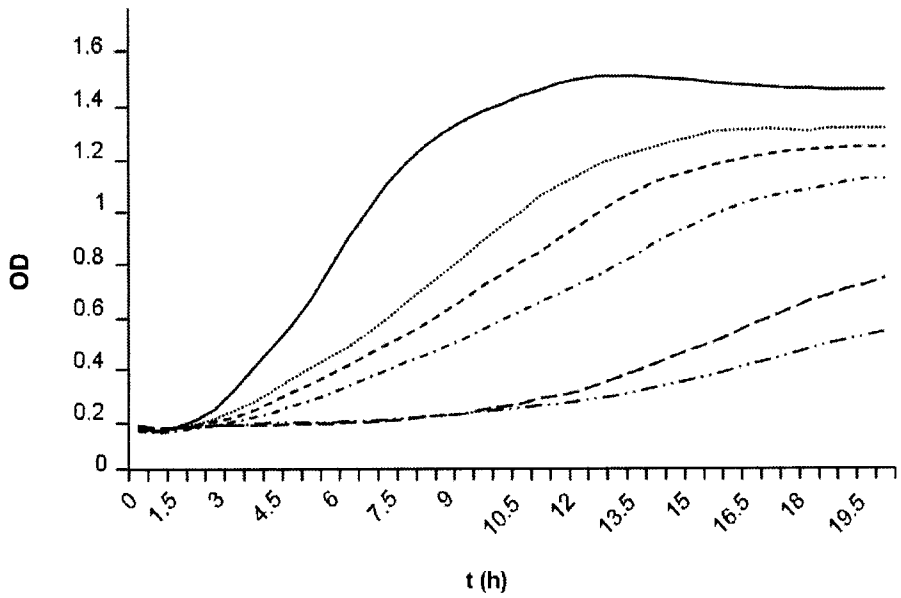

FIGURE 3

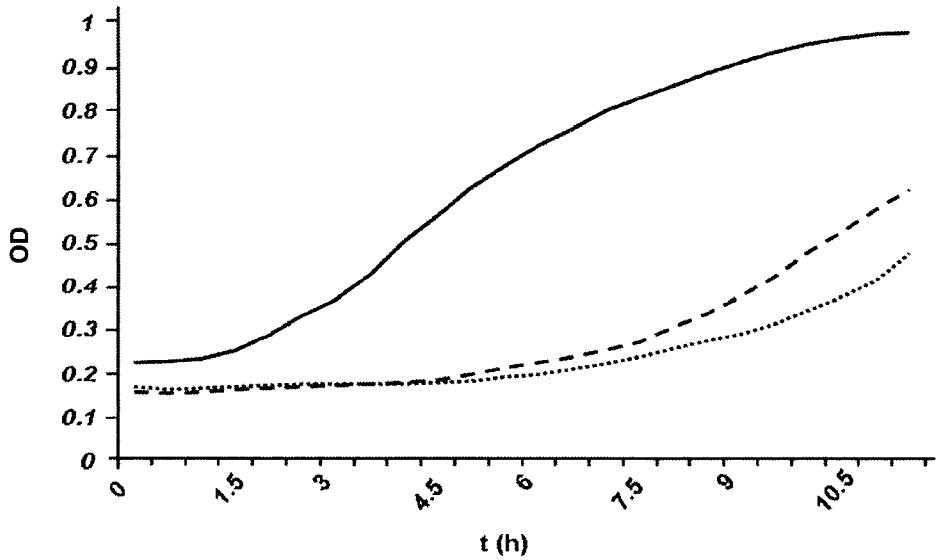

FIGURE 4

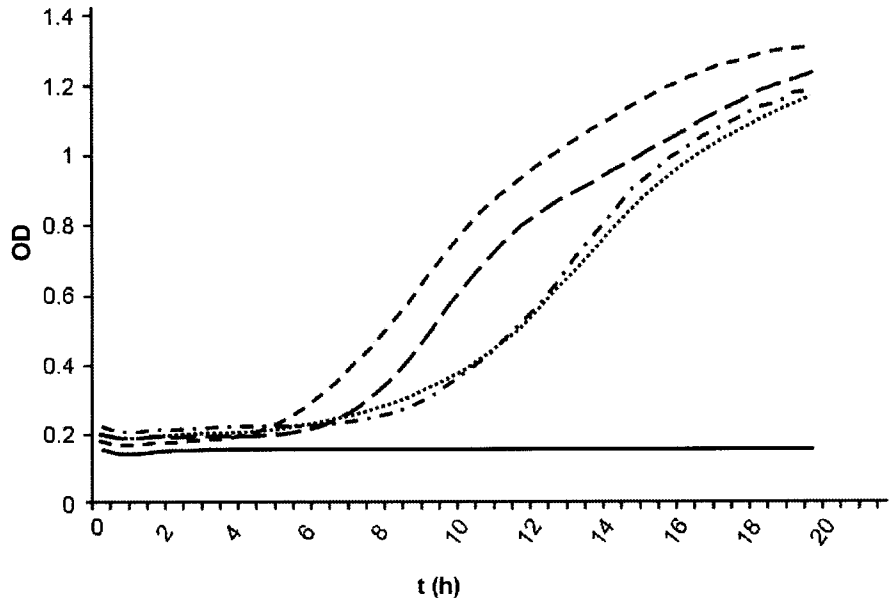

FIGURE 5

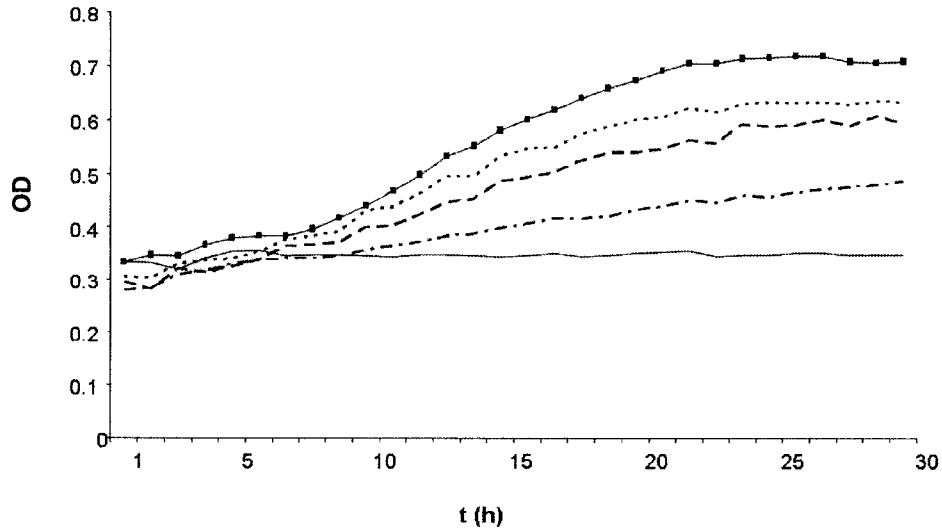

FIGURE 6

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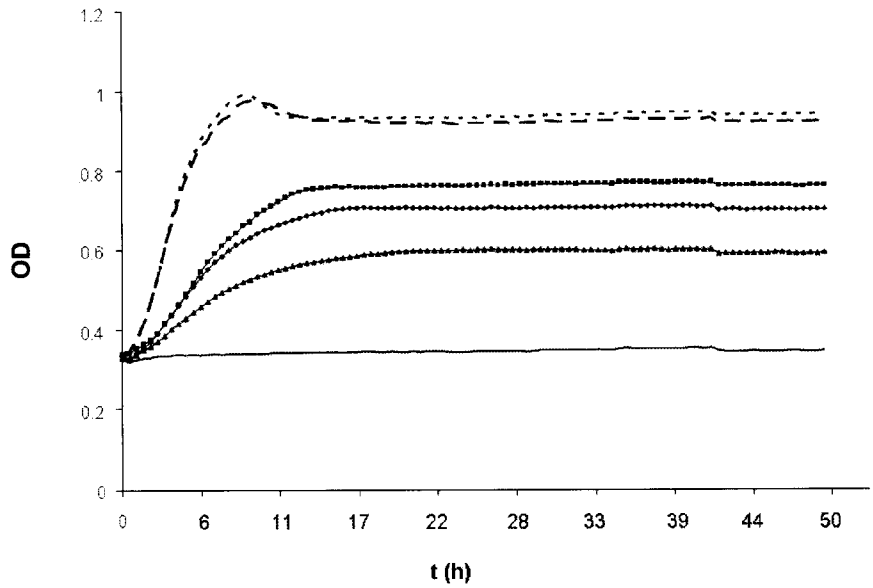
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0.6
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0.2
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OD
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6
11
17
22
28
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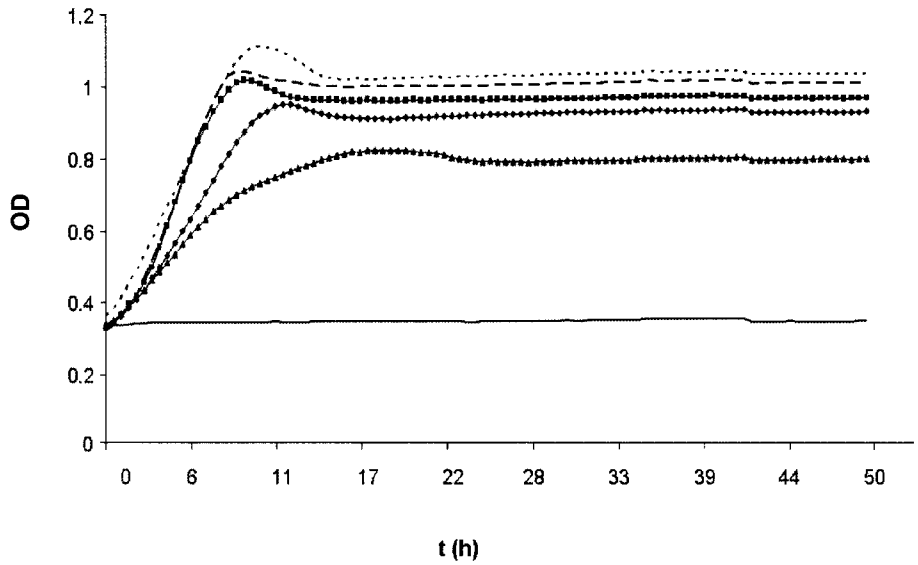
44
50
t (h)

B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50
t (h)

FIGURE 7

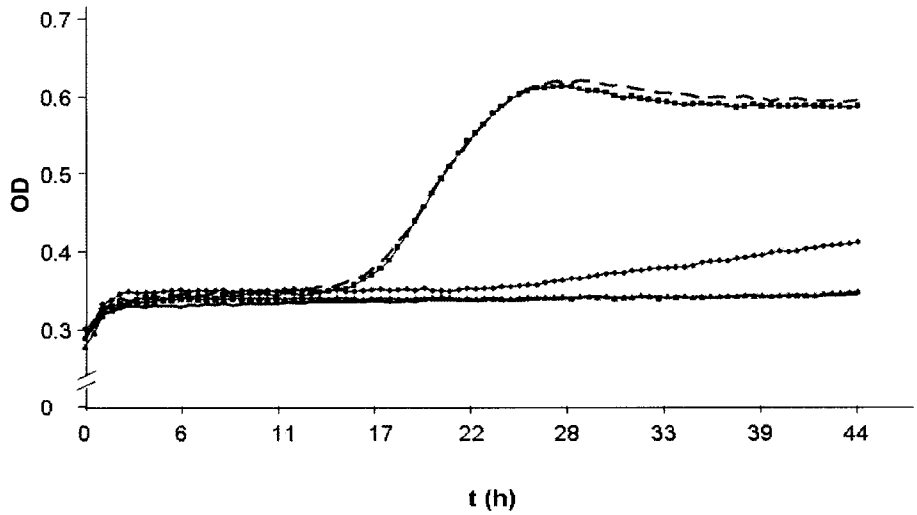


FIGURE 8

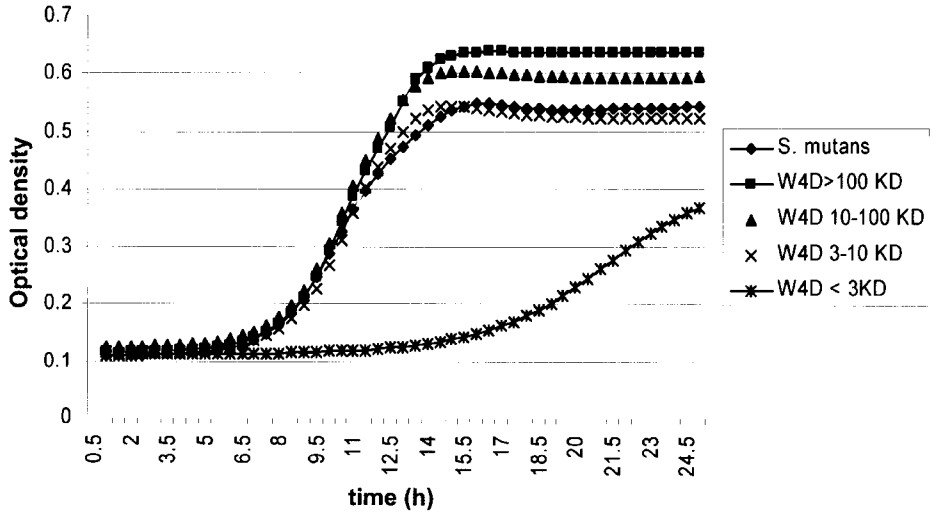


FIGURE 9

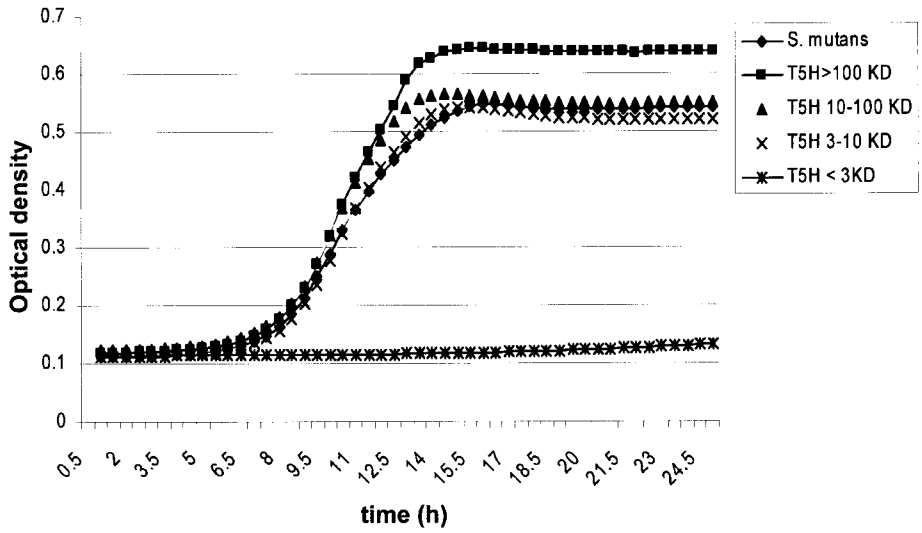


FIGURE 10

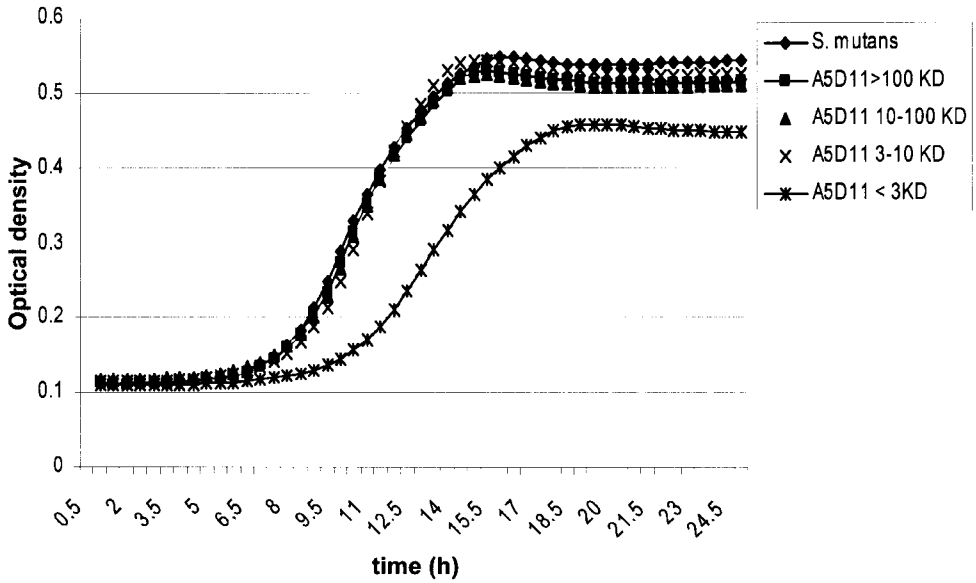
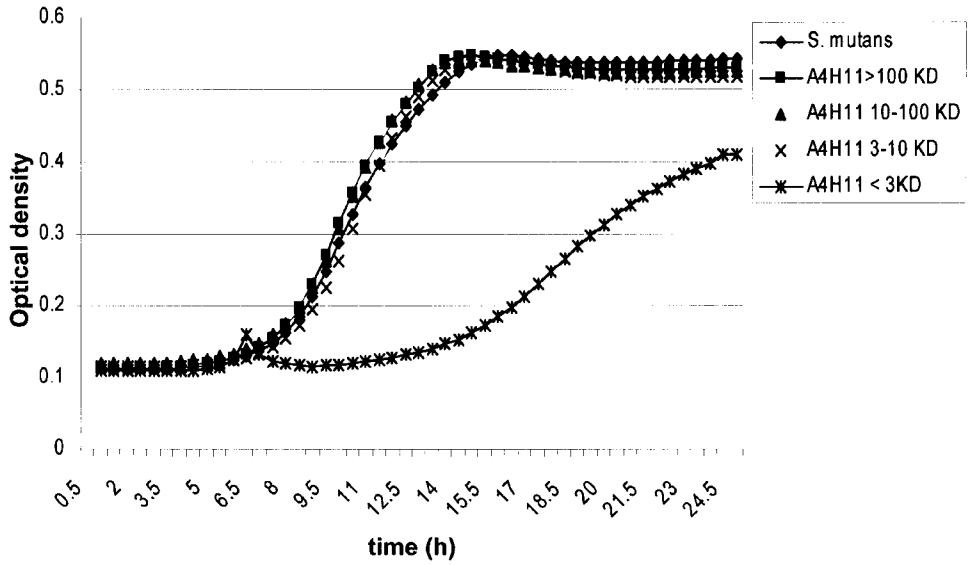


FIGURE 11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0.4
0.3
0.2
0.1
0
Optical density
0.5
2
3.5
5
6.5
8
9.5
11
12.5
14
15.5
17
18.5
20
21.5
23
24.5
time (h)
S. mutans
A4H11>100 KD
A4H11 10-100 KD
A4H11 3-10 KD
A4H11 < 3KD

FIGURE 12

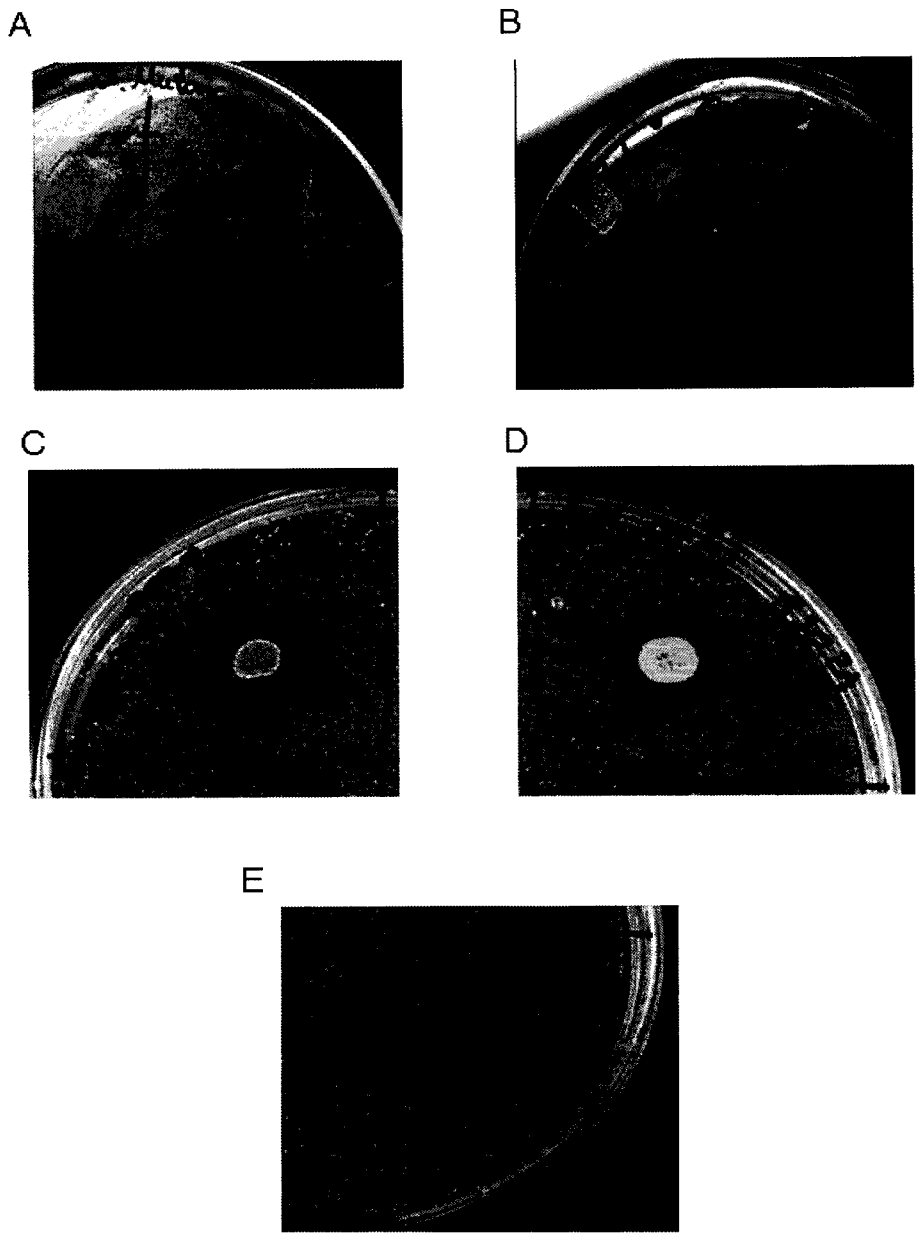
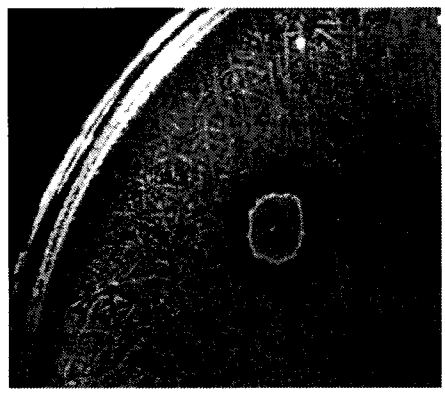


FIGURE 13

A



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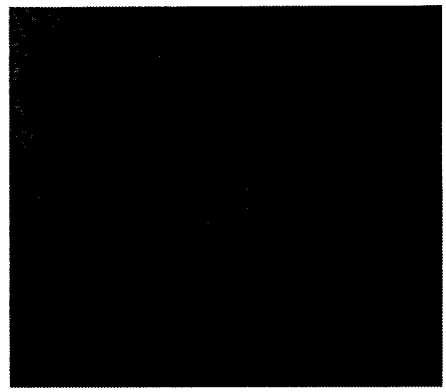

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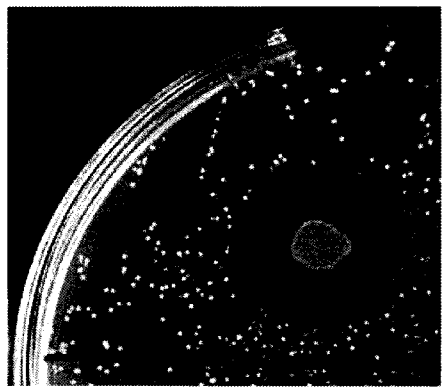


FIGURE 14

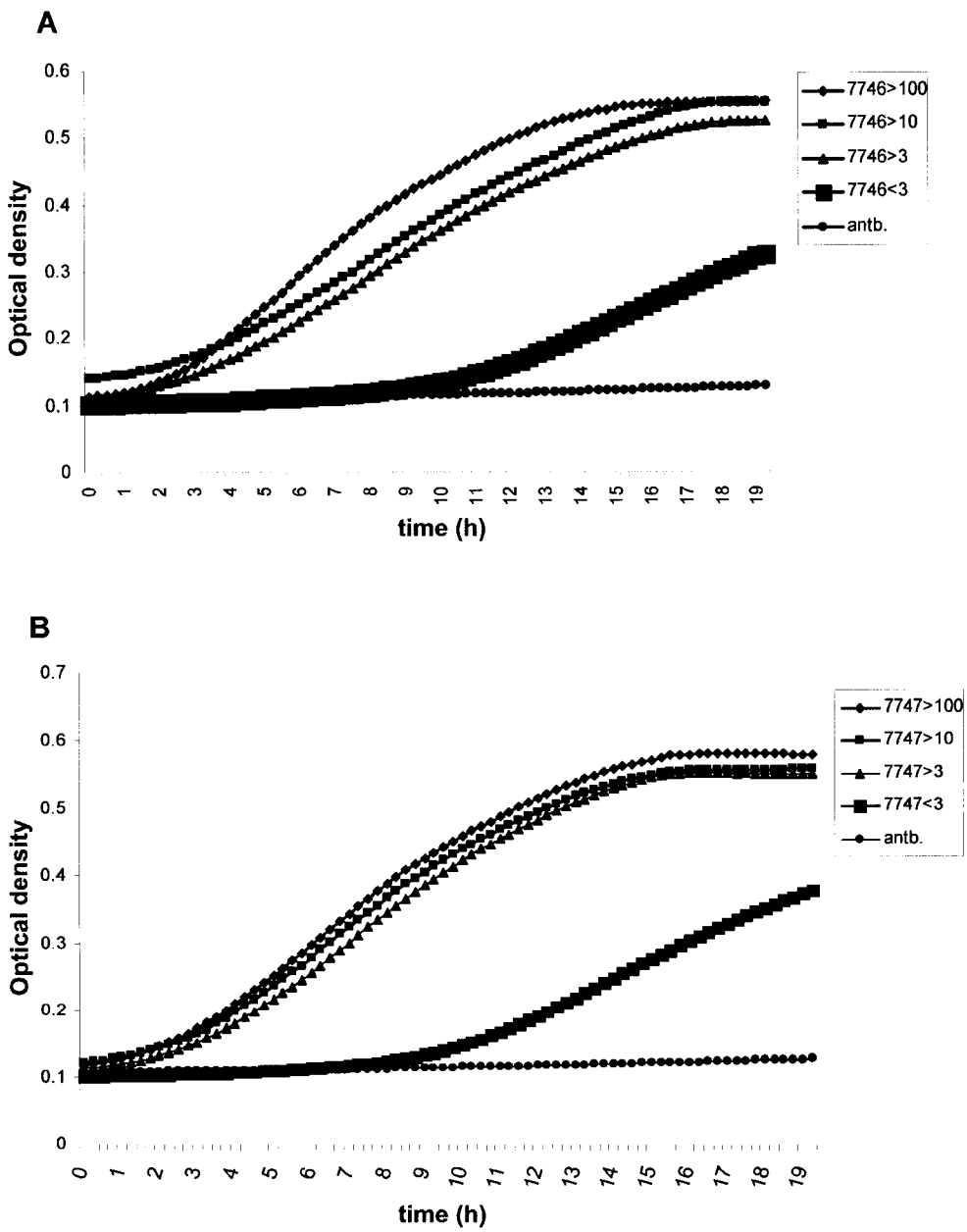
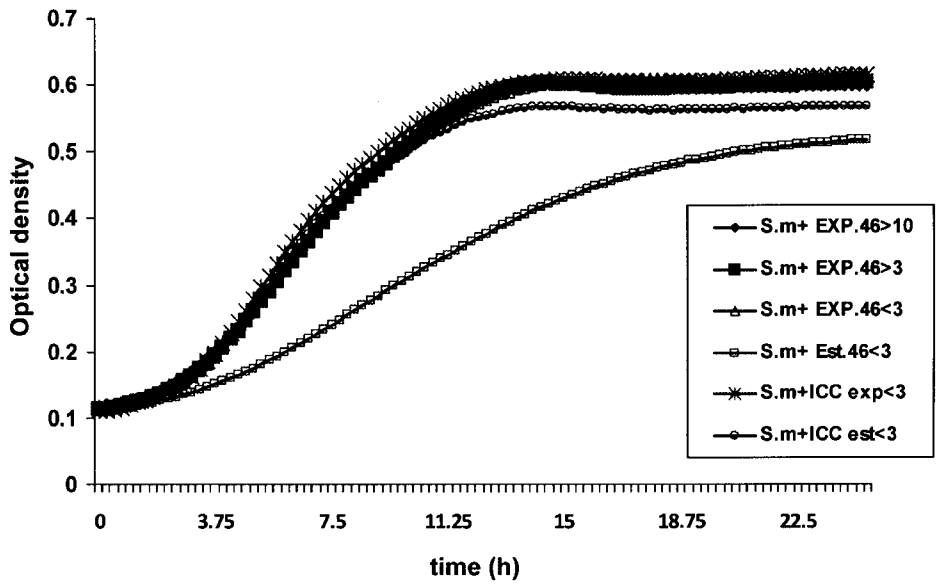

A
Optical density
time (h)
7746>100
7746>10
7746>3
7746<3
antb.
B
Optical density
time (h)
7747>100
7747>10
7747>3
7747<3
antb.

FIGURE 15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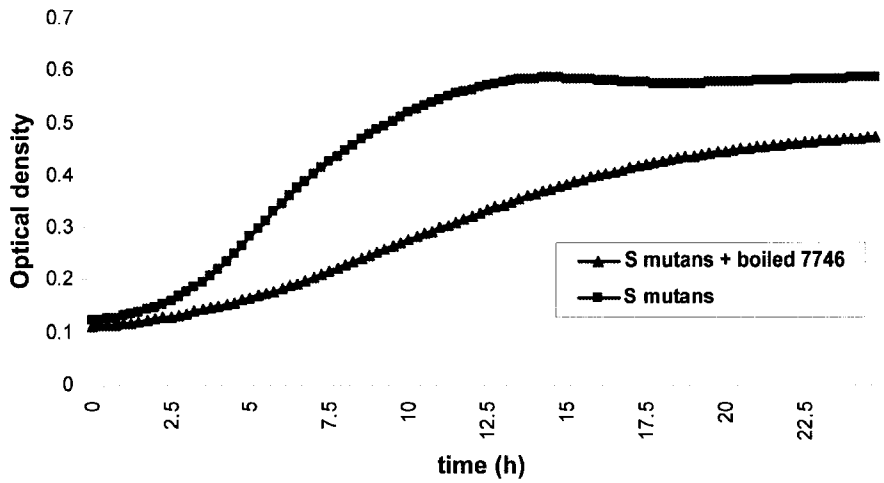
0.3
0.2
0.1
0
Optical density
0
3.75
7.5
11.25
15
18.75
22.5
time (h)
S.m+ EXP.46>10
S.m+ EXP.46>3
S.m+ EXP.46<3
S.m+ Est.46<3
S.m+ICC exp<3
S.m+ICC est<3

FIGURE 16

A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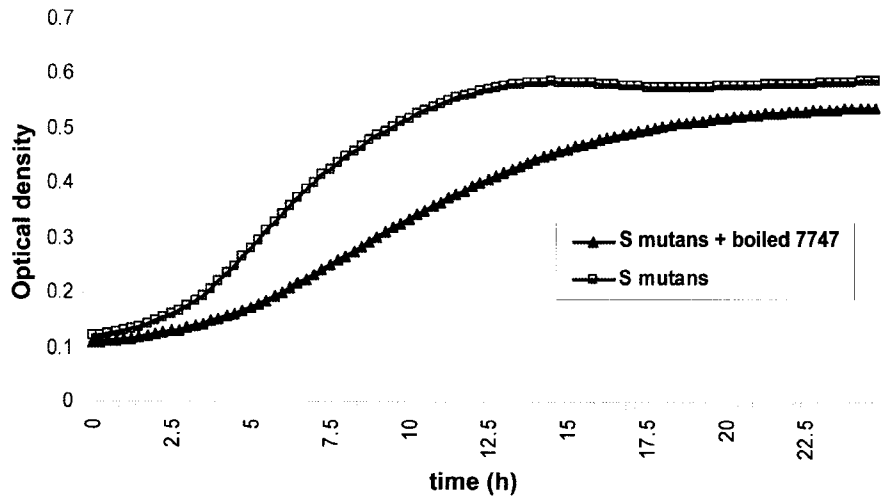
0.6
0.5
0.4
0.3
0.2
0.1
0
Optical density
0
2.5
5
7.5
10
12.5
15
17.5
20
22.5
time (h)
S mutans + boiled 7746
S mutans

B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0.6
0.5
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0.3
0.2
0.1
0
Optical density
0
2.5
5
7.5
10
12.5
15
17.5
20
22.5
time (h)
S mutans + boiled 7747
S mutans

FIGURE 17

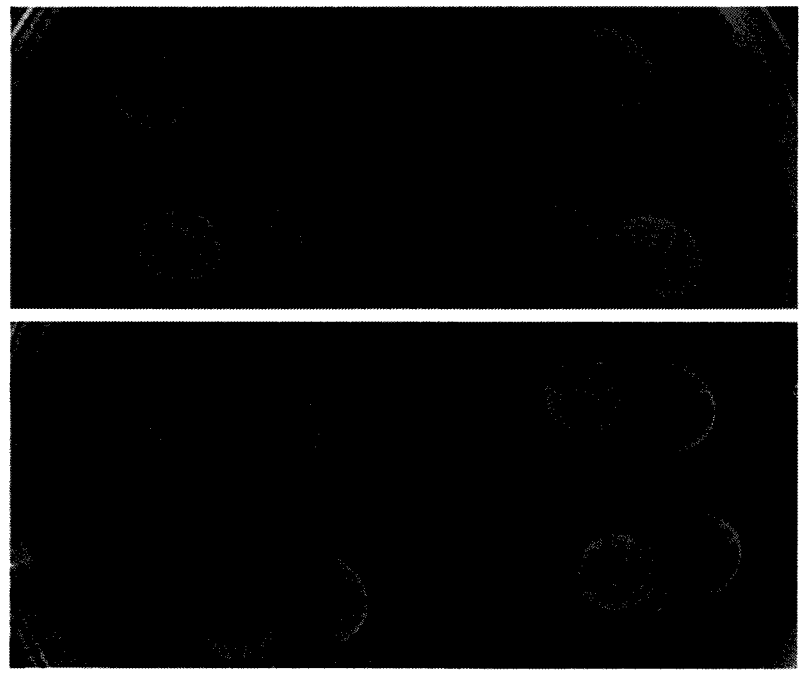
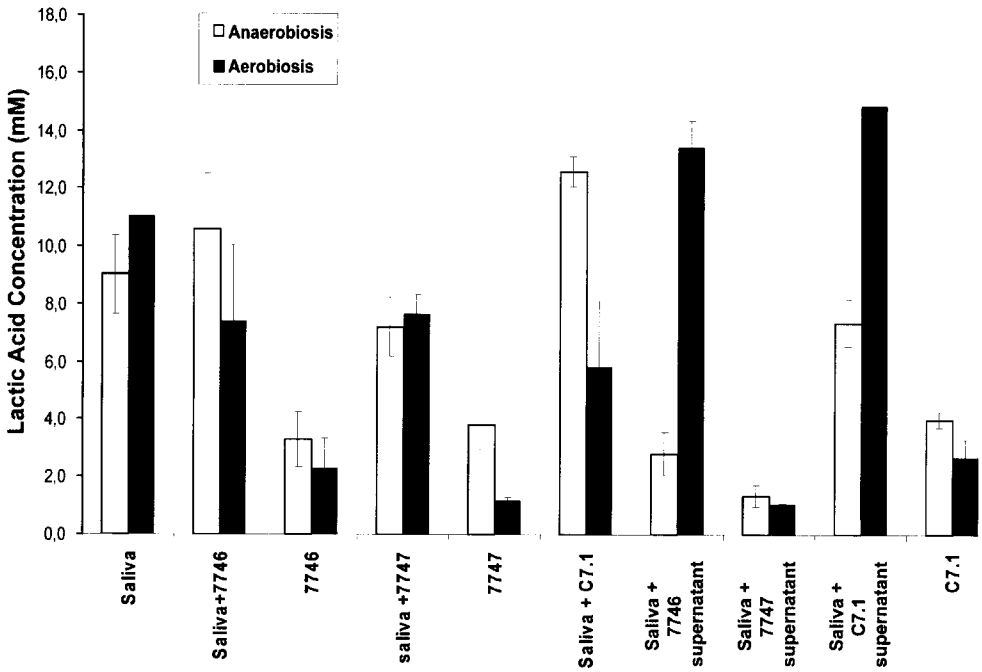


FIGURE 18


Anaerobiosis
Aerobiosis
Lactic Acid Concentration (mM)
18,0
16,0
14,0
12,0
10,0
8,0
6,0
4,0
2,0
0,0
Saliva
Saliva+7746
7746
saliva +7747
7747
Saliva + C7.1
Saliva + 7746 supernatant
Saliva + 7747 supernatant
Saliva + C7.1 supernatant
C7.1