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(54) **COMPOSITION FOR INDUCING PROLIFERATION OR ACCUMULATION OF REGULATORY T CELLS**

ZUSAMMENSETZUNG ZUR INDUZIERUNG DER PROLIFERATION ODER AKKUMULATION VON
REGULATORISCHEN T-ZELLEN

COMPOSITION POUR INDUIRE LA PROLIFÉRATION OU L'ACCUMULATION DE LYMPHOCYTES
T RÉGULATEURS

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Description

[Technical Field]

[0001] Described herein is a composition which has an effect of inducing proliferation or accumulation of regulatory T cells, and which comprises, as an active ingredient, bacteria belonging to the genus *Clostridium*, a physiologically active substance derived from the bacteria, bacterial spores, or the like.

[0002] Also described is a method for inducing proliferation or accumulation of regulatory T cells, as well as a method for inhibiting such proliferation or accumulation. Also described is

a vaccine composition containing at least one strain of bacteria belonging to the genus *Clostridium* or a spore of bacteria, as well as a method for treating or preventing at least one disease or condition selected from infectious diseases and autoimmune diseases by administering the vaccine composition to an individual in need thereof.

[0003] Also described is a method for screening for a compound that promotes proliferation or accumulation of regulatory T cells, as well as a non-human mammal which is used in this method, and in which a reporter gene is expressed under control of IL-10 gene expression.

[Background Art]

Hundreds of species of commensal microorganisms are harbored in gastrointestinal tracts of mammals, and intimately interact with the host immune systems. Results of researches using germ-free (GF) animals have shown that the commensal microorganisms exert great influences on the development of mucosal immune systems such as histogenesis of Peyer's patches (PPs) and isolated lymphoid follicles (ILFs), secretion of antimicrobial peptides from epithelium, and accumulation of unique lymphocytes in mucosal tissues, the unique lymphocytes including immunoglobulin A-producing plasma cells, intraepithelial lymphocytes, IL-17-producing CD4-positive T cells (Th 17), and IL-22-producing NK-like cells (Non-Patent Documents 1 to 7). Consequently, the presence of intestinal bacteria enhances protective functions of the mucous membranes, providing the hosts with robust immune responses against pathogenic microbes invading the bodies. On the other hand, the mucosal immune systems maintain unresponsiveness to dietary antigens and harmless microbes (Non-Patent Document 3). For this reason, abnormality in the regulation of cross-talk between commensal bacteria and an immune system (intestinal dysbiosis) may lead to overly robust immune response to environmental antigens, so that inflammatory bowel disease (IBD) is caused (Non-Patent Documents 8 to 10).

Results of Recent studies have shown that individual commensal bacteria control differentiation of their specific immune cells in the mucosal immune system. For example, *Bacteroides fragilis*, which is a commensal bacterium in humans, specifically induces a systemic Th1 cell response and a mucosal IL-10-producing T cell response in mice, and plays a role in protecting the host from colitis, which would otherwise be caused by a pathogen (Non-Patent Document 3). Segmented filamentous bacteria, which are intestinal commensal bacteria in mice, are shown to induce mucosal Th17 cell response and thereby to enhance resistance against infection of gastrointestinal tracts of the host with a pathogen (Non-Patent Documents 11 to 13). In addition, short-chain fatty acids derived from several commensal bacteria are known to suppress intestinal inflammation (Non-Patent Document 14). Moreover, it is presumed that the presence of some species of intestinal microbiota exerts a great influence on the differentiation of regulatory T cells (hereafter referred to as "Treg cells") which maintain homeostasis of the immune system.

Meanwhile, regulatory T cells which have been identified as a subset suppressing immunity are CD4⁺ T cells in which a transcription factor Foxp3 is expressed, and are known to play an important role in maintaining immunological homeostasis (Non-Patent Documents 8, 9, 15, and 16). Moreover, it has been known that the Foxp3-expressing cells are present in a large number especially in the colon, and only Treg cells present locally in the colon constantly express IL-10, which is an immunosuppressive cytokine, at a high level (Non-Patent Document 17). It is also known that animals having CD4⁺ Foxp3⁺ cells from which IL-10 is specifically removed develop inflammatory bowel disease (Non-Patent Document 18).

Accordingly, if the mechanism of the induction of Treg cells which produce IL-10 in the colon at a high level is elucidated, immunosuppression can be enhanced, which in turn can be applied to treatment of autoimmune diseases such as inflammatory bowel disease, as well as to organ transplantation.

However, mechanisms of how a large number of Treg cells come to be present in the colon and how the Treg cells produce IL-10 in the colon at a high level are still unclear. Moreover, it is also still unclear what species of bacteria constituting the intestinal commensal bacterial flora exerts the influence on the induction of regulatory T cells.

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[0010] GABORIAU-ROUTHIAU et al. (2009), Immunity 31:677 describes Segmented-Filamentous Bacteria (SFBs) which do not belong to the genus Clostridium, and indeed are phylogenetically remote therefrom.

[0011] SOKOL et al. (2008-10-28) "Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients", Proc Natl Acad Sci USA 105 (43): 16731-16736, proposes Faecalibacterium prausnitzii (belonging to Clostridium cluster IV) as candidate probiotic agent in the treatment of Crohn's disease (CD).

[0012] KARIMI et al. (2009), "Lactobacillus reuteri-induced regulatory T cells protect against and allergic airway response in mice" American Journal of Respiratory and Critical Care Medicine 17(3):186-193, describes that *Lactobacillus reuteri* induces Foxp3+ regulatory T cells that have a potential to protect against and allergic airway response in mice.

[0013] EP 1 955 706 A1 relates to a composition containing interferon alpha and natural bile pigment C-Phycocyanin, for treating autoimmune diseases, allergy and cancer, by inducing regulatory T cells.

[0014] ITOH K et al. "Characterization of clostridia isolated from faeces of limited flora mice and their effect on caecal size when associated with germ-free mice." LABORATORY ANIMALS APR 1985 vol. 19, no. 2, April 1985 (1985-04), pages 111-118, discloses the characterization of 115 strains of clostridia accumulated from 3 separate isolations from the faeces of 1 limited flora (LF) mouse produced by inoculation of germ-free mice with chloroform-treated faeces of conventional mice, and the effect on caecal size when associated with germ-free mice was studied.

[0015] BAKKEN (2009) Anaerobe 15:285-289 relates to Faecal bacteriotherapy as a treatment for recurrent *Clostridium difficile* infection.

[Summary of Invention]

[0016] The invention is defined in the claims, and provides a composition for use in a method of treating or preventing an allergic disease by inducing proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells, the composition comprising, as an active ingredient, bacteria belonging to the genus Clostridium of clusters XIVa and/or IV, wherein the bacteria induce said proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells. Other aspects of the invention are also defined in the claims.

[0017] The present inventors have found that a chloroform-treated fraction and a spore-forming fraction of a fecal sample obtained from a mammal induces accumulation of regulatory T cells (Treg cells) in the colon. Moreover, the present inventors have found that bacteria belonging to the genus Clostridium induce proliferation or accumulation of regulatory T cells in the colon. The present inventors have also found that the regulatory T cells induced by these bacteria suppress proliferation of effector T cells. Furthermore, the present inventors have also found that colonization of bacteria belonging to the genus Clostridium and resultant proliferation or accumulation of Treg cells regulate local and systemic immune responses.

[0018] From these findings, the present inventors have found that the use of bacteria belonging to the genus *Clostridium*, spores thereof, or a physiologically active substance derived therefrom makes it possible to induce the proliferation or accumulation of regulatory T cells (Treg cells), and further to suppress immune functions.

5 [Advantageous Effects]

[0019] The compositions described herein containing as an active ingredient bacteria belonging to the genus *Clostridium* or a physiologically active substance derived from the bacteria serves as an excellent composition for inducing the proliferation or accumulation of regulatory T cells (Treg cells). Immunity in a living organism can be suppressed in accordance with the claims through administration of the composition of the present invention as defined in the claims as a pharmaceutical product or ingestion of the composition as a food or beverage. Accordingly, the composition of the present invention can be used, for example, to prevent or treat allergic diseases

[0020] In addition, if a food or beverage such as a health food comprises the composition of the present invention, healthy individuals can ingest the composition easily and routinely. As a result, it is possible to induce the proliferation or accumulation of regulatory T cells and thereby to improve immune functions, as defined in the claims.

[Brief Description of Drawings]

[0021]

[Fig. 1] Fig. 1 is a schematic diagram showing a method of producing *Il10^{venus}* mouse.

[Fig. 2] Fig. 2 is a diagram showing results of Southern blotting performed for analysis as to whether or not the *Il10^{venus}* mice have an *Il10^{venus}* allele.

[Fig. 3] Fig. 3 is a FACS dot-plot diagram showing results obtained when Venus-positive cells and Venus-negative cells from the *Il10^{venus}* mice were sorted.

[Fig. 4] Fig. 4 is a graph showing the results obtained when the amounts of IL-10 mRNA expressed in Venus positive-cells and Venus-negative cells of the *Il10^{venus}* mice were analyzed by real-time RT-PCR.

[Fig. 5] Fig. 5 is a graph showing change in the ratio of Foxp3⁺ cells in CD4⁺ lymphocytes of SPF mice.

[Fig. 6] Fig. 6 shows FACS dot-plot diagrams showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the small intestine, the colon, and the peripheral lymph nodes of GF mice and SPF mice.

[Fig. 7] Fig. 7 is a graph showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the small intestine, the colon, and the peripheral lymph nodes of GF mice and SPF mice.

[Fig. 8] Fig. 8 shows graphs showing analysis results of the numbers of CD4⁺ Foxp3⁺ cells isolated from the small intestine, the colon, and the peripheral lymph nodes of GF mice and SPF mice.

[Fig. 9] Fig. 9 is a plot diagram showing analysis results of the ratios of Venus⁺ cells in CD4⁺ cells in various tissues of SPF mice treated with antibiotics.

[Fig. 10] Fig. 10 shows FACS dot-plot diagrams showing analysis results of the ratio of Foxp3⁺ cell in CD4⁺ lymphocytes isolated from the colonic lamina propria of GF mice to which a fecal suspension of SPF mice was administered.

[Fig. 11] Fig. 11 is a graph showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the lamina propria of the colon and the lamina propria of the small intestine of GF mice to which a fecal suspension of SPF mice was administered.

[Fig. 12] Fig. 12 is a graph showing analysis results of the ratio of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the lamina propria of mice deficient in ILFs, PPs, and colonic-patches.

[Fig. 13] Fig. 13 shows FACS dot-plot diagrams showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the colonic lamina propria of GF mice to which specific commensal bacteria were administered.

[Fig. 14] Fig. 14 shows graphs showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the colonic lamina propria of GF mice to which specific commensal bacteria were administered.

[Fig. 15] Fig. 15 is a graph showing analysis results of the ratios of IFN- γ ⁺ cells in CD4⁺ lymphocytes isolated from the colonic lamina propria of mice in which specific commensal bacteria were colonized.

[Fig. 16] Fig. 16 is a graph showing analysis results of the ratios of IL-17⁺ cells in CD4⁺ lymphocytes isolated from the colonic lamina propria of mice in which specific commensal bacteria were colonized.

[Fig. 17] Fig. 17 is a graph showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the colon of kinds of SPF mice each being deficient in a pathogen-associated molecular pattern recognition receptor-associated factor.

[Fig. 18] Fig. 18 is a graph showing analysis results of the ratios of Foxp3⁺ cells in CD4⁺ lymphocytes isolated from the colonic lamina propria of Myd88^{-/-} mice in which the *Clostridium* was colonized.

[Fig. 19] Fig. 19 shows FACS dot-plot diagrams showing analysis results of the ratios of Venus⁺ cells in lymphocytes isolated from various tissues of *Il10^{venus}* mice.

[Fig. 20] Fig. 20 is a FACS dot-plot diagram showing analysis results of the expression of a T cell receptor β chain on cell surfaces of lymphocytes isolated from the colonic lamina propria of *Il10^{venus}* mice.

[Fig. 21] Fig. 21 shows FACS dot-plot diagrams showing analysis results of the expression of IL-17, IL-4, and IFN- γ in lymphocytes isolated from the colonic lamina propria of *Il10^{venus}* mice.

[Fig. 22] Fig. 22 shows graphs showing analysis results of the amounts of mRNAs of IL-10, CTLA4, Foxp3, and GITR expressed in spleen Foxp3⁺CD4⁺ cells, spleen Foxp3⁺ CD4⁺ cells, colonic lamina propria Venus⁺ cells, and small intestinal lamina propria Venus⁺ cells.

[Fig. 23] Fig. 23 shows FACS dot-plot diagrams showing analysis results of the expression of CD4, Foxp3, and Venus in the lamina propria of the small intestine and the lamina propria of the colon of GF *Il10^{venus}* mice and SPF *Il10^{venus}* mice.

[Fig. 24] Fig. 24 shows FACS dot-plot diagrams showing analysis results of the expression of Venus and Foxp3 of CD4 cells in various tissues of SPF *Il10^{venus}* mice.

[Fig. 25] Fig. 25 shows FACS dot-plot diagrams showing analysis results of the expression of Foxp3 and Venus in *Il10^{venus}* mice in which specific commensal bacteria were colonized.

[Fig. 26] Fig. 26 is a graph showing analysis results of the expression of Foxp3 and/or Venus of CD4⁺ cells in the small intestine of *Il10^{venus}* mice in which specific commensal bacteria were colonized.

[Fig. 27] Fig. 27 is a graph showing analysis results of the expression of Foxp3 and/or Venus of CD4⁺ cells in the colon of *Il10^{venus}* mice in which specific commensal bacteria were colonized.

[Fig. 28] Fig. 28 is a plot diagram showing analysis results of the ratios of Venus⁺ cells in CD4⁺ cells isolated from various tissues of *Il10^{venus}* mice treated with antibiotics.

[Fig. 29] Fig. 29 is a graph showing analysis results of immunoregulatory functions of CD4⁺ Venus⁺ cells from the colonic lamina propria of GF *Il10^{venus}* mice in which the genus *Clostridium* was colonized, CD4⁺ Venus⁺ cells from the colonic lamina propria of SPF *Il10^{venus}* mice, and CD4⁺ GFP⁺ cells from the spleen of Foxp3^{eGFP} reporter mice.

[Fig. 30] Fig. 30 is a graph showing the results obtained when SPF B6 mice were treated with polymyxin B or vancomycin for 4 weeks, and then analyzed for the ratio of Foxp3⁺ cells in the CD4⁺ cell group.

[Fig. 31] Fig. 31 is a graph showing the results obtained when SPF mice-derived chloroform-treated feces were orally administered to GF mice, and then the ratio of Foxp3⁺ cells in the CD4⁺ cell group was analyzed.

[Fig. 32] Fig. 32 is a graph showing the general results of flow cytometry analysis on Helios expression in LP lymphocytes in the thymuses or the colons of SPF mice, GF mice, *Lactobacillus*-colonized mice, or *Clostridium*-colonized mice.

[Fig. 33] Fig. 33 shows plot diagrams showing representative results of flow cytometry analysis on CD4 expression, Foxp3 expression, and Helios expression in the LP lymphocytes in the thymuses or the colons of the SPF mice, the GF mice, the *Lactobacillus*-colonized mice, or the *Clostridium*-colonized mice.

[Fig. 34] Fig. 34 is a graph showing the results obtained when the whole colons derived from GF mice, *Lactobacillus*-colonized mice, or *Clostridium*-colonized mice were cultured, and the culture supernatants thereof were analyzed for the TGF- β 1 concentration by ELISA.

[Fig. 35] Fig. 35 is a graph showing the results obtained when intestinal epithelial cells (IECs) derived from GF mice or *Clostridium*-colonized mice were cultured, and the culture supernatants thereof were analyzed for the TGF- β 1 concentration by ELISA.

[Fig. 36] Fig. 36 is a graph showing the results obtained when splenic CD4⁺ T cells were cultured together with an anti-CD3 antibody and with a culture supernatant of IECs isolated from GF mice or mice colonized with 46 bacterial strains of the genus *Clostridium* (Clost.) in the presence or absence of an anti-TGF- β antibody, and the T cells were collected on day 5 of the culture and analyzed for Foxp3 expression by real-time RT-PCR.

[Fig. 37] Fig. 37 is a graph showing the results obtained when C57BL/6 GF mice were orally inoculated with 46 bacterial strains of the genus *Clostridium* (Clost.) or three bacterial strains of the genus *Lactobacillus* (Lacto.), and IECs were collected three weeks after the inoculation and analyzed for the relative mRNA expression level of the MMP2 gene by real-time RT-PCR.

[Fig. 38] Fig. 38 is a graph showing the results obtained when C57BL/6 GF mice were orally inoculated with 46 bacterial strains of the genus *Clostridium* (Clost.) or three bacterial strains of the genus *Lactobacillus* (Lacto.), and IECs were collected three weeks after the inoculation and analyzed for the relative mRNA expression level of the MMP9 gene by real-time RT-PCR.

[Fig. 39] Fig. 39 is a graph showing the results obtained when C57BL/6 GF mice were orally inoculated with 46 bacterial strains of the genus *Clostridium* (Clost.) or three bacterial strains of the genus *Lactobacillus* (Lacto.), and IECs were collected three weeks after the inoculation and analyzed for the relative mRNA expression level of the MMP13 gene by real-time RT-PCR.

[Fig. 40] Fig. 40 is a graph showing the results obtained when C57BL/6 GF mice were orally inoculated with 46

bacterial strains of the genus *Clostridium* (Clost.) or three bacterial strains of the genus *Lactobacillus* (Lacto.), and IECs were collected three weeks after the inoculation and analyzed for the relative mRNA expression level of the IDO gene by real-time RT-PCR.

[Fig. 41] Fig. 41 is a graph showing the results obtained when control mice (SPF) and *Clostridium*-administered mice (SPF+Clost.) were treated with 2% DSS, observed and measured for the body weight loss, the hardness of stool, and bleeding for six days, and then evaluated numerically.

[Fig. 42] Fig. 42 is a photograph showing the state of the colons collected on day 6 after the control mice (SPF) and the *Clostridium*-administered mice (SPF+Clost.) were treated with 2% DSS.

[Fig. 43] Fig. 43 shows photomicrographs showing the results obtained when the control mice (SPF) and the *Clostridium*-administered mice (SPF+Clost.) were treated with 2% DSS, and the colons thereof were collected on day 6 and analyzed histologically by HE staining.

[Fig. 44] Fig. 44 is a graph showing the results obtained when control mice (SPF) and *Clostridium*-administered mice (SPF+Clost.) were sensitized with oxazolone, and subsequently the inside of each rectum was treated with a 1% oxazolone/50% ethanol solution, and the body weight loss was measured.

[Fig. 45] Fig. 45 shows photomicrographs showing the results obtained when the control mice (SPF) and the *Clostridium*-administered mice (SPF+Clost.) were sensitized with oxazolone, and subsequently the inside of each rectum was treated with a 1% oxazolone/50% ethanol solution, and the colons obtained by the treatment were analyzed histologically by HE staining.

[Fig. 46] Fig. 46 is a graph showing the results obtained when control mice (SPF) and *Clostridium*-administered mice (SPF+Clost.) were immunized by administering alum-absorbed ovalbumin (OVA) twice at a 2-week interval, and the sera were collected therefrom and analyzed for the concentration of OVA-specific IgE in these sera by ELISA.

[Fig. 47] Fig. 47 is a graph showing the results obtained when the control mice (SPF) and the *Clostridium*-administered mice (SPF+Clost.) were immunized by administering the alum-absorbed OVA twice at a 2-week interval, and splenic cells were collected and analyzed for IL-4 production of these splenic cells by in-vitro OVA restimulation.

[Fig. 48] Fig. 48 is a graph showing the results obtained when the control mice (SPF) and the *Clostridium*-administered mice (SPF+Clost.) were immunized by administering the alum-absorbed OVA twice at a 2-week interval, and the splenic cells were collected and analyzed for IL-10 production of these splenic cells by the in-vitro OVA restimulation.

[Fig. 49] Fig. 49 is Phylogenetic tree constructed by the neighbor-joining method with the resulting sequences of the 41 strains of *Clostridium* and those of known bacteria obtained from Genbank database using Mega software.

[Fig. 50] Fig. 50 is histograms showing Foxp3 expression gated CD4 cells from GF mice (Germ-free mouse #1 and #2) or GF mice colonized with three strains of *Clostridium* belonging to cluster IV (3 strains of Clost. mouse #1 and #2).

[Fig. 51] Fig. 51 is histograms showing Foxp3 expression by CD4 positive lymphocytes from GF mice (GF) or GF mice gavaged with chloroform-treated human stool (GF+Chloro.) .

[Fig. 52] Fig. 52 is a graph showing Foxp3 expression by CD4 positive lymphocytes from GF mice (GF) or GF mice gavaged with chloroform-treated human stool (GF+Chloro.) .

[Fig. 53] Fig. 53 is a graph showing amounts of *Clostridium* and *Bacteroides* in feces of mice gavaged with chloroform-treated human stool

[Description]

<Composition Having Effect of Inducing Proliferation or Accumulation of Regulatory T cells>

[0022] Described herein is a composition that induces proliferation or accumulation of regulatory T cells, the composition comprising, as an active ingredient, at least one substance selected from the group consisting of the following (a) to (c):

- (a) bacteria belonging to the genus *Clostridium* or a physiologically active substance derived from the bacteria;
- (b) a spore-forming fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction; and
- (c) a chloroform-treated fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction.

[0023] Herein, "regulatory T cells" mean T cells which have a function of suppressing an abnormal or excessive immune response, and which play a role in immune tolerance. The regulatory T cells of the invention are transcription factor Foxp3-positive CD4-positive T cells. However, other regulatory T cells also include transcription factor Foxp3-negative regulatory T cells that are IL-10-producing CD4-positive T cells.

[0024] The meaning of the " induces proliferation or accumulation of regulatory T cells" in the present invention includes an effect of inducing the differentiation of immature T cells into regulatory T cells, which differentiation leads to the proliferation or the accumulation of regulatory T cells. In addition, the meaning of the " induces proliferation or accumulation of regulatory T cells" in the present invention includes in-vivo effects, in vitro effects, and ex vivo effects. Accordingly, all of the following effects are included: an effect of inducing in vivo proliferation or accumulation of regulatory T cells

through administration or ingestion of the bacteria belonging to the genus *Clostridium* or the physiologically active substance or the like derived from the bacteria; an effect of inducing proliferation or accumulation of cultured regulatory T cells by causing the bacteria belonging to the genus *Clostridium* or the physiologically active substance or the like derived from the bacteria to act on the cultured regulatory T cells; and an effect of inducing proliferation or accumulation of regulatory T cells which are collected from a living organism and which are intended to be subsequently introduced into a living organism, such as the organism from which they were obtained or another organism, by causing the bacteria belonging to the genus *Clostridium* or the physiologically active substance or the like derived from the bacteria to act on the regulatory T cells. The effect of inducing proliferation or accumulation of regulatory T cells can be evaluated, for example, as follows. Specifically, the bacteria belonging to the genus *Clostridium* or the physiologically active substance or the like derived from the bacteria is orally administered to an experimental animal such as a germ-free mouse, then CD4-positive cells in the colon are isolated, and the ratio of regulatory T cells contained in the CD4-positive cells is measured by flow cytometry (refer to Example 7).

[0025] The regulatory T cells of which proliferation or accumulation is induced by the composition of the present invention are transcription factor Foxp3-positive regulatory T cells.

[0026] The "bacteria belonging to the genus *Clostridium*," which are the active ingredient in the composition of the present invention, are defined in the claims, and have the effect of inducing proliferation or accumulation of regulatory T cells.

[0027] One strain of the bacteria alone can be used for the composition of the present invention, but two or more strains of the bacteria can be used together for the composition of the present invention. The use of multiple strains of bacteria belonging to the cluster XIVa or the cluster IV in combination can bring about an excellent effect on regulatory T cells. In addition to the bacteria belonging to these clusters, bacteria belonging to other clusters (for example, bacteria belonging to the cluster III) can also be used in combination. If more than one strain of bacteria is used (e.g., one or more strain belonging to cluster XIVa, one or more strain belonging to cluster IV, one or more strain belonging to a cluster other than cluster XIVa or cluster IV, such as one or more strain belonging to cluster III), the type and number of strains used can vary widely. The type and number to be used can be determined based on a variety of factors (e.g., the desired effect, such as induction or inhibition of proliferation or accumulation of regulatory T cells; the disease or condition to be treated, prevented or reduced in severity; the age or gender of the recipient) The strains can be present in a single composition, in which case they will be consumed or ingested together, or can be present in more than one composition (e.g., each can be in a separate composition), in which case they can be consumed individually or the compositions can be combined and the resulting combination (combined compositions) consumed or ingested. Any number or combination of strains that proves effective (e.g., any number from one to 200, such as 1 to 100, 1 to 50, 1 to 40, 1 to 30, 1 to 20, 1 to 10, 1 to 5 and any number therebetween) can be administered. In certain embodiments of the present invention, a combination of some or all of the 46 strains described in Document (Itoh, K., and Mitsuoka, T. Characterization of clostridia isolated from faeces of limited flora mice and their effect on caecal size when associated with germ-free mice. *Lab. Animals* 19: 111-118 (1985)) is used. For example, at least one, two or more, three, three or more, four, four or more, five, five or more, six, six or more or any other number of the 46 described strains, including 46 strains, can be used. They can be used in combination with one another and in combination with strains not described in the cited reference (e.g., in combination with one or more strains belonging to cluster III). Note that, the cluster of "bacteria belonging to the genus *Clostridium*" can be identified, for example, as follows. Specifically, the bacteria belonging to the genus *Clostridium* are classified by PCR using a primer set consisting of SEQ ID NOs 64 and 65 (for *Clostridium* spp. belonging to the cluster XIVa) or a primer set consisting of SEQ ID NOs 66 and 67 (for *Clostridium* spp. belonging to the cluster IV) (refer to Example 18). In addition, the bacteria belonging to the genus *Clostridium* are classified by sequencing of 16S rRNA gene amplified using a primer set consisting of SEQ ID NOs 19 and 20 (refer to Example 7).

[0028] Viable cells of the bacteria belonging to the genus *Clostridium* can be used for the composition of the present invention, and killed cells thereof may also be used for the composition. In addition, from the viewpoint of stability to heat, resistance to antibiotics and the like, and long storage period, the bacteria belonging to the genus *Clostridium* are preferably in the form of spore.

[0029] The meaning of the "physiologically active substance derived from bacteria belonging to the genus *Clostridium*" of the present invention includes substances contained in the bacteria, secretion products of the bacteria, and metabolites of the bacteria. Such a physiologically active substance can be identified by purifying an active component from the bacteria, a culture supernatant thereof, or intestinal tract contents in the intestinal tract of a mouse in which only bacteria belonging to the genus *Clostridium* are colonized by an already known purification method.

[0030] The active ingredient "spore-forming fraction of a fecal sample obtained from a mammal" in the composition as described herein includes spore-forming bacteria present in feces of a mammal, and has the effect of inducing proliferation or accumulation of regulatory T cells.

[0031] The active ingredient "chloroform-treated fraction of a fecal sample obtained from a mammal" in the composition as described herein is obtained by treating feces of a mammal with chloroform (for example, 3% chloroform), and has the effect of inducing proliferation or accumulation of regulatory T cells.

[0032] Note that the "mammal" herein includes humans, mice, rats, cattle, horses, pigs, sheep, monkeys, dogs, and cats.

[0033] Meanwhile, when the "spore-forming fraction of a fecal sample obtained from a mammal" or the "chloroform-treated fraction of a fecal sample obtained from a mammal" is cultured in a medium, substances contained in the bacteria, secretion products of the bacteria, metabolites of the bacteria are released from the bacteria and the like contained in the fraction. The meaning of the active ingredient "culture supernatant of the fraction" in the composition described herein includes such substances, secretion products, and metabolites. The culture supernatant is not particularly limited, as long as the culture supernatant has the effect of inducing proliferation or accumulation of regulatory T cells. Examples of the culture supernatant include a protein fraction of the culture supernatant, a polysaccharide fraction of the culture supernatant, a lipid fraction of the culture supernatant, and a low-molecular weight metabolite fraction of the culture supernatant.

[0034] The composition of the present invention may be in the form of a pharmaceutical composition, a food or beverage (which may also be an animal feed), or a reagent used for an animal model experiment, the pharmaceutical composition, the food or beverage, and the reagent having the effect of inducing proliferation or accumulation of regulatory T cells. An example herein revealed that regulatory T cells (Treg cells) induced by bacteria or the like belonging to the genus *Clostridium* suppressed the proliferation of effector T-cells. Accordingly, the composition of the present invention can be used suitably as defined in the claims as a composition having an immunosuppressive effect. The immunosuppressive effect can be evaluated, for example, as follows. Specifically, regulatory T cells isolated from an experimental animal, such as a mouse, to which the composition of the present invention is orally administered are caused to act on effector T-cells (CD4⁺ CD25⁻ cells) isolated from the spleen, and then proliferation ability thereof is measured by using the intake amount of [³H]-thymidine as an index (refer to Example 14).

[0035] The composition of the present invention can be used, for example, as claimed as a pharmaceutical composition for preventing or treating an allergic disease such as pollenosis or asthma a food or beverage for improving immune functions; or a reagent for suppressing the proliferation or function of effector T-cells.

[0036] Autoimmune diseases, allergic diseases, and rejection in organ transplantations and the like include inflammatory bowel disease (IBD), ulcerative colitis, Crohn's disease, sprue, autoimmune arthritis, rheumatoid arthritis, Type I diabetes, multiple sclerosis, graft vs. host disease following bone marrow transplantation, osteoarthritis, juvenile chronic arthritis, Lyme arthritis, psoriatic arthritis, reactive arthritis, spondyloarthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, thyroiditis, asthma, psoriasis, dermatitis scleroderma, atopic dermatitis, graft versus host disease, acute or chronic immune disease associated with organ transplantation, sarcoidosis, atherosclerosis, disseminated intravascular coagulation, Kawasaki's disease, Grave's disease, nephrotic syndrome, chronic fatigue syndrome, Wegener's granulomatosis, Henoch-Schoenlejn purpura, microscopic vasculitis of the kidneys, chronic active hepatitis, uveitis, septic shock, toxic shock syndrome, sepsis syndrome, cachexia, acquired immunodeficiency syndrome, acute transverse myelitis, Huntington's chorea, Parkinson's disease, Alzheimer's disease, stroke, primary biliary cirrhosis, hemolytic anemia, polyglandular deficiency type I syndrome and polyglandular deficiency type II syndrome, Schmidt's syndrome, adult (acute) respiratory distress syndrome, alopecia, alopecia areata, seronegative arthropathy, arthropathy, Reiter's disease, psoriatic arthropathy, chlamydia, yersinia and salmonella associated arthropathy spondyloarthritis, atheromatous disease/arteriosclerosis, atopic allergy, food allergies, autoimmune bullous disease, pemphigus vulgaris, pemphigus foliaceus, pemphigoid, linear IgA disease, autoimmune haemolytic anaemia, Coombs positive haemolytic anaemia, acquired pernicious anaemia, juvenile pernicious anaemia, myalgic encephalitis/Royal Free Disease, chronic mucocutaneous candidiasis, giant cell arteritis, primary sclerosing hepatitis, cryptogenic autoimmune hepatitis, Acquired Immunodeficiency Disease Syndrome, Acquired Immunodeficiency Related Diseases, Hepatitis C, common varied immunodeficiency (common variable hypogammaglobulinaemia), dilated cardiomyopathy, fibrotic lung disease, cryptogenic fibrosing alveolitis, postinflammatory interstitial lung disease, interstitial pneumonitis, connective tissue disease associated interstitial lung disease, mixed connective tissue disease associated lung disease, systemic sclerosis associated interstitial lung disease, rheumatoid arthritis associated interstitial lung disease, systemic lupus erythematosus associated lung disease, dermatomyositis/polymyositis associated lung disease, Sjogren's disease associated lung disease, ankylosing spondylitis associated lung disease, vasculitic diffuse lung disease, haemosiderosis associated lung disease, drug-induced interstitial lung disease, radiation fibrosis, bronchiolitis obliterans, chronic eosinophilic pneumonia, lymphocytic infiltrative lung disease, postinfectious interstitial lung disease, gouty arthritis, autoimmune hepatitis, type-1 autoimmune hepatitis (classical autoimmune or lupoid hepatitis), type-2 autoimmune hepatitis (anti-LKM antibody hepatitis), autoimmune mediated hypoglycemia, type B insulin resistance with acanthosis nigricans, hypoparathyroidism, acute immune disease associated with organ transplantation, chronic immune disease associated with organ transplantation, osteoarthritis, primary sclerosing cholangitis, idiopathic leucopenia, autoimmune neutropenia, renal disease NOS, glomerulonephritides, microscopic vasculitis of the kidneys, discoid lupus, erythematosus, male infertility idiopathic or NOS, sperm autoimmunity, multiple sclerosis (all subtypes), insulin independent diabetes mellitus, sympathetic ophthalmia, pulmonary hypertension secondary to connective tissue disease, Goodpasture's syndrome, pulmonary manifestation of polyarteritis nodosa, acute rheumatic fever, rheumatoid spondylitis, Still's disease, systemic sclerosis, Taka-

yasu's disease/arteritis, autoimmune thrombocytopenia, idiopathic thrombocytopenia, autoimmune thyroid disease, hyperthyroidism, goitrous autoimmune hypothyroidism (Hashimoto's disease), atrophic autoimmune hypothyroidism, primary myxoedema, phacogenic uveitis, primary vasculitis, vitiligo, allergic rhinitis (pollen allergies), , anaphylaxis, pet allergies, latex allergies, drug allergies, allergic rhinoconjunctivitis, eosinophilic esophagitis, hypereosinophilic syndrome, eosinophilic gastroenteritis cutaneous lupus erythematosus, eosinophilic esophagitis, hypereosinophilic syndrome ,and eosinophilic gastroenteritis.

[0037] Pharmaceutical preparations can be formulated from the composition of the present invention by already known drug formulation methods. For example, the composition of the present invention can be used orally or parenterally in the forms of capsules, tablets, pills, liquids, powders, granules, fine granules, film-coated preparations, pellets, troches, sublingual preparations, chewables, buccal preparations, pastes, syrups, suspensions, elixirs, emulsions, liniments, ointments, plasters, cataplasms, transdermal absorption systems, lotions, inhalations, aerosols, injections, suppositories, and the like.

[0038] For formulating these preparations, the composition of the present invention can be used in appropriate combination with carriers acceptable pharmacologically or acceptable for a food or beverage, specifically, with sterile water, physiological saline, vegetable oil, solvent, a base material, an emulsifier, a suspending agent, a surfactant, a stabilizer, a flavoring agent, an aromatic, an excipient, a vehicle, a preservative, a binder, a diluent, a tonicity adjusting agent, a soothing agent, a bulking agent, a disintegrating agent, a buffer agent, a coating agent, a lubricant, a colorant, a sweetener, a thickening agent, a flavor corrigent, a solubilizer, other additives, or the like.

[0039] Meanwhile, for formulating a pharmaceutical preparation thereof, and particularly for formulating a pharmaceutical preparation for oral administration, it is preferable to use in combination a composition which enables an efficient delivery of the composition of the present invention to the colon, from the viewpoint of more efficiently inducing the proliferation or accumulation of regulatory T cells in the colon.

[0040] Such a composition or method which enables the delivery to the colon is not particularly limited, and known compositions or methods can be employed as appropriate. Examples thereof include pH sensitive compositions, more specifically, enteric polymers which release their contents when the pH becomes alkaline after the enteric polymers pass through the stomach. When a pH sensitive composition is used for formulating the pharmaceutical preparation, the pH sensitive composition is preferably a polymer whose pH threshold of the decomposition of the composition is 6.8 to 7.5. Such a numeric value range is a range where the pH shifts toward the alkaline side at a distal portion of the stomach, and hence is a suitable range for use in the delivery to the colon.

[0041] Moreover, another example of the composition enabling the delivery to the colon is a composition which ensures the delivery to the colon by delaying the release of the contents by approximately 3 to 5 hours, which corresponds to the small intestinal transit time. In an example of formulating a pharmaceutical preparation using the composition for delaying the release, a hydrogel is used as a shell. The hydrogel is hydrated and swells upon contact with gastrointestinal fluid, so that the contents are effectively released. Furthermore the delayed release dosage units include drug-containing compositions having a material which coats or selectively coats a drug. Examples of such a selective coating material include in vivo degradable polymers, gradually hydrolyzable polymers, gradually water-soluble polymers, and/or enzyme degradable polymers. A preferred coating material for efficiently delaying the release is not particularly limited, and examples thereof include cellulose-based polymers such as hydroxypropyl cellulose, acrylic acid polymers and copolymers such as methacrylic acid polymers and copolymers, and vinyl polymers and copolymers such as polyvinylpyrrolidone.

[0042] Examples of the composition enabling the delivery to the colon further include bioadhesive compositions which specifically adhere to the colonic mucosal membrane (for example, a polymer described in the specification of US Patent No. 6,368,586), and compositions into which a protease inhibitor is incorporated for protecting particularly a biopharmaceutical preparation in the gastrointestinal tracts from decomposition due to an activity of a protease.

[0043] An example of a system enabling the delivery to the colon is a system of delivering a composition to the colon by pressure change in such a way that the contents are released by utilizing pressure change caused by generation of gas in bacterial fermentation at a distal portion of the stomach. Such a system is not particularly limited, and a more specific example thereof is a capsule which has contents dispersed in a suppository base and which is coated with a hydrophobic polymer (for example, ethyl cellulose).

[0044] Another example of the system enabling the delivery to the colon is a system of delivering a composition to the colon, the system being specifically decomposed by an enzyme (for example, a carbohydrate hydrolase or a carbohydrate reductase) present in the colon. Such a system is not particularly limited, and more specific examples thereof include systems which use food components such as non-starch polysaccharides, amylose, xanthan gum, and azopolymers.

[0045] When used as a pharmaceutical composition, the composition of the present invention may be used in combination with an already known pharmaceutical composition for use in immunosuppression. Such a known pharmaceutical composition is not particularly limited, and may be at least one therapeutic composition selected from the group consisting of corticosteroids, mesalazine, mesalamine, sulfasalazine, sulfasalazine derivatives, immunosuppressive drugs, cyclosporin A, mercaptopurine, azathiopurine, prednisone, methotrexate, antihistamines, glucocorticoids, epinephrine,

theophylline, cromolyn sodium, anti-leukotrienes, anti-cholinergic drugs for rhinitis, anti-cholinergic decongestants, mast-cell stabilizers, monoclonal anti-IgE antibodies, vaccines (preferably vaccines used for vaccination where the amount of an allergen is gradually increased), and combinations thereof. It is preferable to use these therapeutic compositions in combination with the composition of the present invention.

[0046] When the composition of the present invention is used as a food or beverage, the food or beverage can be, for example, a health food, a functional food, a food for specified health use, a dietary supplement, a food for patients, or an animal feed. The food or beverage of the present invention can be ingested in the forms of the compositions as described above, and also can be ingested in the forms of various foods and beverages. Specific examples of the foods and beverages include various beverages such as juices, refreshing beverages, tea beverages, drink preparations, jelly beverages, and functional beverages; alcoholic beverages such as beers; carbohydrate-containing foods such as rice food products, noodles, breads, and pastas; paste products such as fish hams, sausages, paste products of seafood; retort pouch products such as curries, food dressed with a thick starchy sauces, and Chinese soups; soups; dairy products such as milk, dairy beverages, ice creams, cheeses, and yogurts; fermented products such as fermented soybean pastes, yogurts, fermented beverages, and pickles; bean products; various confectionery products such as Western confectionery products including biscuits, cookies, and the like, Japanese confectionery products including steamed bean-jam buns, soft adzuki-bean jellies, and the like, candies, chewing gums, gummies, cold desserts including jellies, creme caramels, and frozen desserts; instant foods such as instant soups and instant soy-bean soups; micro-wavable foods; and the like. Further, the examples also include health foods and beverages prepared in the forms of powders, granules, tablets, capsules, liquids, pastes, and jellies. The composition of the present invention can be used for animals including humans. The animals, other than humans, are not particularly limited, and the composition can be used for various livestock, poultry, pets, experimental animals, and the like. Specific examples of the animals include pigs, cattle, horses, sheep, goats, chickens, wild ducks, ostriches, domestic ducks, dogs, cats, rabbits, hamsters, mice, rats, monkeys, and the like, but the animals are not limited thereto.

[0047] Without wishing to be bound by theory, individuals in which the relative abundance of bacteria belonging to the group Firmicutes (the group to which the Clostridium clusters IV and XIVa belong) is large gain more body weight than individuals in which the relative abundance of bacteria belonging to the group Bacteroidetes is large. Accordingly, the composition of the present disclosure is capable of conditioning absorption of nutrients and improving feed efficiency. From such a viewpoint, the composition of the present disclosure can be used for promoting body weight gain, or for an animal feed good in feed efficiency.

[0048] Moreover, the addition of the composition of the present disclosure to an antibiotic-free animal feed makes it possible to increase the body weight of a subject that ingests the animal feed to a level equal to or higher than those achieved by antibiotic-containing animal feeds, and also makes it possible to reduce pathogenic bacteria in the stomach to a level equal to those achieved by typical antibiotic-containing animal feeds. Accordingly, the composition of the present disclosure can be used for an animal feed which does not need the addition of antibiotics.

[0049] In addition, unlike conventional bacteria (Lactobacillus and Bifidobacteria) in commercial use which are not easy to incorporate into the livestock production, the composition of the present invention in the spore form can be pelletized, sprayed, or easily mixed with an animal feed, and also can be added to drinking water.

[0050] The feeding of such an animal feed using the composition described herein is not particularly limited, and the animal feed may be fed to a subject at regular intervals in a selective manner, or may be fed for a certain period (for example, at its birth, during weaning, or when the subject to be fed is relocated or shipped).

[0051] Moreover, from the above-described viewpoint, the composition of the present disclosure can be preferably used for malnourished humans. In other words, also when the subject who ingests the composition is a human, the composition can be used for promoting the body weight gain, and enhancing the energy absorption from foods.

[0052] Food or beverage can be manufactured by a manufacturing technique which is well known in the technical field. To the food or beverage, one or more components (for example, a nutrient) which are effective for the improvement of an immune function by the immunosuppressive effect may be added. In addition, the food or beverage may be combined with another component or another functional food exhibiting a function other than the function of the improvement of an immune function to thereby serve as a multi-functional food or beverage.

[0053] Moreover, the composition described herein can be incorporated into foods requiring a processing step which may destroy ordinary probiotic strains. Specifically, most commercially usable probiotic strains cannot be incorporated into foods which need to be processed by any one of a heat treatment, long term storage, a freezing treatment, a mechanical stress treatment, and a high-pressure treatment (for example, extrusion forming or roll forming). On the other hand, because of an advantageous nature of forming spores, the composition of the present invention can be easily incorporated into such processed foods.

[0054] For example, compositions in the form of spore can survive even in a dried food, and can remain living even after being ingested. Likewise, the composition described herein can withstand low-temperature sterilization processes, typically processes at a temperature in a range from 70°C to the boiling point, both inclusive. Thus, the composition described herein can be incorporated into all kinds of dairy products. Furthermore, the composition described herein

can withstand long-term storage of many years; high-temperature processing such as baking and boiling; low-temperature processing such as freezing and cold storage; and high-pressure treatments such as extrusion forming and roll forming.

[0055] The foods which need to be processed under such harsh conditions are not particularly limited, and examples thereof include foods which need to be processed in a microwave oven to be edible (for example, oatmeal), foods which need to be baked to be edible (for example, muffin), foods which need to be subjected to a sterilization high-temperature treatment for a short period of time to be edible (for example, milk), and foods which need to be heated to be drinkable (for example, hot tea).

[0056] When the composition is administered or ingested, the amount thereof for the administration or ingestion is selected as appropriate depending on the age, body weight, symptoms, health conditions, of a subject, the kind of the composition (a pharmaceutical product, a food or beverage, or the like), and the like. For example, the amount per administration or ingestion is generally 0.01 mg/kg body weight to 100 mg/kg body weight, and preferably 1 mg/kg body weight to 10 mg/kg body weight. The present disclosure also includes a method for suppressing the immunity of a subject, the method being characterized in that the bacteria belonging to the genus *Clostridium* or the physiologically active substance derived from the bacteria is administered into or ingested by the subject as described above.

[0057] A product of the composition of the present invention (a pharmaceutical product, a food or beverage, or a reagent) or a manual thereof may be provided with a note stating that the product can be used to suppress the immunity (including a note stating that the product has an immunosuppressive effect, and a note stating that the product has an effect of suppressing the proliferation or function of effector T-cells). Here, the "provision to the product or the manual thereof with the note" means that the note is provided to a main body, a container, a package, or the like of the product, or the note is provided to a manual, a package insert, a leaflet, or other printed matters, which disclose information on the product.

<Method for Inducing Proliferation or Accumulation of Regulatory T Cells>

[0058] As described above, and as will be shown in Examples, the administration of the composition described herein to an individual makes it possible to induce proliferation or accumulation of regulatory T cells in the individual. Thus, the present disclosure includes a method for inducing proliferation or accumulation of regulatory T cells in an individual, the method comprising a step of administering, to the individual, at least one substance selected from the group consisting of the following (a) to (c):

- (a) bacteria belonging to the genus *Clostridium* or a physiologically active substance derived from the bacteria;
- (b) a spore-forming fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction; and
- (c) a chloroform-treated fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction.

[0059] Note that, the "individual" in the present disclosure is not particularly limited, and examples thereof include humans, various kinds of livestock, poultry, pets, experimental animals, and the like. The "individual" may be in a healthy state or a diseased state.

[0060] Moreover, as will be shown in Example 5 to be described later, Gram-positive commensal bacteria play principal roles in the proliferation or accumulation of regulatory T cells. Accordingly, the present disclosure includes a method for inducing proliferation or accumulation of regulatory T cells in an individual, the method comprising a step of administering an antibiotic against Gram-negative bacteria to the individual.

[0061] As used herein, the "antibiotic against Gram-negative bacteria" is not particularly limited, and examples thereof include aminoglycoside antibiotics (amikacin, gentamicin, kanamycin, neomycin, netilmicin, tobramycin, and paromomycin), cephalosporin antibiotics (cefaclor, cefamandole, cefoxitin, cefprozil, cefuroxime, cefixime, cefdinir, cefditoren, cefoperazone, cefotaxime, ceftazidime, ceftibuten, ceftizoxime, ceftriaxone, and cefoxotin), sulfonamides, ampicillin, and streptomycin. Without wishing to be bound by theory, the "antibiotic against Gram-negative bacteria" according to the present invention is preferably one which reduces Gram-negative bacteria, and contributes to the colonization of Gram-positive bacteria.

[0062] Moreover, a prebiotic composition such as almond skin, inulin, oligofructose, raffinose, lactulose, pectin, hemicellulose (such as xyloglucan and alpha-glucans), amylopectin, and resistant starch which are not decomposed in the upper gastrointestinal tract and promote the growth of intestinal microbes in the intestinal tract, as well as growth factors such as acetyl-Co A, biotin, beet molasses, and yeast extracts, contribute to the proliferation of bacteria belonging to the genus *Clostridium*. Accordingly, the present disclosure includes a method for inducing proliferation or accumulation of regulatory T cells in an individual, the method comprising a step of administering, to the individual, at least one substance selected from the group consisting of these substances.

[0063] Meanwhile, in a "method for inducing proliferation or accumulation of regulatory T cells", the composition of the present disclosure, the above-described "antibiotic against Gram-negative bacteria," and the above-described "prebiotic composition or growth factor" may be used in combination. Such combined use is not particularly limited, and

examples of the combined use are as follows: the "antibiotic against Gram-negative bacteria" is administered to an individual in advance, and then the composition of the present invention is administered; the "antibiotic against Gram-negative bacteria" and the composition of the present invention are simultaneously administered to an individual; the "prebiotic composition or growth factor" is administered to an individual in advance, and then the composition of the present invention is administered; the "prebiotic composition or growth factor" and the composition of the present invention are simultaneously administered to an individual; the composition of the present invention, the "antibiotic against Gram-negative bacteria," and the "prebiotic composition or growth factor" are administered to an individual simultaneously or individually at any appropriate time.

[0064] Moreover, a therapeutic composition may be administered to an individual together with at least one substance selected from the group consisting of the composition of the present disclosure, the "antibiotic against Gram-negative bacteria," and the "prebiotic composition or growth factor."

[0065] Such a therapeutic composition is not particularly limited, and may be at least one therapeutic composition selected from the group consisting of corticosteroids, mesalazine, mesalamine, sulfasalazine, sulfasalazine derivatives, immunosuppressive drugs, cyclosporin A, mercaptopurine, azathiopurine, prednisone, methotrexate, antihistamines, glucocorticoids, epinephrine, theophylline, cromolyn sodium, anti-leukotrienes, anti-cholinergic drugs for rhinitis, anti-cholinergic decongestants, mast-cell stabilizers, monoclonal anti-IgE antibodies, vaccines (preferably, vaccines used for vaccination where the amount of an allergen is gradually increased), and combinations thereof. It is preferable to use these therapeutic compositions in combination with the above-described substance.

[0066] Moreover, there is no particular limitation imposed on the combined use of the therapeutic composition with at least one substance selected from the group consisting of the composition of the present disclosure, the "antibiotic against Gram-negative bacteria," and the "prebiotic composition or growth factor". For example, the "one substance" and the therapeutic composition are administered orally or parenterally to an individual simultaneously or individually at any appropriate time.

[0067] Moreover, in the above-described "method for inducing proliferation or accumulation of regulatory T cells," whether or not the administration of the composition described herein or the like actually induces the proliferation or accumulation of regulatory T cells can be determined by using, as an index, increase or reinforcement of at least one selected from the group consisting of the number of regulatory T cells, the ratio of regulatory T cells in the T cell group of the colon, a function of regulatory T cells, and expression of a marker of regulatory T cells. It is preferable to use one measurement selected from the group consisting of promotion of IL-10 expression, promotion of CTLA4 expression, promotion of IDO expression, and suppression of IL-4 expression, as the index of the induction of proliferation or accumulation of regulatory T cells.

[0068] Note that examples of a method for detecting such expression include the northern blotting, the RT-PCR, and the dot blotting for detection of gene expression at the transcription level; and the ELISA, the radioimmunoassay, the immunoblotting, the immunoprecipitation, and the flow cytometry for detection of gene expression at the translation level.

[0069] Meanwhile, a sample used for measuring such an index is not particularly limited, and examples thereof include blood sampled from an individual and tissue pieces obtained in a biopsy.

<Method for Predicting Response of Individual to Composition of Present Invention and/or Prognosis of Individual>

[0070] Described herein is a method in which the absolute amount or the ratio of bacteria belonging to the genus *Clostridium* in a microbiota of an individual is determined, and, when the ratio or the absolute value of the bacteria belonging to the genus *Clostridium* is reduced in comparison with a base line value obtained by performing a similar determination on an individual in a typical health state, it is determined that the individual is possibly responsive to the composition described herein.

[0071] Also described is a method to predict a subject's response to a substance and/or the subject's prognosis.

[0072] The method comprises measuring the percentage or absolute amounts of *Clostridium* clusters IV and XIV in the microbiota of the subject and comparing them to a baseline value of the same measurements in a prototypical healthy subject, wherein a decreased absolute amount or percentage level of *Clostridium* clusters IV and/or XIV indicates that the subject may respond favorably to the compositions described herein.

[0073] The method may further comprise measuring the composition of the microbiota of the subject after administration of the substance, wherein an increase in the percentage or absolute number of *Clostridium* spp. belonging to clusters IV, XIV after administration of the compositions of the present invention relative to prior to the administering is a positive indicator of enhanced immunosuppression (or immunoregulation). The measurement of the composition of the subject's microbiota can be made with techniques known in the art, such as 16srRNA sequencing.

[0074] Note that, in these methods, the substance is at least one substance selected from the group consisting of the following (a) to (e):

- (a) bacteria belonging to the genus *Clostridium* or a physiologically active substance derived from the bacteria;

- (b) a spore-forming fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction;
- (c) a chloroform-treated fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction;
- (d) an antibiotic against Gram-negative bacteria; and
- (e) at least one substance selected from the group consisting of almond skin, inulin, oligofructose, raffinose, lactulose, pectin, hemicellulose (such as xyloglucan and alpha-glucans), amylopectin, acetyl-Co A, biotin, beet molasses, yeast extracts, and resistant starch.

<Method for Inhibiting Proliferation or Accumulation of Regulatory T Cells>

[0075] As will be shown in Example 5 to be described later, Gram-positive commensal bacteria have principal roles in the proliferation or accumulation of regulatory T cells. Accordingly, the present disclosure also includes a method for inhibiting proliferation or accumulation of regulatory T cells in an individual, the method comprising a step of administering an antibiotic against Gram-positive bacteria to the individual.

[0076] As used herein, the term "antibiotic against Gram-positive bacteria" is not particularly limited, and examples thereof include cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and ceftobiprole); fluoroquinolone antibiotics (cipro, Levaquin, floxin, tequin, avelox, and norflox); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem).

[0077] As described above, the term "individual" is not particularly limited, and examples thereof include humans, various kinds of livestock, poultry, pets, experimental animals, and the like. The "individual" may be in a healthy state or a diseased state. Such a diseased state is not particularly limited, and examples thereof include states of being subjected to cancer immunotherapy and of suffering from an infectious disease.

[0078] Moreover, as another mode of the "method for inhibiting proliferation or accumulation of regulatory T cells," the present disclosure includes a method for inhibiting proliferation or accumulation of regulatory T cells in an individual, the method comprising a step of administering, to the individual, any one of an antibody, an antibody fragment, and a peptide, which are against an antigen that is at least one substance selected from the group consisting of the following (a) to (c):

- (a) bacteria belonging to the genus Clostridium or a physiologically active substance derived from the bacteria;
- (b) a spore-forming fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction; and
- (c) a chloroform-treated fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction.

<Vaccine Composition and Method for Treating or Preventing Infectious Disease or Autoimmune Disease by Using the Vaccine Composition>

[0079] As described above, and as will be shown in Example 15 to be described later, the induction of Treg cells in the colon by the Clostridium has an important role in local and systemic immune responses. Accordingly, the present disclosure includes a "vaccine composition comprising at least one substance selected from the group consisting of the following (a) to (c): (a) bacteria belonging to the genus Clostridium; (b) a spore of bacteria in a spore-forming fraction of a fecal sample obtained from a mammal; and (c) bacteria in a chloroform-treated fraction of a fecal sample obtained from a mammal" and a "method for treating, aiding in treating, reducing the severity of, or preventing at least one disease selected from infectious diseases and autoimmune diseases in an individual, the method comprising administering the vaccine composition to the individual."

[0080] Note that such "autoimmune diseases" are not particularly limited, and examples thereof include those described as the "specific examples of target diseases" in <Composition Having Effect of Inducing Proliferation or Accumulation of Regulatory T cells>. The "infectious diseases" are also not particularly limited, and examples thereof include infectious diseases associated with "infectious pathogens" described as the "example of infectious pathogens" in <Composition Having Effect of Inducing Proliferation or Accumulation of Regulatory T cells>.

<Method for Screening for Compound Having Activity to Promote Proliferation or Accumulation of Regulatory T Cells>

[0081] Also described is a method for screening for a compound having an activity to promote proliferation or accumulation of regulatory T cells, the method comprising:

- (1) preparing a test substance from at least one substance selected from the group consisting of the following (a) to (c):

- (a) bacteria belonging to the genus Clostridium or a physiologically active substance derived from the bacteria;
- (b) a spore-forming fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction; and

(c) a chloroform-treated fraction of a fecal sample obtained from a mammal or a culture supernatant of the fraction.

(2) preparing non-human mammals in which a reporter gene is to be expressed under control of IL-10 gene expression;

(3) bringing the test substance into contact with the non-human mammal;

(4) after the contact with the test substance, detecting cells expressing the reporter gene in a CD4⁺ Foxp3⁺ cell group of the non-human mammal, and determining the number of cells in the CD4⁺ Foxp3⁺ cell group expressing the reporter gene or a ratio of cells in the CD4⁺ Foxp3⁺ cell group expressing the reporter gene to cells in the CD4⁺ Foxp3⁺ cell group not expressing the reporter gene;

(5) detecting cells expressing the reporter gene in a CD4⁺ Foxp3⁺ cell group of the non-human mammal which has not been in contact with the test substance, and determining the number of cells in the CD4⁺ Foxp3⁺ cell group expressing the reporter gene or a ratio of cells in the CD4⁺ Foxp3⁺ cell group expressing the reporter gene to cells in the CD4⁺ Foxp3⁺ cell group not expressing the reporter gene; and

(6) comparing the absolute numbers or the ratios determined in steps (4) with the number or the ratio determined in (5), and determining, when the number or the ratio determined in (4) is greater than that determined in (5), that the test substance is a compound that promotes proliferation or accumulation of Treg cells.

[0082] The term "test substance" as used herein is not particularly limited, as long as the test substance is a substance prepared from at least one substance selected from the group consisting of the substances (a) to (c). Examples of the test substance include proteins, polysaccharides, lipids, and nucleic acids which are derived from at least one substance selected from the group consisting of the above described substances (a) to (c).

[0083] The term "non-human mammal in which a reporter gene is to be expressed under control of IL-10 gene expression" as used herein is not particularly limited, as long as the non-human mammal is a non-human mammal having a reporter gene whose expression is controlled by an IL-10 gene expression control region (for example, a promoter, or an enhancer). Examples of such a reporter gene include genes encoding fluorescent proteins (for example, GFP), and genes encoding luciferase. As the "non-human mammal in which a reporter gene is to be expressed under control of IL-10 gene expression" according to the present invention, an I110^{venus} mouse to be shown later in Examples can be preferably used.

[0084] The term "contact" as used herein is not particularly limited, and examples thereof include administration of the test substance to the non-human mammal orally or parenterally (for example, intraperitoneal injection, or intravenous injection).

[0085] Also described is a non-human mammal which is used for the method, and in which the reporter gene is to be expressed under the control of the IL-10 gene expression.

[0086] Furthermore, described herein is a method for isolating, from a sample of bacteria belonging to the genus *Clostridium*, a compound having an activity to promote proliferation or accumulation of regulatory T cells, the method comprising the following steps (1) to (3) :

(1) preparing a genomic DNA from the sample of bacteria belonging to the genus *Clostridium*;

(2) inserting the genomic DNA into a cloning system, and preparing a gene library derived from the sample of bacteria belonging to the genus *Clostridium*; and

(3) isolating a compound having an activity to promote proliferation or accumulation of regulatory T cells, by use of the gene library obtained in step (2).

[0087] In such steps, methods for the preparation and the isolation are not particularly limited, and known techniques for an in-vitro or in-vivo system can be used as appropriate. Moreover, the compound isolated by this method is not particularly limited, and examples thereof include nucleic acids (for example, a DNA, a mRNA, and a rRNA) derived from bacteria belonging to the genus *Clostridium*, as well as polypeptides and proteins derived from the bacteria belonging to the genus *Clostridium*.

[0088] Also described is a method for determining the composition of a microbiota in an individual, wherein the increase in the ratio or the absolute number of bacteria belonging to the genus *Clostridium* after the administration of the composition of the present invention to the individual with respect to the ratio or the absolute number before the administration is used as an index of increased immunosuppression. In such a method, the method for determining the composition of the microbiota is not particularly limited, and known techniques (for example, 16S rRNA sequencing) can be used as appropriate.

[0089] Also described is a method for measuring differentiation of Treg cells, wherein the increase in differentiation of Treg cells in an individual after administration of the composition described herein to the individual with respect to that before the administration is used as an index of increased immunosuppression (or immunoregulation).

[0090] Moreover, the composition described herein can also be administered to an individual under an antibiotic

treatment. The timing of the administration is not particularly limited, and the composition can be administered before or simultaneously with the antibiotic treatment, for example. Meanwhile, the composition is preferably administered in the spore form from the viewpoint of resistance to antibiotics.

[0091] Moreover, in a preferred mode of such administration, the composition is administered after or simultaneously with administration of an antibiotic against Gram-positive bacteria, for example. Note that such an "antibiotic against Gram-positive bacteria" is not particularly limited, and examples thereof include cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and cef tobirole); fluoroquinolone antibiotics (cipro, Levaquin, floxin, tequin, avelox, and norflox); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem).

[0092] Meanwhile, in another preferred mode of such administration, the composition is administered after (or simultaneously with) a treatment using vancomycin, metronidazole, linezolid, ramoplanin, or fidaxomicin, for example.

[Examples]

[0093] Hereinafter, the present invention is described more specifically on the basis of Examples. However, the present invention is defined in the claims.

[0094] Note that mice used in Examples were prepared or produced as follows. In the following description, mice may be referred to with "SPF" or "GF" attached in front thereof. These "SPF" and "GF" indicate that the mice were maintained in the absence of specific pathogenic bacteria (specific pathogen-free, SPF), and that the mice were maintained under Germ-Free (GF) conditions, respectively.

<Mice>

[0095] C57BL/6, Balb/c, and IQI mice maintained under SPF or GF conditions were purchased from Sankyo Labo Service Corporation, Inc. (Japan), JAPAN SLC, INC. (Japan), CLEA Japan, Inc. (Japan), or The Jackson Laboratory (USA). GF mice and gnotobiotic mice were bred and maintained within the gnotobiotic facility of The University of Tokyo, Yakult Central Institute for Microbiological Research, or Sankyo Labo Service Corporation, Inc. *Myd88^{-/-}*, *Rip2^{-/-}*, and *Card9^{-/-}* mice were produced as described in Non-Patent Documents 1 to 3, and backcrossed for 8 generations or more, so that a C57BL/6 genetic background was achieved. *Foxp3^{eGFP}* mice were purchased from the Jackson Laboratory.

<*Il10^{venus}* mice>

[0096] To form a bicistronic locus encoding both *Il10* and Venus under control of an *Il10* promoter, a targeting construct was first created. Specifically, a cassette (IRES-Venus-SV40 polyA signal cassette, refer to Non-Patent Document 4) which was made of an internal ribosome entry site (IRES), a yellow fluorescent protein (Venus), and a SV40 polyA signal (SV40 polyA) and which was arranged next to a neomycin-resistant gene (*neo*), was inserted between a stop codon and a polyA signal (Exon 5) of a *Il10* gene. Next, the obtained targeting construct was used to cause homologous recombination with the *Il10* gene region in the genome of mice. Thus, *Il10^{venus}* mice having an *Il10^{venus}* alleles were produced (refer to Fig. 1). Note that in Fig. 1 "tk" represents a gene coding thymidine kinase, "neo" represents the neomycin-resistant gene, and "BamH1" represents a cleavage site by the restriction enzyme BamH1.

[0097] Genomic DNAs were extracted from the *Il10^{venus}* mice, treated with BamH1, and Southern blotted by use of a probe shown in Fig. 1. Fig. 2 shows the obtained results. Wild-type and *Il10^{venus}* alleles were detected as bands having sizes of 19 kb and 5.5 kb, respectively. Hence, as is apparent from the results shown in Fig. 2, it was found that the homologous recombination shown in Fig. 1 occurred in the genome of the *Il10^{venus}* mice.

[0098] Further, CD4⁺ Venus⁻ cells or CD4⁺ Venus⁺ cells in the colonic lamina propria of the *Il10^{venus}* mice were sorted by use of a FACSaria. Then, real-time RT-PCR was carried out on an ABI 7300 system by a method to be described later, to determine the amount of IL-10 mRNA expressed. Figs. 3 and 4 show the obtained results. As is apparent from the results shown in Figs. 3 and 4, it was found that, since the development of the IL-10 mRNA was detected only in the CD4⁺ Venus⁺ cells, the expression of IL-10 mRNA in the *Il10^{venus}* mice was correctly reflected in the expression of Venus. Note that the germ-free states of such *Il10^{venus}* mice were established in Central Institute for Experimental Animals (Kawasaki, Japan). The *Il10^{venus}* mice in the germ-free states were maintained in vinyl isolators in Sankyo Labo Service Corporation, Inc. (Tokyo, Japan), and used in the following Examples.

[0099] Meanwhile, experiments and analyses in Examples were carried out as follows.

<Method for Colonization of Mice with Bacteria and Analysis Thereof>

[0100] According to the description in Non-Patent Documents 5 and 6, mice in which SFB or Clostridium were colonized were produced. Cecal contents or feces of the obtained gnotobiotic mice were dissolved in sterile water or an anaerobic dilution solution. The dissolved cecal contents or feces as they were or after a chloroform treatment were orally administered to GF mice. Three strains of the Lactobacillus and 16 strains of the Bacteroides were cultured separately from each other in a BL or EG agar medium in an anaerobic manner. The cultured bacteria were harvested, suspended in an anaerobic TS broth, and orally administered forcibly to GF mice. The state of the colonization of the bacteria in the mice was assessed by microscopic observation conducted on a smear preparation of fecal pellets.

<Cell Separation and Flow Cytometry>

[0101] In order to isolate lymphocytes from the colonic lamina propria and the small intestinal lamina propria, the small intestine and the colon were collected, and cut open longitudinally. Then, fecal content and the like therein were washed to remove. Subsequently, the small intestine and the colon were shaken in HBSS containing 5 mM of EDTA at 37°C for 20 minutes. After removal of epithelium and fat tissue, the intestinal tissues were cut into small pieces. To the small pieces, RPMI 1640 (4% fetal bovine serum (FBS), 1 mg/ml of collagenase D, 0.5 mg/ml of dispase, and 40 µg/ml of DNaseI (all of which were manufactured by Roche Diagnostics K.K.)) were added, and the mixture was shaken in a water bath kept at 37°C for 1 hour. The digested tissues were washed with HBSS containing 5 mM of EDTA, and resuspended in 5 ml of 40% percoll (GE Healthcare). The suspension was overlaid on 2.5 ml of 80% percoll in a 15-ml Falcon tube. Then, centrifugation was carried out at room temperature and at 2000 rpm for 20 minutes to conduct cell separation by percoll density gradient centrifugation. Cells at the interface were collected, and used as lamina propria lymphocytes. The collected cells were suspended in a staining buffer (PBS, 2% FBS, 2 mM EDTA, and 0.09% NaN₃), and stained by use of an anti-CD4 antibody (RM4-5, BD Biosciences) labeled with PE or PE-Cy7. After the staining of CD4, Foxp3 in the cells were stained by use of Cytofix/Cytoperm Kit Plus with GolgiStop (BD Biosciences) or Foxp3 Staining Buffer Set (eBioscience), as well as an anti-Foxp3 antibody (FJK-16s, eBioscience) labeled with Alexa647. Flow cytometry was performed by use of a FACScant II, and the data were analyzed by FlowJo software (TreeStar Inc.). The sorting of the cells were performed by use of a FACSARIA.

<Real-Time RT-PCR>

[0102] From an RNA prepared by using RNeasy Mini Kit (Qiagen), a cDNA was synthesized by use of a MMV reverse transcriptase (Promega KK). The obtained cDNA was analyzed by real-time RT-PCR using Power SYBR Green PCR Master Mix (Applied Biosystems) and ABI 7300 real time PCR system (Applied Biosystems), or real-time RT-PCR using SYBR Premix Ex Taq (TAKARA) and Light Cycler 480. For each sample, a value obtained was normalized for the amount of GAPDH. A primer set was designed by using Primer Express Version 3.0 (Applied Biosystems), and those exhibiting a 90% or higher sequence identity at an initial evaluation were selected. The primer set used was as follows:

Foxp3

5'-GGCAATAGTTCCTTCCCAGAGTT-3' (SEQ ID NO: 1)
5'-GGGTCGCATATTGTGGTACTTG-3' (SEQ ID NO: 2)

CTLA4

5'-CCTTTTGTAGCCCTGCTCACTCT-3' (SEQ ID NO: 3)
5'-GGGTCACCTGTATGGCTTCAG-3' (SEQ ID NO: 4)

GITR

5'-TCAGTGCAAGATCTGCAAGCA-3' (SEQ ID NO: 5)
5'-ACACCGGAAGCCAAACACA-3' (SEQ ID NO: 6)

IL-10

5'-GATTTTAATAAGCTCCAAGACCAAGGT-3' (SEQ ID NO: 7)
5'-CTTCTATGCAGTTGATGAAGATGTCAA-3' (SEQ ID NO: 8)

GAPDH

5'-CCTCGTCCCGTAGACAAAATG-3' (SEQ ID NO: 9)

5'-TCTCCACTTTGCCACTGCAA-3' (SEQ ID NO: 10)

Mmp2

5'-GGACATTGTCTTTGATGGCA-3' (SEQ ID NO: 11)

5'-CTTGTACAGTGGTGTCACTG-3' (SEQ ID NO: 12)

Mmp9

5'-TCTCTGGACGTCAAATGTGG-3' (SEQ ID NO: 13)

5'-GCTGAACAGCAGAGCCTTC-3' (SEQ ID NO: 14)

Mmp13

5'-AGGTCTGGATCACTCCAAGG-3' (SEQ ID NO: 15)

5'-TCGCCTGGACCATAAAGAA-3' (SEQ ID NO: 16)

Idol

5'-AGAGGATGCGTGACTTTGTG-3' (SEQ ID NO: 17)

5'-ATACAGCAGACCTTCTGGCA-3' (SEQ ID NO: 18).

<Preparation and Culturing of Large Intestinal Epithelial Cells (IECs)>

[0103] First, the colon was collected, cut open longitudinally, and rinsed with PBS. Subsequently, the colon was treated with 1mM dithiothreitol (DTT) at 37°C for 30 minutes on a shaker, and then vortexed for one minute to disrupt the epithelial integrity. The released IECs were collected, and suspended in 5 ml of 20% percoll. The suspension was overlaid on 2.5 ml of 80% percoll in a 15-ml Falcon tube. Then, the tube was centrifuged at 25°C and 780 g for 20 minutes to conduct cell separation by percoll density gradient centrifugation. Cells at the interface were collected, and used as colonic IECs (purity: 90% or higher, viability: 95%). The obtained IECs thus collected were suspended in RPMI containing 10% FBS, and 1×10^5 cells of the IECs were cultured in a 24-well plate for 24 hours. Thereafter, the culture supernatant was collected, and measured for active TGF- β 1 level by ELISA (Promega).

[0104] Meanwhile, for culturing T cells in vitro, 1.5×10^5 MACS-purified splenic CD4⁺ T cells were cultured in each well of a round-bottomed 96-well plate, together with a 50% conditioned medium in which IECs isolated from GF mice or Clostridium-colonized mice were cultured, and with 25 ng/ml of hIL-2 (Peprotech), in the presence or absence of 25 μ g/ml of an anti-TGF- β antibody (R&D). Note that 10 μ g/ml of an anti-CD3 antibody and an anti-CD28 antibody (BD Bioscience) were bound to the round-bottomed plate. After a 5-day culture, the CD4⁺ T cells were collected, and subjected to a real-time PCR.

<Colitis Experimental Model>

[0105] A fecal suspension of Clostridium-colonized mice was orally administered to C57BL/6 mice (2-week old), and grown in a conventional environment for six weeks.

[0106] For preparing a DSS-induced colitis model, 2% (wt/vol) DSS (reagent grade, DSS salt, molecular weight = 36 to 50 kD, manufactured by MP Biomedicals), together with drinking water, was given to the mice for six days.

[0107] Meanwhile, for preparing an oxazolone-induced colitis model, the mice were presensitized by transdermally applying, onto the mice, 150 μ l of a 3% oxazolone (4-ethoxymethylene-2-phenyl-2-oxazolin-5-one, Sigma-Aldrich)/100% ethanol solution. Five days after that, 150 μ l of a 1% oxazolone/50% ethanol solution was intrarectally administered again to the presensitized mice under a light anesthesia. Note that the intrarectal administration was conducted by using a 3.5F catheter.

[0108] Each mouse was analyzed daily for body weight, occult blood, bleeding visible with the naked eyes (gross blood), and the hardness of stool. Moreover, the body weight loss percentage, intestinal bleeding (no bleeding, occult blood (hemoccult+), or bleeding visible with the naked eyes), and the hardness of stool (normal stool, loose stool, or diarrhea) were evaluated numerically, and the disease activity index (DAI) was calculated in accordance with the description in "S. Wirtz, C. Neufert, B. Weigmann, M. F. Neurath, Nat Protoc 2, 541 (2007)."

<OVA Specific IgE Reaction>

[0109] BALB/c SPF mice were inoculated with a fecal suspension of Clostridium-colonized mice (2-week old), and grown in a conventional environment. Then, 1 μ g of OVA (grade V, Sigma) and 2 mg of alum (Thermo Scientific), 0.2 ml in total, were intraperitoneally injected to the mice (at their ages of 4 weeks and 6 weeks). Sera were collected every week from the mice at the root of their tail, and OVA-specific IgE was measured by ELISA (Chondrex). Then, at their ages of 8 weeks, splenic cells were collected, inoculated in a 96-well plate at 1×10^6 cells per well, and stimulated with OVA (100 μ g/ml) for three days. Thereafter, the culture supernatant was collected, and measured for IL-4 and IL-10 levels by ELISA (R&D).

<Statistical Analysis>

[0110] The difference between control and experimental groups was evaluated by the Student's t-test.

(Example 1)

[0111] First, it was investigated whether or not accumulation of regulatory T cells (Treg cells) in the colonic lamina propria was dependent on commensal bacteria. Specifically, lymphocytes were isolated from peripheral lymph nodes (pLN) of Balb/c mice bred in the absence of specific pathogenic bacteria (SPF) or from lamina propria of the colon or the small intestine (SI) of the mice. The CD4 and Foxp3 were stained by antibodies. Then, the ratio of Foxp3⁺ cells in CD4⁺ lymphocytes was analyzed by flow cytometry. Fig. 5 shows the obtained results. As is apparent from the results shown in Fig. 5, it was found that Foxp3⁺ Treg cells were present at a high frequency in the lamina propria of the gastrointestinal tracts, especially in the colonic lamina propria, of the mice kept under the environment free from specific pathogenic microorganisms (SPF). In addition, it was also found that the number of the Foxp3⁺ Treg cells in the colonic lamina propria gradually increased up to three months after their birth, whereas the number of the Foxp3⁺ Treg cells in the peripheral lymph nodes was basically constant from the time of two weeks after their birth.

(Example 2)

[0112] Next, it was investigated whether or not the temporal accumulation of the Treg cells in the colon as found in Example 1 had a relationship with the colonization of intestinal commensal microbiota. Specifically, the expression of CD4 and the expression of Foxp3 in lymphocytes isolated from the small intestine, the colon, and the peripheral lymph nodes of mice bred under a germ-free (GF) or SPF environment (8 weeks old: Balb/c mice, IqI mice, and C57BL/6 mice) were analyzed. Similar results were obtained in three or more independent experiments. Figs. 6 and 7 show the obtained results. Note that, in Fig. 7, each white circle represents the absolute number of CD4⁺Foxp3⁺ cells in an individual mouse, and the error bars represent standard deviations (SDs).

[0113] In addition, lamina propria lymphocytes were collected from SPF mice and GF mice (Balb/c mice or C57BL/6 mice). CD4 and Foxp3 were stained with antibodies. Then, the lamina propria lymphocytes were analyzed by FACS. Fig. 8 shows the obtained results. Note that in Fig. 8 each white circle represents the absolute number of CD4⁺ Foxp3⁺ cells in an individual mouse, ** indicates that "P < 0.001", and * indicates that "P < 0.01."

[0114] Further, lymphocytes were isolated from the lamina propria of the colon, the lamina propria of the small intestine (SI), Peyer's patches (PPs), and mesenteric lymph nodes (MLNs) of mice (SPF C57BL/6 mice) to which antibiotics were orally administered with water for eight weeks. CD4 and Foxp3 were stained with antibodies. Then, the lymphocytes were analyzed by FACS. Similar results were obtained in two or more independent experiments. Fig. 9 shows the obtained results (the ratio of the Foxp3⁺ cells in the CD4⁺ cells of an individual mouse). Note that the following antibiotics were used in combination in accordance with the description in the following document:

ampicillin (A; 500 mg/L, Sigma)
 vancomycin (V; 500 mg/L, NACALAI TESQUE, INC.)
 metronidazole (M; 1g/L, NACALAI TESQUE, INC.)
 neomycin (N; 1g/L, NACALAI TESQUE, INC.)

[0115] Rakoff-Nahoum, J. Paglino, F. Eslami-Varzaneh, S. Edberg, R. Medzhitov, Cell 118, 229 (Jul 23, 2004) Fagarasan et al., Science 298, 1424 (Nov 15, 2002)

[0116] In Fig. 9, each white circle represents the absolute number of the CD4⁺ Foxp3⁺ cells in an individual mouse, each horizontal bar represents the average value of the absolute numbers, * indicates that "P < 0.01," and "AVMN" represents the kinds of the administered antibiotics by using the first letters of the antibiotics.

[0117] As is apparent from the results shown in Figs. 6 to 9, the frequencies and the absolute numbers of Foxp3⁺

CD4⁺ cells in the small intestine and the peripheral lymph nodes of the GF mice were equal to or greater than those of the SPF mice (refer to Figs. 6 to 8). In addition, the numbers of the Treg cells in the small intestinal lamina propria, Peyer's patches, and mesenteric lymph nodes of the SPF mice to which the antibiotics were orally administered for eight weeks were equal to or greater than those of the SPF mice (refer to Fig. 9). Meanwhile, the number of the Foxp3⁺ CD4⁺ cells in the colonic lamina propria of the GF mice was decreased significantly in comparison with that of the SPF mice (refer to Figs. 6 and 7). This decrease was commonly observed among mice of different genetic backgrounds (Balb/c, IQI, and C57BL/6), as well as among mice bred in different animal facilities (refer to Fig. 7 for the data regarding the different genetic backgrounds, the data regarding the mice bred in the different animal facilities are not shown in the drawings). In addition, it was also shown that the number of Treg cells in the colonic lamina propria of the SPF C57BL/6 mice to which the antibiotics were administered was decreased significantly (refer to Fig. 9).

(Example 3)

[0118] Next, it was directly checked whether or not the decrease in the number of the Treg cells in the colonic lamina propria of the GF mice shown in Example 2 was attributed to the absence of microbiota. Specifically, a fecal suspension of B6 SPF mice purchased from The Jackson Laboratory was orally administered to GF-IQI mice (conventionalization). Three weeks after the administration, lymphocytes were isolated from the colonic lamina propria, and the expression of Foxp3 in CD4⁺ lymphocytes was analyzed. Figs. 10 and 11 show the obtained results. Note that each white circle in Fig. 11 represents the absolute number of CD4⁺ Foxp3⁺ cells in an individual mouse, the error bars represent standard deviations (SD), * indicates that "P < 0.01" in Student's t-test, and ** indicates that "P < 0.001." As is apparent from the results shown in Figs. 10 and 11, the number of Treg cells in the small intestinal lamina propria did not change. However, the number of the Treg cells in the colonic lamina propria increased significantly. Hence, it was shown that host-microbial interaction played an important role in the accumulation of Foxp3⁺ Treg cells in the colonic lamina propria, while the accumulation of the Treg cells in the small intestinal lamina propria had a different mechanism.

(Example 4)

[0119] Next, the relationship between the gut-associated lymphoid tissues of mice and the number of Foxp3⁺ cells in the colonic lamina propria of the mice was investigated in accordance with the method described in M. N. Kweon et al., J Immunol 174, 4365 (Apr 1, 2005). Specifically, 100 µg of an extracellular domain recombinant protein (a fusion protein (LTβR-Ig) between a lymphotoxin β receptor (LTβR) and a Fc region of human IgG1, refer to Honda et al., J Exp Med 193, 621 (Mar 5, 2001)) was injected intraperitoneally into pregnant C57BL/6 mice 14 days after conception. The LTβR-Ig was again injected intraperitoneally into fetuses obtained from such mice, so that mice from which isolated lymphoid follicles (ILFs), Peyer's patches (PPs), and colonic-patches (CPs) were completely removed were produced. Then, the ratios of Foxp3⁺ cells in CD4⁺ cells in the colonic lamina propria of the mice treated with the LTβR-Ig, and mice treated with rat IgG (control) were analyzed by FACS. Fig. 12 shows the obtained results. Note that in Fig. 12 each white circle represents the ratio of Foxp3⁺ cells in an individual mouse, and the error bars represent standard deviations. As is apparent from the results shown in Fig. 12, it was found that the ratio of the Foxp3⁺ cells in the colonic lamina propria of the mice deficient in isolated lymphoid follicles, Peyer's patches, and the colonic-patches (the mice treated with the LTβR-Ig) rather increased. Accordingly, it was suggested that the decrease in the number of the Treg cells in the colonic lamina propria of the GF mice and the mice treated with the antibiotics was caused because the transmission of specific signals which promotes the accumulation of Treg cells in the colonic lamina propria and which is caused by the intestinal microbes did not occur, rather than simply because of a secondary effect of disorganized gut-associated lymphoid tissues.

(Example 5)

[0120] To investigate whether or not a specific intestinal flora induced the accumulation of colonic Treg cells, vancomycin as an antibiotic against Gram-positive bacteria or polymyxin B as an antibiotic against Gram-negative bacteria was administered to SPF mice (from 4 weeks of age) for four weeks, and analyzed for the ratio of Foxp3⁺ cells in the CD4⁺ cell group ([%] Foxp3⁺ in CD4). Fig. 30 shows the obtained results. Note that, in Fig. 30, "SPF" indicates the result of SPF mice (control), "poly B" indicates the result of the SPF mice to which polymyxin B was administered, and "Vanco." indicates the result of the SPF mice to which vancomycin was administered. Meanwhile, * indicates that "P < 0.01."

[0121] As is apparent from the results shown in Fig. 30, the number of Treg cells in the colon of the mice to which vancomycin was administered was markedly decreased in comparison with that of the control. In contrast, no influence was observed on the number of Treg cells of the mice to which polymyxin B was administered. Those facts suggested that Gram-positive commensal bacteria played a major role in accumulation of Treg cells.

(Example 6)

[0122] A recent report has suggested that spore-forming bacteria play an important role in intestinal T cells response (see V. Gaboriau-Routhiau et al., *Immunity* 31, 677 (Oct 16, 2009)). In this respect, fecal microorganisms (spore-forming fraction) resistant to 3% chloroform were orally administered to GF mice, which were then analyzed for the ratio of Foxp3⁺ cells in the CD4⁺ cell group ([%] Foxp3⁺ in CD4). Fig. 31 shows the obtained results. Note that, in Fig. 31, "GF" indicates the result of GF mice, and "+chloro" indicates the result of the GF mice to which the chloroform-treated feces were administered. Meanwhile, ** indicates that "P < 0.001."

[0123] As is apparent from the results shown in Fig. 31, three weeks after the administration of the chloroform-treated feces, the number of Treg cells in the administered mice was markedly increased to the same level as those of the SPF mice and the GF mice to which the untreated feces was forcibly administered (see Figs. 7 and 11).

[0124] Accordingly, considering the results shown in Example 5 in combination, it was revealed that the specific components of the indigenous microbiota were highly likely to belong to the Gram-positive group, and that the spore-forming fraction played an important role in the induction of Treg cells.

(Example 7)

[0125] Next, the species of the intestinal microbiota which induced the accumulation of Treg cells in the colon as suggested in Examples 4 to 6 were identified. Specifically, segmented filamentous bacteria (SFB), 16 strains of the *Bacteroides* spp. (Bactero. (6 strains of *B. vulgatus*, 7 of the *B. acidifaciens* group 1, and 3 of the *B. acidifaciens* group 2)), 3 strains of the *Lactobacillus* (Lacto. (*L. acidophilus*, *L. fermentum*, and *L. murinum*)), and 46 strains of *Clostridium* spp. (Clost., refer to "Itoh, K., and Mitsuoka, T. Characterization of clostridia isolated from faeces of limited flora mice and their effect on caecal size when associated with germ-free mice. *Lab. Animals* 19: 111-118 (1985)"), or microbiota collected from mice (SPF) bred under a conventional environment was orally administered to GF-Balb/c mice or GF-IQI mice. The mice were maintained in vinyl isolators for three weeks. Then, CD4 cells were isolated from the colon and the small intestine of these mice. The numbers of Treg cells in the colon and the small intestine were analyzed by flow cytometry.

[0126] Fig. 13 shows FACS dot-plots obtained when a gate was set on CD4⁺ cells of the Balb/c mice. Fig. 14 shows the ratio of Foxp3⁺ cells in CD4⁺ cells of each mouse.

[0127] Note that, the bacteria belonging to the genus *Clostridium* are classified by sequencing of 16S rRNA gene, as follows. Specifically, the 16S rRNA genes of the bacteria were amplified by PCR using 16S rRNA gene-specific primer pairs: 5'-AGAGTTTGATCMTGGCTCAG-3' (SEQ ID NO: 19) and 5'-ATTACCGCGGCKGCTG-3' (SEQ ID NO: 20) (see T. Aebischer et al., *Vaccination prevents Helicobacter pylori-induced alterations of the gastric flora in mice. FEMS Immunol. Med. Microbiol.* 46,221-229(2006)). The 1.5-kb PCR product was then introduced into pCR-Blunt Vector. The inserts were sequenced and aligned using the ClustalW software program. The resulting sequences of 16S rRNA genes derived from strain 1-41 of 46 strains of *Clostridium* spp. were shown in SEQ ID NO: 21-61. Phylogenetic tree which was constructed by the neighbor-joining method with the resulting sequences of the 41 strains of *Clostridium* and those of known bacteria obtained from Genbank database using Mega software was shown in Fig.49.

[0128] As is apparent from the results shown in Figs. 13 and 14, no effect on the number of the Treg cells in the colon was observed in the GF mice in which the segmented filamentous bacteria (SFB) were colonized (refer to Fig. 14). Moreover, mice in which the cocktail of three strains of *Lactobacillus* was colonized gave similar results (refer to Fig. 14). On the other hand, it was shown that the accumulation of Foxp3⁺ cells in the colonic lamina propria was strongly induced in the mice in which 46 strains of *Clostridium* spp. were colonized. Importantly, such accumulation was promoted irrespective of the genetic backgrounds of the mice, and led to the increase in number similar to that in the SPF mice although intestinal microbiota of only a single genus were colonized. It was also shown that the colonization of the *Clostridium* did not change the number of Treg cells in the small intestinal lamina propria (refer to Fig. 14). Note that, when the 16 strains of *Bacteroides* spp. were colonized, the number of Treg cells in the colon was increased significantly. However, the extent of the increase varied depending on the genetic background of the mice in which the bacteria were colonized (refer to Figs. 13 and 14).

(Example 8)

[0129] Next, CD4 expression, Foxp3 expression, and Helios expression in LP lymphocytes of the thymuses and the colons of SPF mice, GF mice, *Lactobacillus*-colonized mice, and *Clostridium*-colonized mice were analyzed by flow cytometry.

Figs. 32 and 33 show the obtained results. Note that, in Figs. 32 and 33, "GF" or "Germ Free" indicates the results of the GF mice, "SPF" indicates the results of the SPF mice, "Lacto." indicates the results of the *Lactobacillus*-colonized mice, and "Clost." indicates the results of the *Clostridium*-colonized mice. In Fig. 32, the vertical axis represents the ratio

of Helios⁺ cells in the Foxp3⁺ cell group ([%] Helios⁺ in Foxp3⁺), and ** indicates that "P < 0.001."

[0130] As is apparent from the results shown in Figs 32 and 33, most Foxp3⁺ cells found in the SPF mice or the Clostridium-colonized mice did not express Helios. Note that Helios is a transcription factor known to be expressed in thymic-derived natural Treg cells (see A. M. Thornton et al., J Immunol 184, 3433 (Apr 1, 2010)). Accordingly, it was suggested that most of the Treg cells in the SPF mice and the Clostridium-colonized mice were Treg cells induced in peripheral portions, i.e., so-called iTreg cells.

(Example 9)

[0131] Next, it was investigated whether or not the colonization of the Clostridium or the like had an influence on other T cells. Specifically, SFB, 16 strains of Bacteroides spp. (Bactero.), 46 strains of Clostridium spp. (Clost.), or microbiota collected from mice bred under a conventional environment (SPF) was colonized in GF ICI mice. Three weeks later, lymphocytes in the colonic lamina propria were isolated from these mice, and stimulated with PMA (50 ng/ml) and ionomycin (1 ug/ml) for four hours in the presence of Golgistop (BD Bioscience). After the stimulation was given, intracellular cytokines were stained by using an anti-IL-17 PE antibody (TC11-18H10) and an anti-IFN- γ FITC antibody (BD Bioscience) in accordance with the manual of a cytofix/cytoperm kit (BD Bioscience). Then, the ratio of IFN- γ ⁺ cells or IL-17⁺ cells in CD4⁺ leucocytes was analyzed by flow cytometry. Figs. 15 and 16 show the obtained results. Note that, in Figs. 15 and 16, each white circle represents the absolute number of CD4⁺ IFN- γ ⁺ cells or the absolute number of CD4⁺ IL-17⁺ cells in each individual mouse, and the error bars represent standard deviations (SD). As is apparent from the results shown in Figs. 15 and 16, the colonization of the Clostridium did not have any influence on Th1 cells (CD4⁺ IFN- γ ⁺ cells) in the colon, and caused only a slight increase of Th17 cells (CD4⁺ IL-17⁺ cells). Accordingly, it was suggested that the genus Clostridium was a genus of bacteria which specifically induced Treg cells.

(Example 10)

[0132] It has been reported that 46 strains of Clostridium spp. exert an influence on the accumulation of CD8⁺ intestinal tract intraepithelial lymphocytes (IELs) in the colon. Accordingly, it is conceivable that Clostridium regulates the immune system in various aspects, and that Clostridium exhibits a marked ability to induce and maintain Treg cells especially in the colon, as described above. In addition, a kind of cytokines, transforming growth factor- β (TGF- β), is known to play an important role in regulation of Treg cell generation.

[0133] In this respect, it was examined whether or not the colonization of Clostridium provided a colonic environment rich in TGF- β . Specifically, first, the whole colons of GF mice, Clostridium-colonized mice, and Lactobacillus-colonized mice were cultured for 24 hours, and the culture supernatants thereof were measured for the concentration of active TGF- β (TGF- β 1) by ELISA (the number of mice analyzed was four per group). Fig. 34 shows the obtained results. Note that, in Fig. 34, "GF" indicates the result of the GF mice, "Clost." indicates the result of the Clostridium-colonized mice, and "Lacto." indicates the result of Lactobacillus-colonized mice. Meanwhile, * indicates that "P < 0.02," and ** indicates that "P < 0.001."

[0134] As is apparent from the results shown in Fig. 34, the amount of TGF- β produced in the colons of the Clostridium-colonized mice was significantly larger than those of the GF mice and the Lactobacillus-colonized mice.

[0135] Next, intestinal epithelial cells (IECs) of GF mice and Clostridium-colonized mice were cultured for 24 hours, and the culture supernatants thereof were measured for the concentration of active TGF- β (TGF- β 1) by ELISA (the number of mice analyzed was four per group). Fig. 35 shows the obtained results. Note that, in Fig. 35, "GF" indicates the result of the GF mice, and "Clost." indicates the result of the Clostridium-colonized mice. Meanwhile, ** indicates that "P < 0.001."

[0136] As is apparent from the results shown in Fig. 35, TGF- β was detected in the culture supernatant of the IECs isolated from the Clostridium-colonized mice, whereas no TGF- β was detected in the culture supernatant of the IECs isolated from the GF mice.

[0137] Next, as described above, splenic CD4⁺ T cells were cultured for five days together with a 50% conditioned medium in which IECs isolated from the GF mice or the Clostridium-colonized mice were cultured, and with the anti-CD3 antibody, in the presence or absence of an anti-TGF- β antibody. Then, the T cells were collected, and analyzed for expression of Foxp3 by real-time RT-PCR. Fig. 36 shows the obtained results. Note that, in Fig. 36, "Medium" indicates the result of a medium in which no cells were cultured, "GF" indicates the result of the conditioned medium in which the IECs of the GF mice were cultured, "Clost." indicates the result of the conditioned medium in which the IECs of the Clostridium-colonized mice were cultured, and "Clost. + α TGF β " indicates the result of the conditioned medium to which the anti-TGF- β antibody was added and in which the IECs of the Clostridium-colonized mice were cultured. Meanwhile, ** indicates that "P < 0.001."

[0138] As is apparent from the results shown in Fig. 36, when the culture supernatant of the IECs derived from the Clostridium-colonized mice was added to the splenic CD4⁺ T cells, the differentiation into Foxp3-expressing cells was

accelerated. Meanwhile, the differentiation into the Treg cells was inhibited by the anti-TGF- β antibody.

[0139] Moreover, the expression of MMP2, MMP9, and MMP13, which are thought to contribute to the activation of latent TGF- β was investigated. The expression of indoleamine 2,3-dioxygenase (IDO), which is thought to be involved in the induction of Treg cells, was also investigated. Specifically, 46 bacterial strains of the genus *Clostridium* (Clost.), or three bacterial strains of the genus *Lactobacillus* (Lacto.) were orally administered to C57BL/6 germ-free mice. Three weeks after the administration, IECs were collected, and analyzed for relative mRNA expression levels of MMP2, MMP9, MMP13, and IDO genes by real-time RT-PCR (the number of mice analyzed was three per group). Figs. 37 to 40 show the obtained results. Note that, in Figs. 37 to 40, "GF#1 to 3" indicate the results of GF mice, "Clost.#1 to 3" indicate the results of the *Clostridium*-colonized mice, and "Lacto.#1 to 3" indicate the results of the *Lactobacillus*-colonized mice.

[0140] For the relationship between the activation of latent TGF- β and the above-describe MMP, see D'Angelo et al., J. Biol. Chem. 276, 11347-11353, 2001; Heidinger et al., Biol. Chem. 387, 69-78, 2006; Yu et al., Genes Dev. 14, 163-176, 2000. For the relationship between IDO and the induction of Treg cells, see G. Matteoli et al., Gut 59, 595 (May, 2010).

[0141] As is apparent from the results shown in Figs 37 to 39, in agreement with the production of TGF- β described above, transcription products of the genes encoding MMP2, MMP9, and MMP13 were expressed at higher levels in the IECs derived from the *Clostridium*-colonized mice than those in the GF mice and in the *Lactobacillus*-colonized mice.

[0142] Moreover, as is apparent from the results shown in Fig. 40, IDO was expressed only in the *Clostridium*-colonized mice.

[0143] Accordingly, it was revealed that the *Clostridium* activated the IECs, and led to the production of TGF- β and other Treg cell-inducing molecules in the colon.

(Example 11)

[0144] Next, it was investigated whether or not the Treg cell accumulation induced by the colonization of the *Clostridium* was dependant on signal transmission by pathogen-associated molecular pattern recognition receptors. Specifically, the numbers of Treg cells in the colonic lamina propria of each of SPF mice of *Myd88*^{-/-} (deficient in Myd88 (signaling adaptor for Toll-like receptor)), *Rip2*^{-/-} (deficient in Rip2 (NOD receptor adaptor)), and *Card9*^{-/-} (deficient in Card9 (essential signal transmission factor for Dectin-1 signal transmission)) were examined. In addition, *Clostridium* spp. were caused to be colonized in the *Myd88*^{-/-} GF mice, and the change in the number of Treg cells was investigated. Figs. 17 and 18 show the obtained results. As is apparent from the results shown in Figs. 17 and 18, the number of Treg cells of each kind of the SPF mice deficient in the associated factors of the pathogen-associated molecular pattern recognition receptors did not change relative to that of wild-type mice of the same litter, which served as a control. In addition, it was found that also when *Clostridium* spp. were colonized in GF mice deficient in Myd88, the accumulation of Treg cells in the colonic lamina propria was induced. Accordingly, it has been suggested that the mechanism of inducing the accumulation of Treg cells in the colonic lamina propria relies not on activation of recognition pathway for major pathogen-associated molecular patterns as is caused by most of bacterium, but on specific commensal bacterial species.

(Example 12)

[0145] Intestinal tract Foxp3⁺ Treg cells are known to exert some immunosuppressive functions through IL-10 production (refer to Non-Patent Document 9). Meanwhile, animals having CD4⁺ Foxp3⁺ cells from which IL-10 is specifically removed are known to develop inflammatory bowel disease (refer to Non-Patent Document 18). In this respect, first, the expression of IL-10 in lymphocytes of various tissues was examined. Specifically, lymphocytes were isolated from various tissues of SPF *Il10*^{venus} mice, and the expression of CD4 and the expression of Venus were analyzed by flow cytometry. Fig. 19 shows the obtained results. Note that each numeric value in Fig. 19 represents the ratio of cells within the corresponding one of regions divided into four.

[0146] Moreover, lymphocytes in the colonic lamina propria were isolated from *Il10*^{venus} mice, and the expression of T cell receptor β chain (TCR β) on the surfaces of the cells was detected by FACS. Fig. 20 shows the obtained results (FACS dot-plots obtained when a gate was set on CD4⁺ cells). Note that each numeric value in Fig. 20 represents the ratio of cells within the corresponding one of regions divided into four.

[0147] Furthermore, lymphocytes in the colonic lamina propria were isolated from *Il10*^{venus} mice. The lymphocytes were stimulated with PMA (50 ng/ml) and ionomycin (1 μ g/ml) for four hours in the presence of Golgistop (BD Bioscience). Then, after the stimulation was given, intracellular cytokines were stained by using an anti-IL-17 PE antibody, an anti-IL-4 APC antibody (11B11), and an anti-IFN- γ FITC antibody (BD Bioscience) in accordance with the manual of a cytofix/cytoperm kit (BD Bioscience). Fig. 21 shows the obtained results (FACS dot-plots obtained when a gate was set on CD4⁺ cells).

Note that each numeric value in Fig. 21 represents the ratio of cells within the corresponding one of regions divided into four.

[0148] In addition, Foxp3⁺ CD4⁺ cells and Foxp3⁻ CD4⁺ cells were isolated from the spleen (Spl) of Foxp3^{eGFP} reporter

mice, and Venus⁺ cells were isolated from the colonic lamina propria and the small intestine (SI) lamina propria of Il10^{venus} mice. Then, the obtained cells were analyzed in terms of the expression of predetermined genes. The gene expression was analyzed by real-time RT-PCR using a Power SYBR Green PCR Master Mix (Applied Biosystems) and an ABI 7300 real time PCR system (Applied Biosystems). Here, the value for each cell was normalized for the amount of GAPDH. Fig. 22 shows the obtained results. Note that in Fig. 22 the error bars represent standard deviations. As is apparent from the results shown in Figs. 19 to 22, almost no Venus⁺ cells (IL-10-producing cells) were detected in the cervical lymph nodes (peripheral lymph nodes), thymus, peripheral blood, lung, and liver of mice kept under the SPF conditions. Meanwhile, in the spleen, Peyer's patches, and mesenteric lymph nodes thereof, Venus⁺ cells were slightly detected (refer to Fig. 19). On the other hand, many Venus⁺ cells were found in the lymphocytes in the small intestine lamina propria and colonic lamina propria. In addition, most of the Venus⁺ cells in the intestines were positive for CD4, and also positive for T cell receptor β chain (TCR β) (refer to Figs. 19 and 20). Moreover, it was found that the Venus⁺ CD4⁺ T cells expressed Foxp3 and other Treg cell-associated factors such as a cytotoxic T-Lymphocyte antigen (CTLA-4) and a glucocorticoid-induced TNFR-associated protein (GITR) although the Venus⁺ CD4⁺ T cells showed none of the phenotypes of Th2 (IL-4-producing) and Th17 (IL-17-producing) (refer to Figs. 21 and 22). In addition, it was shown that the expression level of CTLA-4 in the intestinal Venus⁺ cells was higher than that in the splenic GFP⁺ Treg cells isolated from the Foxp3^{eGFP} reporter mice (refer to Fig. 22).

(Example 13)

[0149] Venus⁺ cells can be classified into at least two subsets, namely, Venus⁺ Foxp3⁺ double positive (DP) Treg cells and Venus⁺ Foxp3⁻ Treg cells on the basis of intracellular Foxp3 expression. Cells of the latter subset correspond to type 1 regulatory T cells (Tr1) (refer to Non-Patent Documents 8 and 9). In this respect, the Venus⁺ cells (IL-10-producing cells) observed in Example 8 were investigated in terms of the expression of Foxp3. Specifically, the expression of CD4, Foxp3, and Venus in the lamina propria of the colon and the lamina propria of the small intestine of Il10^{venus} mice kept under GF or SPF conditions was analyzed by FACS, and the numbers of Venus⁺ cells in the intestinal tract lamina propria were compared between SPF and GF Il10^{venus} mice. Fig. 23 shows the obtained results (dot-plots obtained when a gate was set on CD4⁺ cells).

[0150] In addition, the intracellular expression of Venus and Foxp3 in CD4 cells in various tissues of SPF Il10^{venus} mice was analyzed by flow cytometry. Fig. 24 shows the obtained results (dot-plots obtained when a gate was set on CD4⁺ cells). Note that each numeric value in Fig. 24 represents the ratio of cells within the corresponding one of regions divided into four.

[0151] Moreover, in order to investigate whether or not the presence of commensal bacteria had any influence on the expression of IL-10 in regulatory cells in the gastrointestinal tracts, germ-free (GF) Il10^{venus} mice were prepared. Then, predetermined species of bacteria were caused to be colonized in the obtained GF Il10^{venus} mice. Three weeks after the species of bacteria were colonized, a CD4⁺ cell group (V⁺F⁻, Venus⁺ Foxp3⁻ cells; V⁺F⁺, Venus⁺ Foxp3⁺ cells; and V⁻F⁺, Venus⁻ Foxp3⁺ cells) in which Foxp3 and/or Venus were expressed in the colon and the small intestine was analyzed by flow cytometry. Fig. 25 shows dot-plots obtained when a gate was set on colonic CD4⁺ cells, and Figs. 26 and 27 show the ratios in the CD4⁺ cell group of each mouse. Note that each numeric value in Fig. 25 represents the ratio of cells within the corresponding one of regions divided into four. Meanwhile, the error bars in Figs. 26 and 27 represent standard deviations, * indicates that "P < 0.02," and ** indicates that "P < 0.001."

[0152] Moreover, in order to check whether or not the presence of commensal bacteria had any influence on the expression of IL-10 in regulatory cells in the gastrointestinal tracts, antibiotics were orally given with water to five or six Il10^{venus} mice per group for 10 weeks. The following antibiotics were used in combination.

ampicillin (A; 500 mg/L Sigma)

vancomycin (V; 500 mg/L NACALAI TESQUE, INC.)

metronidazole (M; 1 g/L NACALAI TESQUE, INC.)

neomycin (N; 1 g/L NACALAI TESQUE, INC.)

[0153] Then, CD4 and Foxp3 of lymphocytes in the lamina propria of the colon, the lamina propria of the small intestine (SI) mesenteric lymph nodes (MLN), and Peyer's patches (PPs) were stained with antibodies, and analyzed by FACS. The results were obtained from two or more independent experiments which gave similar results. Fig. 28 shows the obtained results (the ratio of Venus⁺ cells in CD4⁺ cells in each sample). Note that each white circle in Fig. 28 represents an individual sample, each horizontal bar represents an average value, * indicates that "P < 0.02," and "AVMN" represents the kinds of the administered antibiotics by using the first letters of the antibiotics.

[0154] As is apparent from the results shown in Figs. 23 and 24, it was shown that the small intestinal lamina propria was rich in Venus⁺ Foxp3⁻ cells, namely, Tr1-like cells, and that the Venus⁺ Foxp3⁺ DP Treg cells were present at a high frequency in the colon of the SPF mice (refer to Figs. 23 and 24). In contrast, although sufficient numbers of Foxp3⁺ cells were observed also in other tissues, the expression of Venus was not observed in almost all of the cells (refer to Fig. 24).

[0155] In addition, as is apparent from the results shown in Figs. 23 and 25 to 28, it was shown that all regulatory T cell fractions of Venus⁺ Foxp3⁻, Venus⁺ Foxp3⁺, and Venus⁻ Foxp3⁺ in the colon significantly decreased under the GF conditions (Figs. 23 and 26 to 27). Moreover, similar decrease in Venus⁺ cells was observed also in the SPF IL10^{Venus} mice treated with the antibiotics (refer to Fig. 28).

[0156] Moreover, as is apparent from the results shown in Figs. 25 to 27, the colonization of *Clostridium* spp. strongly induced all regulatory T cell fractions of Venus⁺ Foxp3⁻, Venus⁺ Foxp3⁺, and Venus⁻ Foxp3⁺ in the colon, and the degrees of the induction thereof were equal to those in the SPF mice (refer to Figs. 25 and 27). In addition, it was found that the colonization of the three strains of *Lactobacillus* or the colonization of SFB had an extremely small influence on the number of Venus⁺ and/or Foxp3⁺ cells in the colon (refer to Figs. 25 and 27). Moreover, the colonization of 16 strains of *Bacteroides* spp. also induced Venus⁺ cells, but the influence of the colonization was specific to Venus⁺ Foxp3⁻ Tr1-like cells (refer to Figs. 25 and 27). On the other hand, it was found that none of the bacterial species tested exerted any significant influence on the number of IL-10-producing cells in the small intestinal lamina propria (refer to Fig. 26).

[0157] Hence, it was shown that the genus *Clostridium* colonized in the colon or a physiologically active substance derived from the bacteria provided a signal for inducing the accumulation of IL-10⁺ regulatory T cells in the colonic lamina propria or the expression of IL-10 in T cells. Meanwhile, it was shown that the number of Venus⁺ cells in the small intestine was not significantly influenced by the situation where no commensal bacteria were present or commensal bacteria were decreased (refer to Figs. 23 and 26 to 28) and that IL-10⁺ regulatory cells (Tr1-like cells) accumulated in the small intestinal lamina propria independently of commensal bacteria.

(Example 14)

[0158] It was investigated whether or not Venus⁺ cells induced by the genus *Clostridium* had an immunosuppressive function similar to that of Venus⁺ cells in the colon of SPF mice. Specifically, CD4⁺ CD25⁻ cells (effector T cells, Teff cells) isolated from the spleen were seeded in a flat-bottomed 96-well plate at 2×10^4 /well, and cultured for three days together with 2×10^4 splenic CD11c⁺ cells (antigen-presenting cells) subjected to 30 Gy radiation irradiation treatment, 0.5 μ g/ml of an anti-CD3 antibody, and a lot of Treg cells. In addition, for the last six hours, the CD4⁺ CD25⁻ cells were cultured, with [³H]-thymidine (1 μ Ci/well) was added thereto. Note that, Treg cells used in Example 14 were CD4⁺ GFP⁺ T cells isolated from the spleen of Foxp3^{eGFP} reporter mice, or CD4⁺ Venus⁺ T cells in the colonic lamina propria of GF IL10^{Venus} mice in which *Clostridium* spp. were colonized or SPF IL10^{Venus} mice. Then, proliferation of the cells was determined based on the uptake amount of [³H]-thymidine, and represented by a count per minute (cpm) value.

[0159] As is apparent from the results shown in Fig. 29, Venus⁺ CD4⁺ cells of the mice in which the genus *Clostridium* was colonized suppressed in vitro proliferation of CD25⁻ CD4⁺ activated T cells. The suppression activity was slightly inferior to that of GFP⁺ cells isolated from the Foxp3^{eGFP} reporter mice, but equal to that of Venus⁺ cells isolated from the SPF IL10^{Venus} mice. Accordingly, it has been shown that the genus *Clostridium* induces IL-10-expressing T cells having sufficient immunosuppressive activities, and thereby plays a critical role in maintaining immune homeostasis in the colon.

(Example 15)

[0160] Next, the influence, on the local immune response, of the colonization of a large number of *Clostridium* and the resultant proliferation of Treg cells was investigated.

<Dextran Sulfate Sodium (DSS)-Induced Colitis Model>

[0161] First, the DSS-induced colitis model was prepared as described above, and the influence, on the model mice, of the inoculation of the *Clostridium* and the proliferation of Treg cells was investigated. Specifically, control mice and *Clostridium*-inoculated mice were treated with 2% DSS, then observed and measured for six days for the body weight loss, the hardness of stool, and bleeding, and then were evaluated numerically. In addition, on day 6, the colons were collected, dissected, and analyzed histologically by HE staining. Figs. 41 to 43 show the obtained results. Note that, in Figs. 41 to 43, "SPF+Clost." or "SPF+Clost.#1 to 3" indicate the results of C57BL/6 mice inoculated with a fecal suspension of *Clostridium*-colonized mice, and grown in a conventional environment for six weeks, and "SPF" or "SPF#1 to 3" indicate the results of C57BL/6 mice (control mice) grown in a conventional environment for six weeks without being inoculated with the fecal suspension. In addition, in Fig. 41, the vertical axis "Disease score" represents the disease activity index (DAI) described above, and the horizontal axis "post 2% DSS (d)" represents the days elapsed after the initial administration of 2% DSS to the mice. Moreover, in Fig. 41, * indicates that "P < 0.02," and ** indicates that "P < 0.001." Meanwhile, Treg cells induced by regulatory dendritic cells are known to play a preventive role in a DSS-induced colitis model (see S. Manicassamy et al., Science 329, 849 (Aug 13, 2010)).

[0162] As is apparent from the results shown in Figs. 41 to 43, the symptoms of the colitis such as body weight loss

and rectal bleeding were significantly suppressed in the mice having a large number of Clostridium (hereinafter also referred to as "Clostridium-abundant mice") in comparison with the control mice (see Fig. 41). All the features typical for colonic inflammation, such as shortening of the colon, edema, and hemorrhage, were observed markedly in the control mice in comparison with the Clostridium-abundant mice (see Fig. 42). Moreover, histological features such as mucosal erosion, edema, cellular infiltration, and crypt loss were less severe in the DSS-treated Clostridium-abundant mice than in the control mice (see Fig. 43).

<Oxazolone-Induced Colitis Model>

[0163] Next, the oxazolone-induced colitis model was prepared as described above, and the influence, on the model mice, of the inoculation of Clostridium and the proliferation of Treg cells was investigated. Specifically, control mice and Clostridium-inoculated mice were sensitized with oxazolone, and subsequently the inside of the rectums thereof were treated with a 1% oxazolone/50% ethanol solution. Then, the body weight loss was observed and measured. In addition, the colons were dissected, and analyzed histologically by HE staining. Figs. 44 and 45 show the obtained results. Note that, in Figs. 44 and 45, "SPF+Clost." indicates the results of C57BL/6 mice (Clostridium-abundant mice) inoculated with a fecal suspension of Clostridium-colonized mice, and grown in a conventional environment for six weeks, and "SPF" indicates the results of C57BL/6 mice (control mice) grown in a conventional environment for six weeks without being inoculated with the fecal suspension. In addition, in Fig. 44, the vertical axis "Weight (% of initial)" represents the body weight after the administration of 1% oxazolone where the body weight before the administration was taken as 100%, and the horizontal axis "post 1% oxazolone (d)" represents the days elapsed after the administration of 1% oxazolone to the mice. Meanwhile, it is known that Th2-type T cells are involved in colitis induced by oxazolone. (see M. Boirivant, I. J. Fuss, A. Chu, W. Strober, J Exp Med 188, 1929 (Nov 16, 1998)).

[0164] As is apparent from the results shown in Figs. 44 and 45, the colitis proceeded along with persistent body weight loss in the control mice. Meanwhile, the body weight loss of the Clostridium-abundant mice was reduced (see Fig. 44). In addition, it was also revealed that portions having histological diseases such as mucosal erosion, edema, cellular infiltration, and hemorrhage were reduced in the colon of the Clostridium-abundant mice (see Fig. 45).

(Example 16)

[0165] Next, the influence, on the systemic immune response (systemic IgE production), of the colonization of a large number of Clostridium and the resultant proliferation of Treg cells was investigated. Specifically, as described above, control mice and Clostridium-inoculated mice were immunized by administering alum-absorbed ovalbumin (OVA) twice at a 2-week interval. Then, sera were collected from these mice, and the OVA-specific IgE level thereof was investigated by ELISA. In addition, splenic cells were collected from the mice in each group, and IL-4 and IL-10 production by in-vitro OVA restimulation was investigated. Figs. 46 to 48 show the obtained results. Note that, in Figs. 46 to 48, "SPF+Clost." indicates the results of BALB/c SPF mice (Clostridium-abundant mice) inoculated with a fecal suspension of Clostridium-colonized mice, and grown in a conventional environment, "SPF" indicates the results of BALB/c SPF mice (control mice) grown in a conventional environment without being inoculated with the fecal suspension, and ** indicates that "P < 0.001." Meanwhile, in Fig. 46, the vertical axis "OVA-specific IgE (ng/ml)" represents the concentration of OVA-specific IgE in the sera. Moreover, in Fig. 46, the horizontal axis represents the days elapsed after the initial administration of the alum-absorbed ovalbumin to the Clostridium-abundant mice or the control mice (4-week old), and "OVA+Alum" indicates the timing of the administration of the alum-absorbed ovalbumin. In addition, in Figs. 47 and 48, "OVA" on the horizontal axis indicates the results in the case where the in-vitro OVA restimulation was performed, and "-" indicates the results in the case where no in-vitro OVA restimulation was performed. Moreover, in Figs. 47 and 48, the vertical axes "IL-4 (pg/ml)" and "IL-10 (pg/ml)" show the IL-4 concentration and the IL-10 concentration in culture supernatants of splenic cells, respectively.

[0166] As is apparent from the results shown in Figs. 46 to 48, the IgE level was significantly lower in the Clostridium-abundant mice than in the control mice (see Fig. 46). Moreover, the IL-4 production by the OVA restimulation was reduced (see Fig. 47) and the IL-10 production thereby was increased (see Fig. 48) in the splenic cells of the Clostridium-abundant mice sensitized with OVA and alum, in comparison with those of the control mice.

[0167] Accordingly, in consideration of the results shown in Example 15 in combination, it has been revealed that the induction of Treg cells by Clostridium in the colon plays an important role in local and systemic immune responses.

(Example 17)

[0168] Next, GF Balb/c were colonized with three strains of Clostridium belonging to cluster IV (strains 22, 23 and 32 listed in Fig. 49). Three weeks later, colonic Foxp3⁺ Treg cells were analyzed by FACS. Fig. 50 shows the obtained results. As is apparent from the results shown in Fig. 50, gnotobiotic mice colonized with three strains of Clostridium

showed an intermediate pattern of Treg induction between GF mice and mice inoculated with all 46 strains.

(Example 18)

[0169] Next, it was investigated whether or not a spore-forming (for example, a chloroform resistant) fraction of a fecal sample obtained from humans had the effect of inducing proliferation or accumulation of regulatory T cells similar to the spore-forming fraction of the fecal sample obtained from mice.

[0170] Specifically, human stool from a healthy volunteer (Japanese, male, 29years old) was suspended with phosphate-buffered saline (PBS), mixed with chloroform (final concentration 3%), and then incubated in a shaking water bath for 60 min. After evaporation of chloroform by bubbling with N₂ gas, the aliquots containing chloroform-resistant (for example, spore-forming) fraction of human intestinal bacteria were orally inoculated into germ-free (GF) mice (IQL, 8 weeks old). The treated mice were kept in a vinyl isolator for 3 weeks. The colon was collected and opened longitudinally, washed to remove fecal content, and shaken in Hanks' balanced salt solution (HBSS) containing 5 mM EDTA for 20 min at 37°C. After removing epithelial cells and fat tissue, the colon was cut into small pieces and incubated with RPMI1640 containing 4% fetal bovine serum, 1 mg/ml collagenase D, 0.5 mg/ml dispase and 40µg/ml DNase I (all manufactured by Roche Diagnostics) for 1 hour at 37°C in a shaking water bath. The digested tissue was washed with HBSS containing 5 mM EDTA, resuspended in 5 ml of 40% Percoll (manufactured by GE Healthcare) and overlaid on 2.5 ml of 80% Percoll in a 15-ml Falcon tube. Percoll gradient separation was performed by centrifugation at 780 g for 20 min at 25°C. The interface cells were collected and suspended in staining buffer containing PBS, 2% FBS, 2 mM EDTA and 0.09% NaN₃ and stained for surface CD4 with Phycoerythrin-labeled anti-CD4 Ab (RM4-5, manufactured by BD Biosciences). Intracellular staining of Foxp3 was performed using the Alexa647-labeled anti-Foxp3 Ab (FJK-16s, manufactured by eBioscience) and Foxp3 Staining Buffer Set (manufactured by eBioscience). The percentage of Foxp3positive cells within the CD4 positive lymphocyte population was analyzed by flow cytometry. Figs. 51 and 52 show the obtained results.

[0171] In figures, representative histograms (Fig. 51) and combined data (Fig. 52) for Foxp3 expression by CD4 positive lymphocytes from GFmice (GF) or GF mice gavaged with chloroform-treated human stool (GF+Chloro.) are shown. In addition, numbers in Fig. 51 indicate the percentages of cells in the gate. Each circle in Fig. 52 represents a separate animal, error bars indicate the SD, and ** indicates that "P < 0.001."

[0172] As is apparent from the results shown in Figs. 51 and 52, it was found that also when the spore-forming (for example, the chloroform resistant) fraction of human intestinal bacteria was colonized in GF mice, the accumulation of Foxp3⁺ regulatory (Treg) cells in the colonic lamina propria of the mice was induced.

[0173] Next, it was investigated what species of bacteria grew by gavaging with chloroform-treated human stool.

[0174] Specifically, using a QIAamp DNA Stool mini kit (manufactured by QIAGEN), bacterial genomic DNA was isolated from the human stool from a healthy volunteer as described above (human stool) or fecal pellets from GFmice gavaged with chloroform-treated human stool (GF+Chloro.). Quantitative PCR analysis was carried out using a Light-Cycler 480 (manufactured by Roche). Relative quantity was calculated by the ΔCt method and normalized to the amount of total bacteria, dilution, and weight of the sample. The following primer sets were used:

total bacteria

5'-GGTGAATACGTTCCCGG-3' (SEQ ID NO: 62) and
5'-TACGGCTACCTTGTTACGACTT-3' (SEQ ID NO: 63)

Clostridium cluster XIVa (Clostridium coccoides subgroup)

5'-AAATGACGGTACCTGACTAA-3' (SEQ ID NO: 64) and
5'-CTTTGAGTTTCATTCTTGCGAA-3' (SEQ ID NO: 65)

Clostridium cluster IV (Clostridium leptum)

5'-GCACAAGCAGTGGAGT-3' (SEQ ID NO: 66) and
5'-CTTCTCCGTTTTGTCAA-3' (SEQ ID NO: 24)

Bacteroides

5'-GAGAGGAAGGTCCCCCAC-3' (SEQ ID NO: 67) and
5'-CGCTACTTGGCTGGTTCAG-3' (SEQ ID NO: 68).

[0175] Fig. 53 shows the obtained results.

[0176] As is apparent from the results shown in Fig. 53, mice gavaged with chloroform-treated human stool exhibited high amounts of spore-forming bacteria, such as Clostridium clusters XIVa and IV, and a severe decrease of non-spore-forming bacteria, such as Bacteroides, compared with the human stool before chloroform treatment.

[Industrial Applicability]

[0177] As has been described above, the present disclosure makes it possible to provide an excellent composition for inducing proliferation or accumulation of regulatory T cells (Treg cells) by utilizing bacteria belonging to the genus Clostridium or a physiologically active substance or the like derived from the bacteria. Since the composition of the present invention has immunosuppressive effects, the composition can be used as defined in the claims.

[0178] Healthy individuals can easily and routinely ingest the composition as a food or beverage, such as a health food, to improve their immune functions.

[Sequence Listing]

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SEQ ID NO:21 to 61

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<120> COMPOSITION FOR INDUCING PROLIFERATION OR ACCUMULATION OF REGULATORY T CELLS

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<151> 2010-06-04

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25	agggagcgta ggcggggagga taagttgaat gtgaaatcta tgggctcaac ccatagctgc	600
	gttcaaactg ttcttcttga gtgaagtaga ggagggcgga attcctagt tagcgggtgaa	660
	atgcgtagat attaggagga caccagtggc gaaggcgggc tgctgggctt tactgacgct	720
30	gaggctcgaa agcgtgggta gcaaacagga ttagataccc tggtagtcca cgcggtaaac	780
	gatgattact aggtgtgggt ggactgacct catccgtgcc ggagttaaca caataagtaa	840
35	tccacctggg gagtacggcc gcaaggttga aactcaaagg aattgacggg ggcccgcaca	900
	agcagtggag tatgtggttt aattcgacgc aacgcgaaga acctaccag gtcttgacat	960
	cgagtgcgg acatagagat atgtctttcc ttcgggacac gaagacaggt ggtgcatggt	1020
40	tgctcgtcagc tcgtgtcgtg agatgttggg ttaagtcccg caacgagcgc aacccttacc	1080
	attagttgct acgcaagagc actctaattg gactgccgtt gacaaaacgg aggaaggtgg	1140
	ggatgacgtc aaatcatcat gcccttatg acctgggcga cacacgtact acaatggcgg	1200
45	tcaacagagg gaggcaaagc cgcgaggcag agcaaaccct taaaagccgt ctcagttcgg	1260
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50	ccgcgggtgaa tacgttcccg ggccttgtag acaccgcccg tcacaccatg agagccggta	1380
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<210> 26

<211> 1474

<212> DNA

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<213> Clostridium coccooides

<220>

<221> rRNA

<222> (1)..(1474)

<223> 16S rRNA coding gene sequence of Clostridium strain 6

<400> 26

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10      agagtttgat catggctcag gatgaacgct ggcgggcgtgc ctaacacatg caagtcgaac      60
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15      taacgcgtgg gcaacctggc ctgtacaggg ggataacact tagaaatagg tgctaatacc      180
      gcataacggg ggaagccgca tggcttttcc ctgaaaactc cgggtgtaca ggatgggccc      240
      gcgtctgatt agccagttgg cagggtaacg gcctaccaa gcgacgatca gtagccggcc      300
20      tgagagggcg gacggccaca ctgggactga gacacggccc agactcctac gggaggcagc      360
      agtgggggat attgcacaat ggggggaacc ctgatgcagc gacgccgcgt ggggtgaagaa      420
      gcgcctcggc gcgtaaagcc ctgtcagcag ggaagaaaat gacgggtacct gaagaagaag      480
25      ccccggttaa ctacgtgcca gcagccgcgg taatacgtag gggggcaagc gttatccgga      540
      tttactgggt gtaaaggggg cgagacggc gatgcaagcc aggagtgaag gcccggggcc      600
      caaccccggg actgctcttg ggaactgctg ggctggagtg cagagggcag cggaattcct      660
30      ggtgaaatgc gtagatatca gaagacacgg tgcgaggcgg cctgctgact gactgacgt      720
      tgagccgaag cgtgggggagc aaacaggatt agataccgtg gtagtcacgc cgtaaaccgat      780
35      gattactagg tgtcggggag cagagactgc ccggtgccgc agccaacgca ttaagtaatc      840
      cacctgggga gtacgttcgc aagaatgaaa ctcaaaggaa ttgacgggga cccgcacaag      900
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      cagaatgtcg cggtgaatac gttcccgggt cttgtacaca ccgcccgtca caccatggga      1380
      gtcggaaatg cccgaagtca gtgacctaac cgaaaggaag gagctgccga aggtggagcc      1440
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<210> 27

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<211> 1484
<212> DNA
<213> Clostridium leptum

5 <220>
<221> rRNA
<222> (1)..(1484)
<223> 16S rRNA coding gene sequence of Clostridium strain 7

10 <400> 27

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	taacgcgtga gcaatctgcc ttggagtggg gaataacggt tggaaacagc cgctaatacc	180
	gcatgatgcg tctgggaggg atctctctgg acgccaaaga tttatcgctc tgagatgagc	240
20	tcgcgtctga ttagcttggt ggcggggtaa aggccacca aggcgacgat cagtagccgg	300
	actgagaggt tggccggcca cattgggact gagacacggc ccagactcct acgggaggca	360
	gcagtgggga atattgggca atgggcgcaa gcctgaccca gcaacgccgc gtgaaggaag	420
25	aaggctttcg gggtgtaaac ttcttttctg agggacgaag aaagtgacgg tacctcagga	480
	ataagccacg gctaactacg tgccagcagc cgcggttaata cgtaggtggc aagcgttatc	540
30	cggatttatt gggtgtaaag ggcgtgtagg cgggaaagca agtcagatgt gaaaactcag	600
	ggctcaaccc tgagcctgca tttgaaactg tttttcttga gtgctggaga ggcaatcgga	660
	attccgtgtg tagcggtgaa atgcgtagat atacggagga caccagtggc gagcggattg	720
35	ctggacagta ctgacgctga agcgcgaaaag cgtgggagca aacagataga tacctggtag	780
	tcacgcgtaa acgatggata ctaggtgtgg ggggactgac cccctccgtg ccgcagctaa	840
	cgcaataagt atcccacctg gggagtacga tcgcaagggt gaaactcaa ggaattgacg	900
40	ggggcccgca caagcgggtg agtatgtggt ttaattcgaa gcaacgcgaa gaaccttacc	960
	agggcttgac atcctgctaa cgaaccagag atggattagg tgcccttcgg ggaaagcaga	1020
45	gacagggtgg gcatggttgt cgtcagctcg tgtcgtgaga tgttgggtta agtcccgcaa	1080
	cgagcgcaac ccttattggt agttgctacg caagagcact ctagcgagac tgccgttgac	1140
	aaaacggagg aaggtgggga cgacgtcaaa tcatcatgcc ccttacgtcc tgggccacac	1200
50	acgtactaca atggcggcca acaaagagag gcaagaccgc gaggtggagc aaatctcaaa	1260
	aagccgtccc agttcggatc gcaggctgca acccgccctgc gtgaagttgg aatcgctagt	1320
55	aatcgcggat cagcatgccg cggatgaatac gttcccgggc cttgtacaca ccgcccgtca	1380
	caccatgaga gtcgggaaca cccgaagtcc gtagcctaac cgcaaggggg gcgcggccga	1440
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<210> 28
<211> 1483
<212> DNA
<213> Clostridium leptum

<220>
<221> rRNA
<222> (1)..(1483)
<223> 16S rRNA coding gene sequence of Clostridium strain 8

<400> 28

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gtaacgcgtg aggaacctgc cttccagagg gggacaacag ttggaaacga ctgctaatac      180
cgcatgatgc gttggagccg catgactccg acgtcaaaga tttatcgctg gaagatggcc      240
tcgcgtctga ttagctagtt ggtgaggtaa cggccacca aggcgacgat cagtagccgg      300
actgagaggt tggccggcca cattgggact gagatacggc ccagactcct acgggaggca      360
gcagtgggga atattgggca atggacgcaa gtctgaccca gcaacgccgc gtgaaggaag      420
aaggctttcg ggttgtaaac ttcttttaag ggggaagagc agaagacggt accccttgaa      480
taagccacgg ctaactacgt gccagcagcc gcgtaatac gtaggtggca agcgttgtcc      540
ggatttactg ggtgtaaagg gcgtgcagcc ggagagacaa gtcagatgtg aaatccacgg      600
gctcaacccg tgaactgcat ttgaaactgt ttcctttgag tgtcggagag gtaatcggga      660
ttccttgtgt agcgggtgaat gcgtagatat agagaccaca gtgccgacgc cgaataactga      720
cgatactgac ggtgagcgcg aaagcgtggg gagcaaacag gattagatac cctggtagtc      780
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acaataagta tcgcacctgg ggagtacgat cgcaagggtg aaactcaaag gaattgacgg      900
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gggcttgaca tcctgctaac gaagtagaga tacattaggt gcccttcggg gaaagcagag     1020
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cgtaatacaa tggcgggtta caaagggatg caaagccgcg aggcagagcg aaccccaaaa     1260
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	atcgcggatc agcatgccgc ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcac	1380
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5	ggtgggttcg ataattgggg tgaagtcgta acaaggtagc cgt	1483

<210> 29

<211> 1480

<212> DNA

10 <213> Clostridium coccoides

<220>

<221> rRNA

<222> (1)..(1480)

15 <223> 16S rRNA coding gene sequence of Clostridium strain 9

<400> 29

20

25

30

35

40

45

50

55

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	ggagtttgat cctggctcag gatgaacgct ggcggcgtgc ttaacacatg caagtcgaac	60
	gggctcatat tgaaacctag tgatgtatga gttagtggcg gacgggtgag taacgcgtgg	120
5	agaacctgcc gtatactggg ggataacact tagaaatagg tgctaatacc gcataagcgc	180
	acagcttcgc atgaagcagt gtgaaaaact ccggtggat acgatggatc cgcgtctgat	240
10	tagctggttg gcggggtaac agcccaccaa ggcgacgatc agtagccggc ctgagagggg	300
	gaacggccac attgggactg agacacggcc caaactccta cgggaggcag cagtggggaa	360
	tattgcacaa tgggggaaac cctgatgcag cgacgcccg tgagtgaaga agtatttcgg	420
15	tatgtaaagc tctatcagca gggaagaaat actgacctta cggtcagcag acggtacctg	480
	actaagaagc cccgggctaa ctacgtgcc a gcagcccgcg taatacgtag gggcaagcgt	540
	tatccggatt tactgggtgt aaagggggcg cagacggcga tgcaagccag gagtgaagc	600
20	cggggcccaa ccccgggact gctcttgac tgcgtggctg gagtgcagag ggcagcgaat	660
	tcctgtgtag cgtgaatgcg tagattcaga ggacacgtgc gagcgctgc tgactgact	720
	gacgtgagcc cgaagcgtgg ggagcaaaca ggattagata cctggtagtc cacgccgtaa	780
25	acgatgatta ctaggtgtcg gggagcagag actgcccggt gccgcagcca acgcattaag	840
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	catccccctg gatggcccgt aacgggggtca gcctttcggg gcaggggaga cagggtggtgc	1020
	atggttgctg tcagctcgtg tcgtgagatg ttgggttaag tcccgcacag agcgcaaccc	1080
35	ctgcccgcag tagccagcat tttagatggg gactctgcgg ggactgccgg ggacaacccg	1140
	gaggaaggcg gggatgacgt caaatcatca tgccccttat ggcctgggct acacacgtgc	1200
	tacaatggcg ccgacagagg gaggcgaagc ggcgacgcgg agcgaacccc aaaaacggcg	1260
40	tcccagttcg gattgtagtc tgcaacccga ctacatgaag ccggaatcgc tagtaatcgc	1320
	ggatcagaat gccgcggtga atacgttccc gggctcttgta cacaccgccc gtcacaccat	1380
45	gggagccggg aatgcccga gtctgtgacc gaacccgtaa ggggaggggc agccgaaggc	1440
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<210> 30

<211> 1489

<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1489)

<223> 16S rRNA coding gene sequence of Clostridium strain 10

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<400> 30

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	gtaacgcgtg ggcaacctgc cttacacagg gggataacaa ttagaaatga ttgctaatac	180
10	cgcataagac cacgggtactg catggtacag tggtaaaaac tgagggtggg taagatgggc	240
	ccgcgtctga ttaggtagtt ggtggggtag aagcctacca agccgacgat cagtagccga	300
	cctgagaggg cgaccggcca cattgggact gagacacggc ccaaactcct acgggaggca	360
15	gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgagtgagg	420
	aagtatttctg gtatgtaaag ctctatcagc aggggaagaa atgacgggtac ctgactaaga	480
	agcccccggc taactacgtg ccagcagccg cggtaatagc tagggggcaa gcgttatccg	540
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	cccaaccggg gactgcattg aaactgtatt ttttgagggg gtccgaggag gcaagtggaa	660
	tcctgggtag cggtgaaatg gcgtagaatt cagggaggaa caccagtggc ggaaggcgaa	720
25	ttactggacg ataactgacg gtgaggcgcg aagcgtggga gcaaacaaga attagatacc	780
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	cgtcacacca tgagagtcgg gaacacccga agtccgtagc ctaaccgcaa ggagggcgcg	1440
50	gccgaagggtg ggttcgataa ttggggtgaa gtcgtaacaa ggtagccgt	1489

<210> 31

<211> 1490

<212> DNA

<213> Clostridium leptum

55

<220>

<221> rRNA

<222> (1)..(1490)

EP 3 552 613 B1

<223> 16S rRNA coding gene sequence of Clostridium strain 11

<400> 31

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10	taacgcgtga gcaatctgcc ttggagtggg gaataacggt tggaaacagc cgctaatacc	180
	gcatgatgcg tctgggaggc atctctctgg acgccaaaga tttatcgctc tgagatgagc	240
	tcgcgtctga ttagcttggt ggcggggtaa agggccacca aggcgacgat cagtagccgg	300
15	actgagaggt tggccggcca cattgggact gagacacggc ccagactcct acgggaggca	360
	gcagtgggga atattgggca atgggcgcaa gcctgaccca gcaacgccgc gtgaaggaag	420
	aaggctttcg gggtgtaaac ttcttttctg agggacgaag aaagtgacgg tacctcagga	480
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25	ggctcaaccc tgagcctgca tttgaaactg tttttcttga gtgctggaga ggcaatcgga	660
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	gcggattgct ggaacagtaa ctgacgctga ggcgccgaaa gcgtggggag caaacaggat	780
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40	ccgcaacgag cgcaaccctt attgttagtt gctacgcaag agcactctag cgagactgcc	1140
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45	ctcaaaaagc cgtcccagtt cggatcgag gctgcaaccc gcctgctgta agttggaatc	1320
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50	ccgtcacacc atgagagtcg ggaacacccg aagtccgtag cctaaccgca aggggggagc	1440
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<210> 32

<211> 1489

<212> DNA

<213> Clostridium coccoides

<220>

EP 3 552 613 B1

<221> rRNA

<222> (1)..(1489)

<223> 16S rRNA coding gene sequence of Clostridium strain 12

5 <400> 32

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acagcttcgc atgaagcagt gtgaaaaact ccggtgggat acgatggatc cgcgtctgat 240

15 tagctggttg gcggggtaac agcccaccaa ggcgacgatc agtagccggc ctgagagggg 300

gaacggccac attgggactg agacacggcc caaactccta cgggaggcag cagtggggaa 360

tattgcacaa tgggggaaac cctgatgcag cgacgcccgcg tgagtgaaga agtatttcgg 420

20 tatgtaaagc tctatcagca ggaagaaat actgacctta cggtcagcag acggtacctg 480

actaagaagc cccggctaac tacgtgccag cagccgcggg aatacgtagg gggcaagcgt 540

25 tatccggatt tactgggtgt aaaggagcgc tagacggcag cgcaagtctg aagtgaaatc 600

ccatggctta accatggaac tgctttggaa actgtgcagc tggagtgcag gagaggtgag 660

cggaattcct agtgtagcgc tgaatgcgta gatattagag gacaccagtg gcgatgcggc 720

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45 tacacacgtg ctacaatggc gtaaacaaag ggaagcgaga cggtgacgtt aagcaaatcc 1260

caaaaataac gtcccagttc ggattgtagt ctgcaactcg actacatgaa gctggaatcg 1320

ctagtaatcg cgaatcagaa tgctcgcggtg aatacgttcc cgggtcttgt acacaccgcc 1380

50 cgtcacacca tgggagtcgg aaatgcccga agtcagtac ctaaccgaaa ggaaggagct 1440

gccgaagggtg gagccggtaa ctggggtgaa gtcgtaacaa ggtagccgt 1489

<210> 33

<211> 1456

<212> DNA

<213> Clostridium coccoides

EP 3 552 613 B1

<220>

<221> rRNA

<222> (1)..(1456)

<223> 16S rRNA coding gene sequence of Clostridium strain 13

5

<400> 33

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10 gaagcacttg agaacgattc ttcggatgag gactttttgtg actgagtggc ggacgggtga      120
gtaacgcgtg ggtaacctgc cctatacagg gggataacag ttagaaatga ctgctaatac      180
15 cgcataagcg cactaaaacc gcatggttcg gtgtgaaaaa ctgaggtggg ataggatgga      240
cccgcgtctg attagcttgt tgggtgggta acggctcacc aaggcgacga tcagtagccg      300
gcctgagagg gcgaccggcc acattgggac tgagacacgg cccaaactcc tacgggaggc      360
20 agcagtgggg gatattgcac aatgggggga accctgatgc agcgacgccg cgtgggtgaa      420
gaagcgcctc ggcgcgtaaa gccctgtcag cagggaagaa aatgacggta cctgaagaag      480
aagccccggc taactacgtg ccagcagccg cggtaatacg taggggcaag cgttattccg      540
25 ggatttactg ggtgtaaagg gggcgagac ggcgatgcaa gccaggagtg aagccccggg      600
cccacccggg actgctcttg gactgcgtgc tggagtgcag aaggggcagc gatcctgtgt      660
accgtgaatt gcgtagatat cagagacacg ttgcgagcgc tgctgactgc actgacgtga      720
30 gcgaagctgg agcacagata gatactgtag tcagcgtaac gatgatacta gtgtcgggag      780
cagagactgc ccgttgccgc agcccaacgc attagtattc cacttgggga gtacgtttcg      840
35 cagaatgaac ttcaaggaaa tgacggggac ccgcacaagg cggaggagca tgtggtttaa      900
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50 gttcccggtt cttgtacaca ccgcccgtca caccatggga gccgggaatg cccgaagtct      1380
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55 gtaacaaggt agccgt      1456

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<210> 34

<211> 1475

<212> DNA

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<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1475)

<223> 16S rRNA coding gene sequence of Clostridium strain 14

<400> 34

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      gtaacgcgtg aggaacctgc cttccagagg gggacaacag ttggaaacga ctgctaatac      180
15      cgcatgatgc gttggagccg catgactccg acgtcaaaga tttatcgctg gaagatggcc      240
      tcgcgtctga ttagctagtt ggtgaggtaa cggccacca aggcgacgat cagtagccgg      300
20      actgagaggt tggccggcca cattgggact gagatacggc ccagactcct acgggaggga      360
      gcagtgggga atattgggca atggacgcaa gtctgaccca gcaacgccgc gtgaaggaag      420
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25      taagccacgg ctaactacgt gccagcagcc gcggtataac gtaggtggca agcgttgtcc      540
      ggatttactg ggtgtaaagg gcgtgcagcc ggagagacaa gtcagatgtg aaatccacgg      600
      gctcaacccg tgaactgcat ttgaaactgt ttcccttgag tgtcggagag gtaatcgga      660
30      tttccttggt tagcggtgaa tgcgtagata taaggaagga cacagtggcg agcggattac      720
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50      cagttcggat cgcaggctgc aaccgcctg cgtgaagtcg gaatcgctag taatcgcgga      1320
      tcagcatgcc gcggtgaata cgttcccggg ccttgtacac accgcccgtc acaccatgag      1380
      agtcgggaac acccgaagtc cgtagcctaa ccgcaaggag ggcgcgccg aaggtgggtt      1440
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<210> 35

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<211> 1480
<212> DNA
<213> Clostridium coccooides

5 <220>
<221> rRNA
<222> (1)..(1480)
<223> 16S rRNA coding gene sequence of Clostridium strain 15

10 <400> 35

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	agaacctgcc gtatactggg ggataaacact tagaaatagg tgctaatacc gcataagcgc	180
	acagcttcgc atgaagcagt gtgaaaaact ccggtgggat acgatggatc cgcgtctgat	240
20	tagctggttg gcggggtaac agcccaccaa ggcgacgatc agtagccggc ctgagagggg	300
	gaacggccac attgggactg agacacggcc caaactccta cgggaggcag cagtggggaa	360
	tattgcacaa tgggggaaac cctgatgcag cgacgcccg	420
25	tatgtaaagc tctatcagca gggaagaaat actgacctta cggtcagcag acggtacctg	480
	actaagaagc cccggctaac tacgtgccag cagccgcggg aatacgtagg ggcaagcggt	540
30	atccggattt actgggtgta aaggagcgt agacggcagc gcaagtctga agtgaaatcc	600
	catggcttaa cccatggaac tgctttggaa actgtgcagc tggagtgcag gagaggtaag	660
	cggaattcct agtgtagcgt gaaatgcgta gattattagg aggacaacag tgcgagcgct	720
35	actgacgtga ggctcgaagc gtgggagcaa acaggattag atacctggtg gtcacgcgta	780
	aacgatgatt actaggggtg tgggggacca aggtcttcgg tgccggcgca aacgcattaa	840
	gtaatccacc tggggagtag gttcgcaaga atgaaactca aaggaattga cggggacccg	900
40	cacaagcggg ggagcatgtg gtttaattcg aagcaacgcg aagaacctta cctggtcttg	960
	acatcccgat gacgagttag caaagtcact ttcccttcgg ggcatggag acagggtggg	1020
45	catggttggt gtcagctcgt gtcgtgagat gttgggttaa gtcccgaac gagcgcaacc	1080
	cctattttcca gtagccagca ggtagagctg ggcactctgg agagactgcc cgggataacc	1140
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	cgtcccagtt cggattgtag tctgcaactc gactacatga agctggaatc gctagtaatc	1320
55	gcgaatcaga atgtcgcggg gaatacgttc ccgggtcttg tacacaccgc ccgtcacacc	1380
	atgggagtcg gaaatgcccg aagtcagtga cctaaccgaa aggaaggagc tgccgaagg	1440
	ggagccggta actggggtga agtcgtaaca aggtagccgt	1480

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<210> 36
 <211> 1486
 <212> DNA
 <213> Clostridium papyrosolvens

<220>
 <221> rRNA
 <222> (1)..(1486)
 <223> 16S rRNA coding gene sequence of Clostridium strain 16

<400> 36

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agcaacctgc ctatcagagg ggaataacag tgagaaatca ttgctaatac cgcatatgct      180
cacagtatca catgatacag tgaggaaagg agcaatccgc tgatagatgg gcttgcgctt      240
gattagttag ttggtggggt aacggcctac caagacgacg atcagtagcc ggactgagag      300
gttgaacggc cacattggga ctgagatacg gccagactc ctacgggagg cagcagtcgg      360
gaatattgcg caatggagga aactctgacg cagtgcgcc gcgtatagga agaaggTTTT      420
cggattgtaa actattgtcg ttagggaaga taaaagactg tacctaagga ggaagccccg      480
gctaactatg tgccagcagc cgcggttaata catagggggc aagcgttatc cggaattatt      540
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aggaactgca accaaaacta ttctccttga gtgtcggaga ggaaagtgga attcctagtg      660
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ataactgacg ttgaggcagc aaagtgtggg gagcaaacag gattagatac cctggtagtc      780
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gataaatcgg aggaagggtg ggatgacgtc aaatcatcat gccctttatg tcctgggcta     1200
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	gtaatggcag gtcagcatac tgccgtgaat acgttccccg gccttgtaca caccgcccgt	1380
	cacaccatga gagttggaaa taccggaagc ctgtgagcta actgtaaaga ggcagcagtc	1440
5	gaaggtagag ccaatgattg gggatgaagtc gtaacaaggt agccgt	1486

<210> 37

<211> 1493

<212> DNA

10 <213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1493)

15 <223> 16S rRNA coding gene sequence of Clostridium strain 17

<400> 37

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25

30

35

40

45

50

55

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	gagaaccaac ggattgagga ttcgtccaaa tgaagttggg gaaagtggcg gacgggtgag	120
5	taacgcgtga gcaatctgcc ttggagtggg gaataacggt tggaacagc cgctaatacc	180
	gcatgatgcg tctgggaggc atctctctgg acgccaaaga tttatcgctc tgagatgagc	240
10	tcgcgtctga ttagctagtt ggcggggcaa cggcccacca aggcgacgat cagtagccgg	300
	actgagaggt tggccggcca cattgggact gagacacggc ccagactcct acgggaggca	360
	gcagtgggga atattgggca atgggcgcaa gcctgaccca gcaacgccgc gtgaaggaag	420
15	aaggctttcg gggtgtaaac ttcttttaag ggggacgaac aaatgacggt accccttgaa	480
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	gctggacagt aactgacgct gaggcgcgaa agcgtgggga gcaaacaggg attagatacc	780
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	aaccttacca gggcttgaca tcctgctaac gaaccagaga tggatcaggt gcccttcggg	1020
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45	cgcgcgtcac accatgagag tcgggaacac ccgaagtccg tagcctgacc gcaagggggg	1440
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50 <210> 38
 <211> 1493
 <212> DNA
 <213> Clostridium leptum

55 <220>
 <221> rRNA
 <222> (1)..(1493)
 <223> 16S rRNA coding gene sequence of Clostridium strain 18

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<400> 38

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	agtaacacgt gagcaacctg cctttcagag ggggataaca gttggaaacg actgctaata	180
10	ccgcataacg ctgcgatggg gcatcccgat gcagccaaag gagcaatccg ctgaaagatg	240
	ggctcgcggc cgattagcta gttggtgggg caacggccca ccaaggcgac gatcggtagc	300
	cggactgaga ggttgatcgg ccacattggg actgagacac ggcccagact cctacgggag	360
15	gcagcagtgg gggatattgc acaatggagg aaactctgat gcagcgacgc cgcgtgaggg	420
	aagacggtct tcggattgta aacctctgtc tttggggaag aaaatgacgg tacccaaaga	480
	ggaagctccg gctaactacg tgccagcagc cgcggtaata cgtacggagc gagcgttgctc	540
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	ggcttaactg gtagctgcgt tcaaaacttc ttgtcttgag tgaagtagag gcaggcggaa	660
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	aagaacctta ccaggtcttg acatcgtgcg catagcctag agataggtga agcccttcgg	1020
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	tcccgcgaacg agcgcgaaccc ttattattag ttgctacgca agagcactct aatgagactg	1140
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	ggctacacac gtactacaat ggcactgaaa cagagggaag cgacatcgcg aggtgaagcg	1260
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	cgcccgtcac accatgggag tcggtaacac ccgaagccag tagcctaacc gcaaggaggg	1440
50	cgctgtcgaa ggtgggattg atgactgggg tgaagtcgta acaaggtagc cgt	1493

<210> 39

<211> 1483

<212> DNA

<213> Clostridium leptum

55

<220>

<221> misc_feature

<222> (1)..(1483)

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<223> 16S rRNA coding gene sequence of Clostridium strain 19

<400> 39

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	ggagtgaaga tgcttgcatac tgaacttagt ggcggacggg tgagtaacac gtgagcaacc	120
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	tcgcatggca ctgatatcaa aggagcaatc cgctgaaaga tgggctcgcg tccgattagg	240
	cagttggcgg ggtaacggcc caccaaaccg acaatcggtg gccggactga gaggttgaac	300
15	ggccacattg ggactgagac acggcccaga ctctacggg aggcagcagt gggggatatt	360
	gcacaatggg ggaaacctg atgcagcgat gccgcgtgaa tgaagacggc cttcggttg	420
	taaagttctg tcgcagggga cgaaaatgac ggtaccctgc aagaaagctc cggctaacta	480
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	agggagcgta ggcgggagga taaagttgaa tgtgaaatct atgggctcaa cccatagctg	600
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25	aaatgcgtag atattaggag gaacaccagt ggcgaaagcg gcctgctggg cttttactga	720
	cgctgaggct cgaaagcgtg ggtagcaaac agaattagat taccctgtta ttcacggcgg	780
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	atcgcgatc agcatgccgc ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcac	1380
	accatgagag ccggtaacac ccgaagtcaa tagtctaacc gcaaggagga cattgccgaa	1440
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<210> 40

<211> 1511

55 <212> DNA

<213> Clostridium coccoides

<220>

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<221> rRNA

<222> (1)..(1511)

<223> 16S rRNA coding gene sequence of Clostridium strain 20

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	agaacctgcc gtatactggg ggataacact tagaaatagg tgctaatacc gcataagcgc	180
	acagcttcgc atgaaacagt gtgaaaaact ccggtggtat acgatggatc cgcgtctgat	240
15	tagctggttg gcggggtaac agcccaccaa ggcgacgatc agtagccggc ctgagagggg	300
	gaacggccac attgggactg agacacggcc caaactccta cgggaggcag cagtggggaa	360
	tattgcacaa tgggggaaac cctgatgcag cgacgccgcg tgagtgaaga agtatttcgg	420
20	tatgtaaagc tctatcagca ggaagaaat actgacctta cggtcagcag acggtacctg	480
	actaagaagc cccggctaac tacgtgccag cagccgcggt aatacgtagg ggcaagcgtt	540
25	atccggatth actgggtgta aaggagcgt agacggcagc gcaagtctga gtgaaatccc	600
	atggcttaac catggaactg ctttggaac tgtgcagctg gagtgcagga gaggtaaagc	660
	ggaattccta gtgtagcggg tgaaatgctg agatatagga ggaacaacag tggcgggaagg	720
30	cggctactgg gactgtaact gacgttgagg ctcgaaagcg tggggagcaa acaggattag	780
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	ccgggtcttg tacacaccgc ccgtcacacc atgggagtcg gaaatgcccg aagtcagtga	1440
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55	aaggtagccg t	1511

<210> 41

<211> 1495

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<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1495)

<223> 16S rRNA coding gene sequence of Clostridium strain 21

<400> 41

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<210> 42
<211> 1491
<212> DNA
<213> Clostridium leptum

<220>
<221> rRNA
<222> (1)..(1491)
<223> 16S rRNA coding gene sequence of Clostridium strain 22

<400> 42

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5	cccgtcacac catgagagtc gggaacaccc gaagtccgta gcctaaccgc aaggggggcg	1440
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	<211> 1495
	<212> DNA
	<213> Clostridium leptum
15	<220>
	<221> rRNA
	<222> (1)..(1495)
	<223> 16S rRNA coding gene sequence of Clostridium strain 23
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25

30

35

40

45

50

55

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	ccgcatgatg cgtctgggag gcatctctct ggacgccaaa gatttatcgc tctgagatga	240
	gctcgcgtct gattagctag ttggcggggc aacggcccac caaggcgacg atcagtagcc	300
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45	accgcccgtc acaccatgag agtcgggaac acccgaagtc cgtagcctga ccgcaagggg	1440
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<210> 44

<211> 1440

<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1440)

<223> 16S rRNA coding gene sequence of Clostridium strain 24

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<400> 44

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	taaagttctg tcgcagggga cgaaaatgac ggtaccctgc aagaaagctc cggctaacta	480
	cgtgccagca gccgcggtaa tacgtaggga gcaagcgttg tccggaatta ctgggtgtaa	540
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	gttcaaaact gttcttcttg agtgaagtag aggcaggcgg aattcctagt gtagcggtaga	660
25	aatgcgtaga tattagagga acaccagtgg cgaagcggcc tgctgggctt ttactgacgc	720
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<210> 45

<211> 1495

<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1495)

<223> 16S rRNA coding gene sequence of Clostridium strain 25

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<400> 45

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	taacgcgtga gcaatctgcc ttggagtggg gaataacggc tggaaacagc cgctaatacc	180
10	gcatgatata gctgggaggg atctccctgg ctgtcaaaga tttatcgctc tgagatgagc	240
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	actgagaggt tggccggcca cattgggact gagacacggc ccagactcct acgggaggca	360
15	gcagtgggga atattgggca atgggcgcaa gcctgaccca gcaacgccgc gtgaaggaag	420
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50	ggcgcgggccg aaggtgggtt cgataattgg ggtgaagtcg taacaaggta gccgt	1495

<210> 46

<211> 1495

<212> DNA

<213> Clostridium leptum

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<220>

<221> rRNA

<222> (1)..(1495)

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<223> 16S rRNA coding gene sequence of Clostridium strain 26

<400> 46

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<210> 47

<211> 1509

<212> DNA

<213> Clostridium leptum

<220>

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<221> rRNA

<222> (1)..(1509)

<223> 16S rRNA coding gene sequence of Clostridium strain 27

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<210> 48

<211> 1583

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<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1583)

<223> 16S rRNA coding gene sequence of Clostridium strain 28

<400> 48

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	<210> 49
	<211> 1519
15	<212> DNA
	<213> Clostridium coccoides
	<220>
	<221> rRNA
20	<222> (1)..(1519)
	<223> 16S rRNA coding gene sequence of Clostridium strain 29
	<400> 49

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	gggtgtacgg gaaggaaggc ttcggccgga aaacctgtgc atgagtggcg gacgggtgag	120
5	taacgcgtgg gcaacctggc ctgtacaggg ggataaact tagaaatagg tgctaatacc	180
	gcataacggg ggaagccgca tggcttttcc ctgaaaactc cgggtgtaca ggatgggccc	240
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	agtgggggat attgcacaat ggggggaacc ctgatgcagc gacgccgct ggggtgaagaa	420
	gcgcctcggc gcgtaaagcc ctgtcagcag ggaaagaaaa tgacggtagc tgaagaagaa	480
15	gccccgggct aactacgtgc cagcagccgg cggttaattac gtaggggggc aggcgttatc	540
	cggatttact ggggtggtaaa ggggggcgca aacggcgatg gcaggccagg aatggaaagc	600
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	gggcaggcgg aaattccttg tggtagcggg ggaaaatggc taaaaatcaa gaagaaaaac	720
	cgggtggggaa aggcggcctg gtgggactgc gaactgacgt tgaaggcccg aaagcgtggg	780
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	tttaattcga agcaacgcga agaaccttac ctggtcttga catcccgatg acgagtgagc	1020
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45	aatacgttcc cgggtcttgt acacaccgcc cgtcacacca tgggagtcgg aaatgcccga	1440
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	gtcgtatacaa ggtagccgt	1519
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	<211> 1497	
	<212> DNA	
	<213> Clostridium coccoides	
55	<220>	
	<221> rRNA	
	<222> (1)..(1497)	

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<223> 16S rRNA coding gene sequence of Clostridium strain 30

<400> 50

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	taacgcgtgg gcaacctgcc ccgtgccggg ggataccgcc tggaaacagg cgctaatacc	180
10	gcataagcgc atacagccgc atgggtgtat gcggaagct ccggcggcac gggatgggcc	240
	cgcgcccgat tagccagttg gcggggtaac ggcccaccaa agcgacgatc ggtagccggc	300
	ctgagagggc ggacggccac attgggactg agacacggcc caaactccta cgggaggcag	360
15	cagtggggaa tattgcacaa tgggggaaac cctgatgcag caacgcccg cggtgaagg	420
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20	agccccggct aactacgtgc cagcagccgc ggtaatacgt agggggcgag cgttatccgg	540
	aattactggg tgtaaaggga gcgtagacgg cgaggtaagc ctgaagtga agcccgcggc	600
	ccaaccgcgg aactgctttg ggaactgttt tgctggagta tgggaggggt aagcgggaatt	660
25	cctggtgtag cggtgaaatg cgtagatatc aggaggaaca ccggtggcga aggcggctta	720
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	gcagcgaacg cagtaagtaa tccacctggg gtagtacctc gcaagaatga aactcaaagg	900
	aattgacggg gacccgcaca agcgggtggag catgtggttt aattcgaagc aacgcgaaga	960
35	accttaccgg gccttgacat cccctggaca gcatatgtaa tgtatgtttc cttcgggacc	1020
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40	cgcaacgagc gcaaccctg cccccagtag ccagcattta agatgggcac tctgggggga	1140
	ctgccggggg taacccggag gaaggcgggg atgacgtcaa atcatcatgc cccttatggc	1200
	cggggctaca cacgtgctac aatggcgtaa acagagggag gcgagacagc gatgttaagc	1260
45	gaaccccaaa aataacgtcc cagttcggat tgcagcctgc aactcggctg catgaagctg	1320
	gaatcgctag taatcgcgga tcagaatgcc gcggtgaata cgttcccggg tcttgtacac	1380
	accgcccgtc acaccatggg agtcgggaac gccgaagcc ggtgaccgaa cccgaaaggg	1440
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<210> 51

<211> 1475

55 <212> DNA

<213> Clostridium leptum

<220>

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<221> rRNA

<222> (1)..(1475)

<223> 16S rRNA coding gene sequence of Clostridium strain 31

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aaatctgcct atcagagggg aataacagtg agaaatcact gctaataccg catatgccat 180

agttatcgca tgataatagt gggaaagaag caattcgctg atagatgagc ttgcggctga 240

15 ttagctagtt ggtggggtaa cggcctacca aggcgacgat cagtagccgg cctgagaggg 300

tgaacggcca cattgggact gagacacggc ccaaactcct acgggaggca gcagtgggga 360

atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgagtgaag aagtatttcg 420

20 gtatgtaaag ctctatcagc agggaagaaa atgacggtag ctgactaaga aagccccggc 480

taactacgtg ccagcagccg cggtaatacg tagggggcaa gcgttatccg gatttactgg 540

tgtaaagggg gcgtagacgg cagcgcgaagt ctgagtgaat tcccatggct taccatgaa 600

25 actgcttttg aaactgtgca gctggagtgc aggagaggta agcgggaatcc tagtgtagcg 660

gttgaaatgc gtagattatc agaaggaaca ccggtggccg aggcggcctg ctgggctttt 720

30 actgacgctg aggctcgaag cgtgggtagc aaacaggatt agataccctg gtagtccacg 780

cggtaaacga tgattactag gtgtgggtgg actgacccca tccgtgccgg agttaacaca 840

ataagtaatc cacctgggga gtacggccgc aaggttgaaa ctcaaaggaa ttgacggggg 900

35 cccgcacaag cagtggagta tgtggtttta ttcgacgcaa cgcgaagaac cttaccaggt 960

cttgacatcg agtgacggac atagagatat gtctttcctt cgggacacga agacaggtgg 1020

tgcatgggtg tcgtcagctc gtgtcgtgag atgttgggtt aagtcccgca acgagcgcaa 1080

40 cccttaccat tagttgctac gcaagagcac tctaattggga ctgccgttga caaaacggag 1140

gaaggtgggg atgacgtcaa atcatcatgc cccttatgac ctgggcgaca cacgtactac 1200

45 aatggcgggtc aacagaggga ggcaaagccg cgaggcagag caaacccta aaagccgtct 1260

cagttcggat tgcaggctgc aactcgcctg catgaagtcg gaattgctag taatcgcgga 1320

tcagcatgcc gcggtgaata cgttcccggg ccttgtacac accgcccgtc acaccatgag 1380

50 agccggtaac acccgaagtc aatagtctaa ccgcaaggag gacattgccg aaggtgggat 1440

tggttaattgg ggtgaagtcg taacaaggta gccgt 1475

55 <210> 52
<211> 1491
<212> DNA
<213> Clostridium leptum

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<220>

<221> rRNA

<222> (1)..(1491)

<223> 16S rRNA coding gene sequence of Clostridium strain 32

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<400> 52

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    taacgcgtga gcaatctgcc ttggagtggg gaataacggc tggaaacagc cgctaatacc      180
    gcatgataca gttgggaggg atctctctga ctgtcaaaga tttatcgctc tgagatgagc      240
15  tcgcgtctga ttagctagtt ggcggggtaa cggccaccca aggcgacgat cagtagccgg      300
    actgagaggt tggccggcca cattgggact gagacacggc ccagactcct acgggaggca      360
20  gcagtgggga atattgggca atgggcgcaa gcctgacca gcaacgccgc gtgaaggaa      420
    aaggctttcg ggttgtaaac ttcttttctg ggggacgaac aaatgacggg accccaggaa      480
    taagccacgg ctaactacgt gccagcagcc gcgtaatac gtaggtggca agcgttatcc      540
25  ggatttattg ggtgtaaagg gcgtgtaggc gggaatgcaa gtcagatgtg aaaactatgg      600
    gctcaaccca tagcctgcat ttgaaactgt atttcttgag tgctggagag gcaatcggaa      660
    ttccgtgtgt agcggtgaaa tgcgtagata tacggaggaa caccagtggc gaagcggatt      720
30  gctggacagt aactgacgct gaggcgcgaa agcgtgggga gcaaacagga ttagataccc      780
    tggtagtcca cgccgtaacg atggatacta gtgtgggggg actgaccccc tccgtgccgc      840
35  agctaacgca ataagtatcc ccacctgggg agtacgatcg caaggttgaa actcaaagga      900
    attgacgggg gcccgcacaa gcggtggagt atgtggttta attcgaagca acgcgaagaa      960
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45  cgttgacaaa acggagggaag gtggggacga cgtcaaatca tcatgccctt tacgtcctgg      1200
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50  cgctagtaat cgcggatcag catgccgcgg tgaatacgtt cccgggcctt gtacacaccg      1380
    cccgtcacac catgagagtc gggaacaccc gaagtccgta gcctaaccgc aaggggggcg      1440
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55

<210> 53

<211> 1495

<212> DNA

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<213> Clostridium coccooides

<220>

<221> rRNA

<222> (1)..(1495)

<223> 16S rRNA coding gene sequence of Clostridium strain 33

<400> 53

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    taacgcgtgg gcaacctggc ctgtacaggg ggataacact tagaaatagg tgctaatacc      180
15  gcataacggg ggaagccgca tggcttttcc ctgaaaactc cggtggtaca ggatgggccc      240
    gcgtctgatt agccagttgg cagggtaacg gcctaccaa gcgacgatca gtagccggcc      300
    tgagagggcg gacggccaca ctgggactga gacacggccc agactcctac gggaggcagc      360
20  agtgggggat attgcacaat ggggggaacc ctgatgcagc gacgccgcgt gggngaagaa      420
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25  ccccggttaa ctacgtgcca gcagccgcgg taatacgtag ggggcaagcg ttatccggat      540
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    aaccccgga ctgctcttgg aactgcgtgg ctggagtga ggaggggcag gcggaattcc      660
30  tgggtgtacg gtgaaatgcg tagatatcag aggaacaccg gtggcgaaag cggcctgctg      720
    gactgcaact gacgttgagg cccgaaagcg gtgggagcaa acaggattag ataccctggt      780
35  agtccacgcc gtaaaccgat attactaggt gtcggggagc agagactgcc cggtgccgca      840
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45  caacgagcgc aaccctgcc cgagtagcc agcattttag atggggactc tgcggggact      1140
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    atcgctagta atcgcggatc agaataccgc ggtgaatacg ttcccgggtc ttgtacacac      1380
    cgcgcgtcac accatgggag ccgggaatgc ccgaagtctg tgaccgaacc cgtaagggga      1440
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<210> 54

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<211> 1493
<212> DNA
<213> Clostridium leptum

<220>
<221> rRNA
<222> (1)..(1493)
<223> 16S rRNA coding gene sequence of Clostridium strain 34

<400> 54

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gtaacgcgtg aggaacctgc cttccagagg gggacaacag ttggaaacga ctgctaatac      180
cgcatgatgc gttggagccg catgactccg acgtcaaaga tttatcgctg gaagatggcc      240
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gtcccgcacg gagcgcaacc cctattgtta gttgctacgc aagagcactc tagcgagact     1140
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cgcccgtcac accatgagag tcgggaacac ccgaagtccg tagcctaacc gcaaggaggg     1440
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<210> 55
<211> 1498
<212> DNA
<213> Clostridium coccooides

<220>
<221> rRNA
<222> (1)..(1498)
<223> 16S rRNA coding gene sequence of Clostridium strain 35

<400> 55

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taacgcgtgg gcaacctggc ctgtacaggg ggataacact tagaaatagg tgctaatacc      180
gcataacggg ggaagccgca tggcttttcc ctgaaaactc cggtggtaca ggatgggccc      240
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gccccggcta actacgtgcc agcagccgcg gtaatacgtg aggggcaagc gttatccgga      540
tttactgggt gtaaaggggg cgacagacggc gatgcaagcc aggagtgaag gcccggggcc      600
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aaccttacca ggccttgaca tccccctgga tggcccgtaa cggggtcagc ctttcggggc     1020
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	cgaaccccaa aaacggcgtc ccagttcgga ttgtagtctg caaccgact acatgaagcc	1320
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	caccgcccgt cacaccatgg gagccgggaa tgcccgaagt ctgtgaccga acccgtaagg	1440
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20	<220> <221> rRNA <222> (1)..(1491) <223> 16S rRNA coding gene sequence of Clostridium strain 36	
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	ggagcgccta tgaaggagat ttcggtcaac ggaataggct gcttagtggc tgacgggtga	120
5	gtaacgcgtg aggaacctgc ctttcagagg gggacaacag ttggaaacga ctgctaatac	180
	cgcataacac ataggtgtcg catggcattt atgtcaaaga tttatcgctg aaagatggcc	240
10	tcgcgtctga ttagctagtt ggtgaggtaa cggctcacca aggcgacgat cagtagccgg	300
	actgagaggt tagccggcca cattgggact gagatacggc ccagactcct acgggaggca	360
	gcagtgggga atattgggca atggacgcaa gtctgaccca gcaacgccgc gtgaaggaag	420
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	gatttactgg gtgtaaaggg cgtgtagccg ggctgacagt cagatgtgaa attccggggc	600
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35	cccgcaacga gcgcaaccct tattgttagt tgctacgcaa gagcactcta gcgagactgc	1140
	cgttgacaaa acggaggaag gtggggacga cgtcaaatac tcatgccctt tatgtcctgg	1200
40	gctacacacg taatacaatg gcggtaaaca gagggatgca atactgcgaa gtggagcgaa	1260
	cccctaaaag ccgtcccagt tcagattgca gtctgcaact cgactgcatg aagtcggaat	1320
	cgctagtaat cgcggatcag catgccgcgg tgaatacgtt cccgggcctt gtacacaccg	1380
45	cccgtcacac catgagagtc gggaacaccc gaagtccgta gcctaaccgc aaggagggcg	1440
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50 <210> 57
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 <213> Clostridium coccoides

55 <220>
 <221> rRNA
 <222> (1)..(1493)
 <223> 16S rRNA coding gene sequence of Clostridium strain 37

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<400> 57

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	taacgcgtgg gcaacctggc ctgtacaggg ggataacact tagaaatagg tgctaatacc	180
	gcataacggg ggaagccgca tggcttttcc ctgaaaactc cgggtgtaca ggatgggccc	240
10	gcgtctgatt agccagttgg cagggtaacg gcctaccaa gcgacgatca gtagccggcc	300
	tgagagggcg gacggccaca ctgggactga gacacggccc agactcctac gggaggcagc	360
	agtgggggat attgcacaat ggggggaaac cctgatgcag cgacgccgcg tgagtgaaga	420
15	agtatttcgg tatgtaaagc tctatcagca gggaagaaaa tgacgggtacc tgactaagaa	480
	gccccggcta actacgtgcc agcagccgcg gtaatacgta gggggcaagc gttatccgga	540
20	tttactgggt gtaaaggag cgtagacggc agcgcaagtc tgaagtgaaa tcccatggct	600
	taaccatgga actgcttttg aaactgtgca gctggagtgc aggagaggta agcggaattc	660
	ctagtgtagc ggtgaaatgc gtagatatta ggaggaacac cagtggcgaa ggcggcttac	720
25	tggactgtac tgacgttgag gctcgaaagc gtggggagca aacaggatta gataccctgg	780
	tagtccacgc cgtaaacgat gattactagg tgttggggga ccaaggtctt cggtgccggc	840
30	gcaaacgcat taagtaatcc acctggggag tacgttcgca agaataaaac tcaaaggaat	900
	tgacggggac ccgcacaagc ggtggagcat gtggtttaat tcgaagcaac gcgaagaacc	960
	ttacctgggtc ttgacatccc gatgacgagt gagcaaagtc actttccctt cggggcattg	1020
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40	gccccgggata accgggagga aggcggggat gacgtcaa atcatgccc cttatgatca	1200
	gggctacaca cgtgctacaa tggcgtaa acgaggaagc gagacggtga cgttgagcaa	1260
	atccccaaaa taacgtccca gttcggattg tagtctgcaa ctcgactaca tgaagctgga	1320
45	atcgctagta atcgcgaa atcagaatgtc ggtgaatacg ttcccgggtc ttgtacacac	1380
	cgccccgtcac accatgggag tcggaaatgc ccgaagtcag tgacctaacc gaaaggaagg	1440
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<211> 1493

<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1493)

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<223> 16S rRNA coding gene sequence of Clostridium strain 38

<400> 58

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	gtaacgcgtg aggaacctgc cttccagagg gggacaacag ttggaaacga ctgctaatac	180
10	cgcatgatgc gttggagccg catgactccg acgtcaaaga tttatcgctg gaagatggcc	240
	tcgcgtctga ttagctagtt ggtgaggtaa cggcccacca aggcgacgat cagtagccgg	300
	actgagaggt tggccggcca cattgggact gagatacggc ccagactcct acgggaggca	360
15	gcagtgggga atattgggca atggacgcaa gtctgacctc gcaacgccgc gtgaaggaag	420
	aaggctttcg ggttgtaaac ttcttttaag ggggaagagc agaagacggg accccttgaa	480
20	taagccacgg ctaactacgt gccagcagcc gcgtaatac gtagtggcaa gcgttgtccg	540
	gatttactgg gtgtaaaggg cgtgcagccg gagagacaag tcagatgtga aatccacggg	600
	ctcaacccgt gaactgcatt tgaaaactgtt tcccttgagt gtcggagagg taatcggaat	660
25	tccttggtga gcggtgaaat gcgtagatat aaggaagaac accagtggcg aaggcggatt	720
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30	ctggtagtcc acgctgtaaa cgatcgatac taggtgtgcg gggactgacc ccctgcgtgc	840
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	gaattgacgg gggcccgcac aagcggtgga ttatgtggtt taattcgaag caacgcgaag	960
35	aaccttacca gggcttgaca tcctgctaac gaagtagaga tacattaggt gcccttcggg	1020
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	atcgctagta atcgcggatc agcatgccgc ggtgaatacg ttcccgggcc ttgtacacac	1380
	cgcccgtcac accatgagag tcgggaacac ccgaagtccg tagcctaacc gcaaggaggg	1440
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<211> 1511

55 <212> DNA

<213> Clostridium leptum

<220>

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<221> rRNA

<222> (1)..(1511)

<223> 16S rRNA coding gene sequence of Clostridium strain 39

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    ctggacgata actgacggtg aggcgcgaaa gcgtggggag caaacaggat tagataacctg      780
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35   aaactcaaaa gaaatggacg gggggccccg cccaagcgg gtgggattat gttggtttat      960
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50   cccgggcctt gtacacaccg cccgtcacac catgagagtc gggaacaccc gaagtccgta      1440
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<210> 60

<211> 1499

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<212> DNA

<213> Clostridium leptum

<220>

<221> rRNA

<222> (1)..(1499)

<223> 16S rRNA coding gene sequence of Clostridium strain 40

<400> 60

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15     gtaacgcgtg aggaacctgc ctacagagag ggataaacac accgaaaggt gtgctaatac      180
      cgcataacat atgagagggg catccctttc atatcaaaga tttattgctt tgagatggcc      240
20     tcgcgtccaa ttagctagtt ggtgaggtaa cgccccacca aggcgacgat tggtagccgg      300
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      gcagtgggga atattgcaca atgggggggaa ccctgatgca gcaatgccgc gtgaaggatg      420
25     aaggttttcg gattgtaaac ttcttttgta cgggacgaag aaagtgacgg taccgtaaga      480
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55     cacaccgccc gtcacaccat gagagtcgga aacacccgaa gcctgtagcc caaccgcaag      1440
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<210> 61
<211> 1512
<212> DNA
<213> Clostridium coccoides

<220>
<221> rRNA
<222> (1)..(1512)
<223> 16S rRNA coding gene sequence of Clostridium strain 41

<400> 61

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cggacgggtg agtaacgcgt gggtaacctg ccttgcaactg ggggataaca ctagaaata      180
ggtgctaata ccgcataaca gtaggagacg catgtctttt acttgaaaac tccggtggtg      240
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	catgcccctt atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag	1260
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	ccgggtcttg tacacaccgc ccgtcacacc atgggagtcg gaaatgcccg aagtctgtga	1440
15	cccaacctga gaaggaggga gcagccgaag gcaggtcgga tgactgggggt gaagtcgtaa	1500
	caaggtagcc gt	1512

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 <213> Artificial

<220>
 <223> Artificially synthesized primer sequence

<400> 62
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<210> 63
 <211> 22
 <212> DNA
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<220>
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<400> 63
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<210> 64
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 <212> DNA
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<210> 68
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cgctactgg ctggtcag 19

Claims

- 50
1. A composition for use in a method of treating or preventing an allergic disease by inducing proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells, the composition comprising, as an active ingredient, bacteria belonging to the genus Clostridium of clusters XIVa and/or IV, wherein the bacteria induce said proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells.
 2. A composition for use according to claim 1 wherein the bacteria belong to Clostridium clusters XIVa and IV in combination.
- 55

3. The composition for use according to claim 1 or claim 2 wherein the composition further comprises bacteria belonging to a Clostridium cluster other than Clostridium cluster XIVa or cluster IV.
- 5 4. The composition for use according to claim 2 or 3 wherein the bacteria belonging to Clostridium clusters XIVa and IV in combination comprise multiple strains of bacteria belonging to Clostridium cluster XIVa or cluster IV in combination as an active ingredient.
- 10 5. The composition for use according to any one of the preceding claims wherein said bacteria according to any one of the preceding claims are in the form of spores.
- 15 6. The composition for use according to any one of the preceding claims wherein said bacteria are obtained from a fecal sample obtained from a human.
- 20 7. A composition for use in a method of treating or preventing an allergic disease by inducing proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells, the composition comprising, as an active ingredient, a spore-forming fraction of human fecal matter, wherein the spore-forming fraction induces said proliferation or accumulation of transcription factor Foxp3-positive regulatory T cells.
- 25 8. The composition for use according to claim 7, wherein the spore-forming fraction is obtainable by chloroform treatment of human fecal matter.
9. The composition for use according to any one of the preceding claims wherein the allergic disease is food allergy.
10. The composition for use according to any one claims 1-8, wherein the allergic disease is pollenosis or asthma.
11. The composition for use according to any one of the preceding claims, wherein the composition suppresses proliferation of effector T cells.
12. The composition for use according to any one of the preceding claims wherein the composition is formulated as a pharmaceutical preparation for oral administration.
13. The composition for use according to any one of the preceding claims, wherein the composition is formulated as a pharmaceutical preparation using a composition that enables delivery to the colon.
14. The composition for use according to claim 13, wherein the composition is formulated as a delayed release dosage unit having a coating material suitable for delaying release by 3-5 hours.
15. The composition for use according to claim 13, wherein the composition is formulated as a pharmaceutical preparation employing a pH sensitive composition comprising an enteric polymer.

Patentansprüche

1. Zusammensetzung zur Verwendung in einem Verfahren zum Behandeln oder Vorbeugen einer allergischen Krankheit durch Induzieren von Proliferation oder Akkumulieren von Transkriptionsfaktor-Foxp3-positiven regulatorischen T-Zellen, die Zusammensetzung umfassend, als einen Wirkstoff, Bakterien, welche zum Genus Clostridium des Clusters XIVa und/oder IV gehören, wobei die Bakterien die Proliferation oder Akkumulation von Transkriptionsfaktor-Foxp3-positiven regulatorischen T-Zellen induzieren.
2. Zusammensetzung zur Verwendung gemäß Anspruch 1, wobei die Bakterien zu den Clostridium-Clustern XIVa und IV in Kombination gehören.
3. Zusammensetzung zur Verwendung gemäß Anspruch 1 oder Anspruch 2, wobei die Zusammensetzung weitergehend Bakterien umfasst, welche zu einem anderen Clostridium-Cluster als Clostridium-Cluster XIVa oder -Cluster IV gehören.
4. Zusammensetzung zur Verwendung gemäß Anspruch 2 oder 3, wobei die Bakterien, welche zu den Clostridium-Clustern XIVa und IV in Kombination gehören, mehrere Stämme von Bakterien in Kombination als einen Wirkstoff

umfassen, welche zum Clostridium-Cluster XIVa oder -Cluster IV gehören.

- 5 5. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die Bakterien gemäß irgendeinem der vorstehenden Ansprüche in Form von Sporen vorliegen.
- 6 6. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die Bakterien von einer von einem Menschen erhaltenen Fäkalprobe erhalten werden.
- 10 7. Zusammensetzung zur Verwendung in einem Verfahren zum Behandeln oder Vorbeugen einer allergischen Krankheit durch Induzieren von Proliferation oder Akkumulieren von Transkriptionsfaktor-Foxp3-positiven regulatorischen T-Zellen, die Zusammensetzung umfassend, als einen Wirkstoff, eine Sporen-bildende Fraktion humaner Fäkalien, wobei die Sporen-bildende Fraktion die Proliferation oder Akkumulation von Transkriptionsfaktor-Foxp3-positiven regulatorischen T-Zellen induziert.
- 15 8. Zusammensetzung zur Verwendung gemäß Anspruch 7, wobei die Sporen-bildende Fraktion durch Chloroform-Behandlung menschlicher Fäkalien erhältlich ist.
- 9 9. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die allergische Krankheit Lebensmittelallergie ist.
- 20 10. Zusammensetzung zur Verwendung gemäß irgendeinem der Ansprüche 1-8, wobei die allergische Krankheit Heuschnupfen (pollenosis) oder Asthma ist.
- 25 11. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die Zusammensetzung Proliferation von Effektor-T-Zellen supprimiert.
12. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die Zusammensetzung als eine pharmazeutische Zusammensetzung für orale Verabreichung formuliert ist.
- 30 13. Zusammensetzung zur Verwendung gemäß irgendeinem der vorstehenden Ansprüche, wobei die Zusammensetzung als eine pharmazeutische Zusammensetzung unter Verwendung einer Zusammensetzung, welche Abgabe in den Dickdarm ermöglicht, formuliert ist.
- 35 14. Zusammensetzung zur Verwendung gemäß Anspruch 13, wobei die Zusammensetzung als eine Dosierungseinheit mit verzögerter Wirkstoffabgabe formuliert ist, welche ein Überzugsmaterial aufweist, welches geeignet ist, um die Abgabe für 3-5 Stunden zu verzögern.
- 40 15. Zusammensetzung zur Verwendung gemäß Anspruch 13, wobei die Zusammensetzung als eine pharmazeutische Zusammensetzung formuliert ist, unter Verwendung einer pH-empfindlichen Zusammensetzung, welche ein enterisches Polymer umfasst.

Revendications

- 45 1. Composition destinée à être utilisée dans un procédé de traitement ou de prévention d'une maladie allergique en induisant une prolifération ou accumulation de lymphocytes T régulateurs positifs au facteur de transcription Foxp3, la composition comprenant, en tant que principe actif, des bactéries appartenant aux groupes XIVa et/ou IV de Clostridium, dans laquelle les bactéries induisent ladite prolifération ou accumulation de lymphocytes T régulateurs positifs au facteur de transcription Foxp3.
- 50 2. Composition pour son utilisation selon la revendication 1 dans laquelle les bactéries appartiennent aux groupes XIVa et IV de Clostridium en combinaison.
- 55 3. Composition pour son utilisation selon la revendication 1 ou 2 dans laquelle la composition comprend en outre des bactéries appartenant à un groupe de Clostridium autre que le groupe XIVa ou le groupe IV de Clostridium.
4. Composition pour son utilisation selon la revendication 2 ou 3 dans laquelle les bactéries appartenant aux groupes XIVa et IV de Clostridium en combinaison comprennent de multiples souches de bactéries appartenant au groupe

XIVa ou au groupe IV de Clostridium en combinaison en tant que principe actif.

5 **5.** Composition pour son utilisation selon l'une quelconque des revendications précédentes dans laquelle lesdites bactéries selon l'une quelconque des revendications précédentes sont sous la forme de spores.

10 **6.** Composition pour son utilisation selon l'une quelconque des revendications précédentes dans laquelle lesdites bactéries sont obtenues à partir d'un échantillon fécal obtenu auprès d'un humain.

15 **7.** Composition destinée à être utilisée dans un procédé de traitement ou de prévention d'une maladie allergique en induisant une prolifération ou accumulation de lymphocytes T régulateurs positifs au facteur de transcription Foxp3, la composition comprenant, en tant que principe actif, une fraction sporulée de matière fécale humaine, dans laquelle la fraction sporulée induit ladite prolifération ou accumulation de lymphocytes T régulateurs positifs au facteur de transcription Foxp3.

20 **8.** Composition pour son utilisation selon la revendication 7, dans laquelle la fraction sporulée peut être obtenue par traitement au chloroforme de matière fécale humaine.

25 **9.** Composition pour son utilisation selon l'une quelconque des revendications précédentes dans laquelle la maladie allergique est une allergie alimentaire.

30 **10.** Composition pour son utilisation selon l'une quelconque des revendications 1 à 8, dans laquelle la maladie allergique est la pollinose ou l'asthme.

35 **11.** Composition pour son utilisation selon l'une quelconque des revendications précédentes, dans laquelle la composition supprime la prolifération de lymphocytes T effecteurs.

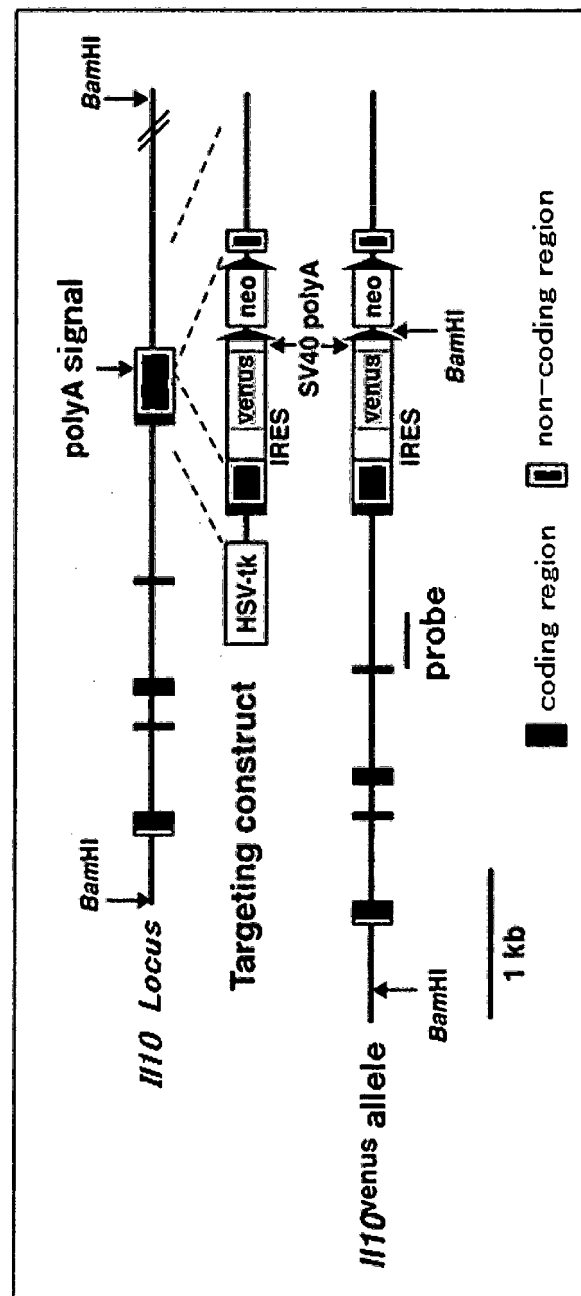
40 **12.** Composition pour son utilisation selon l'une quelconque des revendications précédentes dans laquelle la composition est formulée en tant que préparation pharmaceutique pour administration orale.

45 **13.** Composition pour son utilisation selon l'une quelconque des revendications précédentes, dans laquelle la composition est formulée en tant que préparation pharmaceutique utilisant une composition qui permet la distribution au côlon.

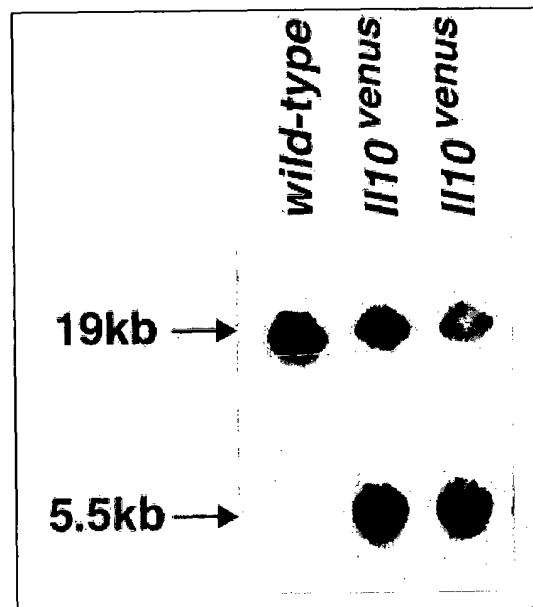
50 **14.** Composition pour son utilisation selon la revendication 13, dans laquelle la composition est formulée en tant qu'unité de dosage à libération différée présentant un matériau d'enrobage approprié pour différer la libération de 3 à 5 heures.

55 **15.** Composition pour son utilisation selon la revendication 13, dans laquelle la composition est formulée en tant que préparation pharmaceutique employant une composition sensible au pH comprenant un polymère entérique.

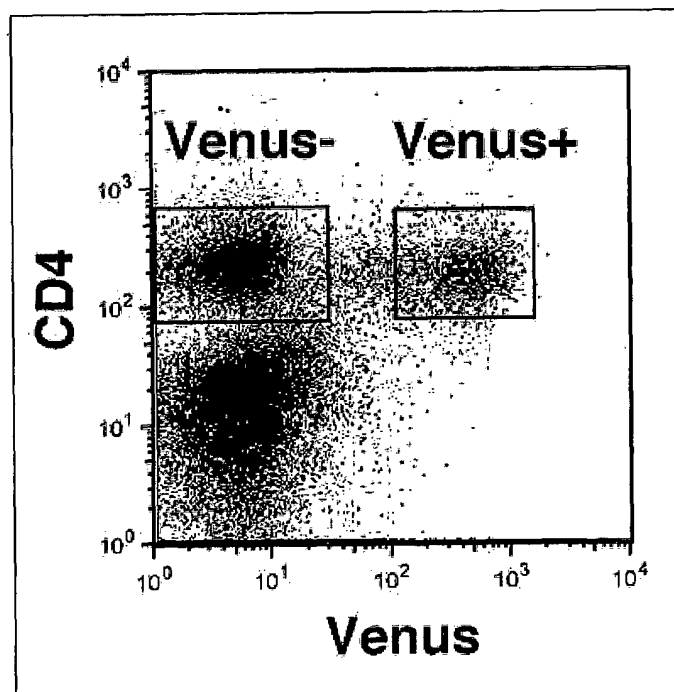
[Fig. 1]



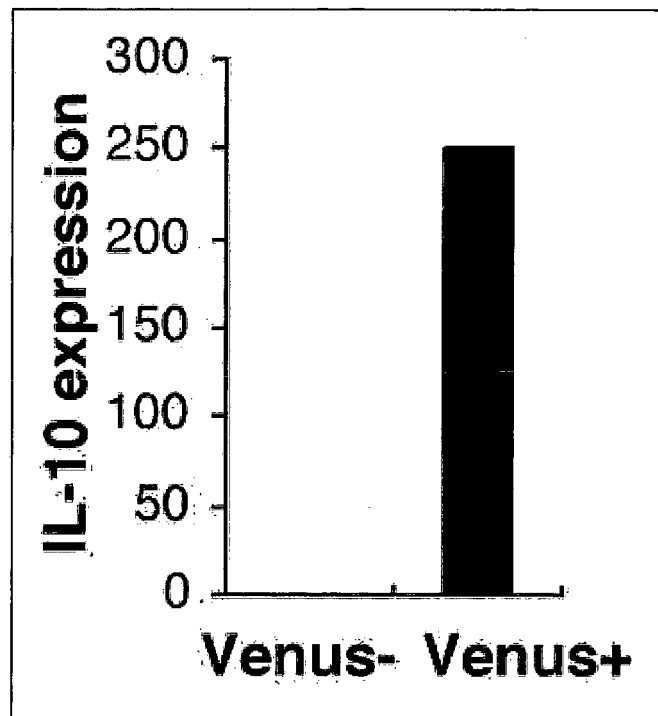
[Fig. 2]



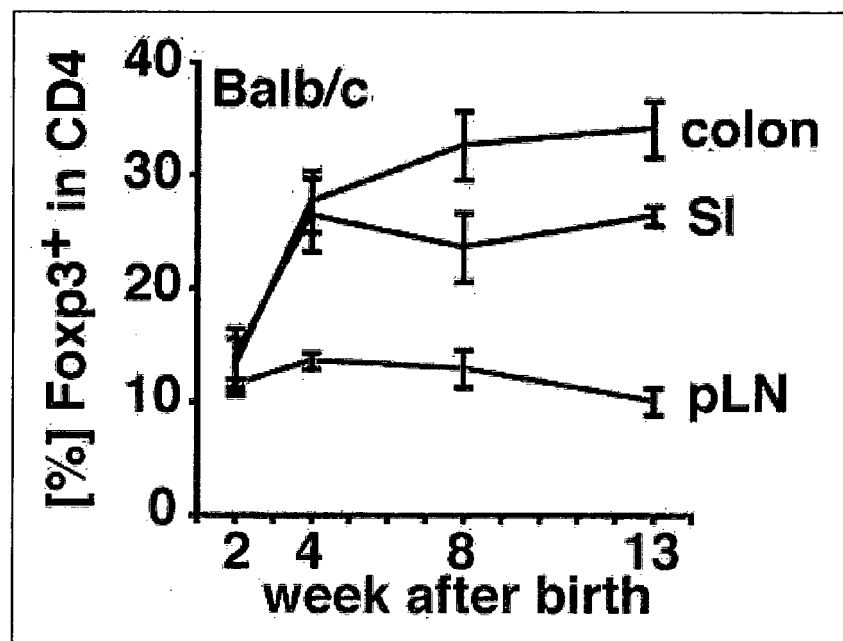
[Fig. 3]



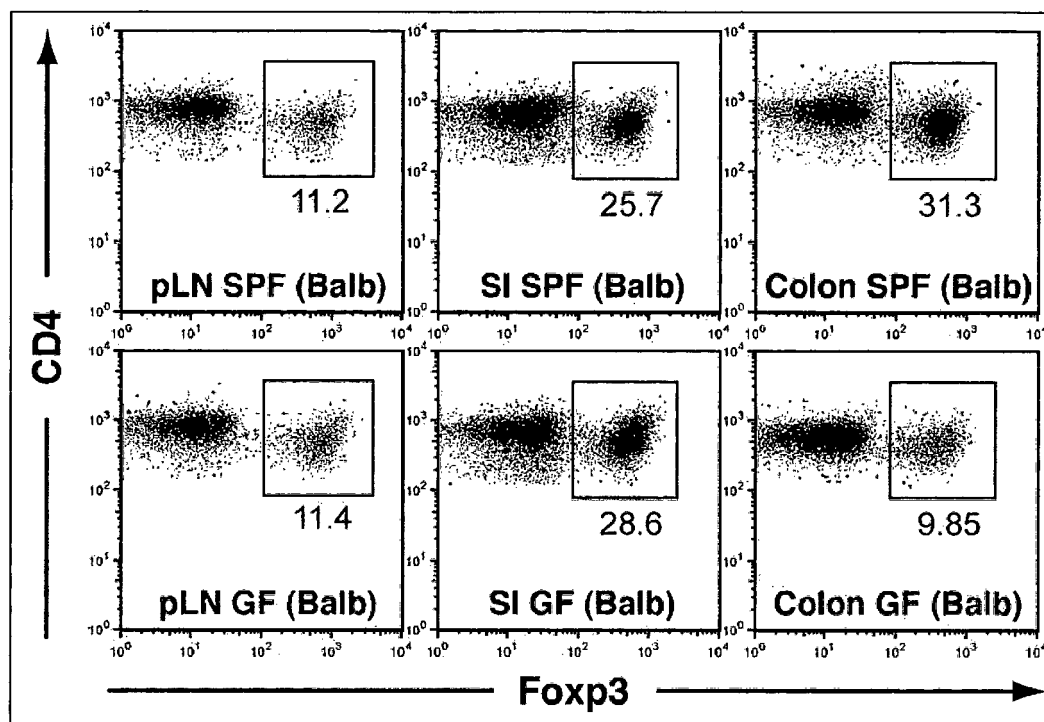
[Fig. 4]



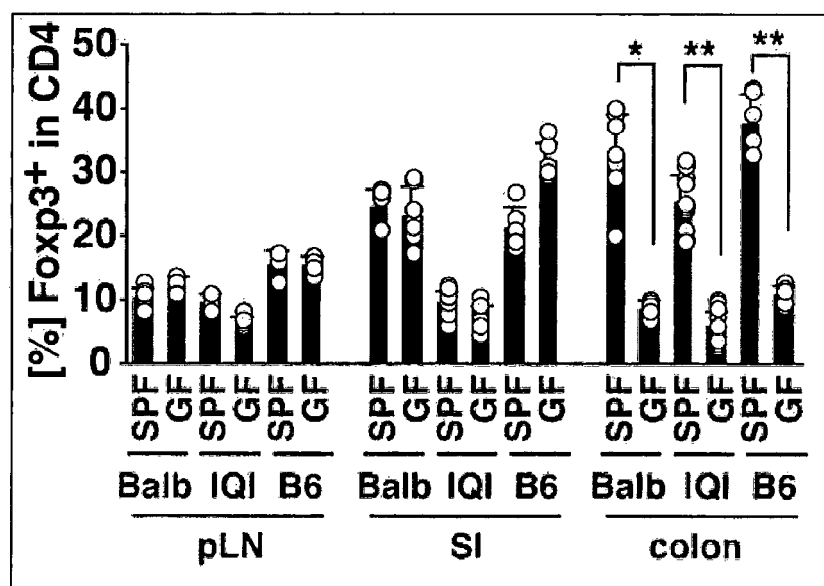
[Fig. 5]



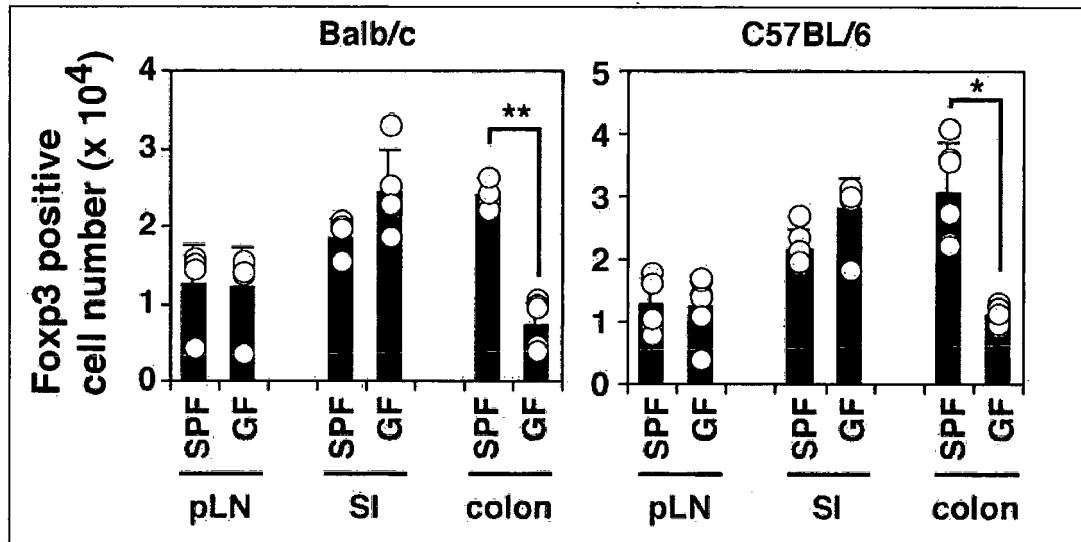
[Fig. 6]



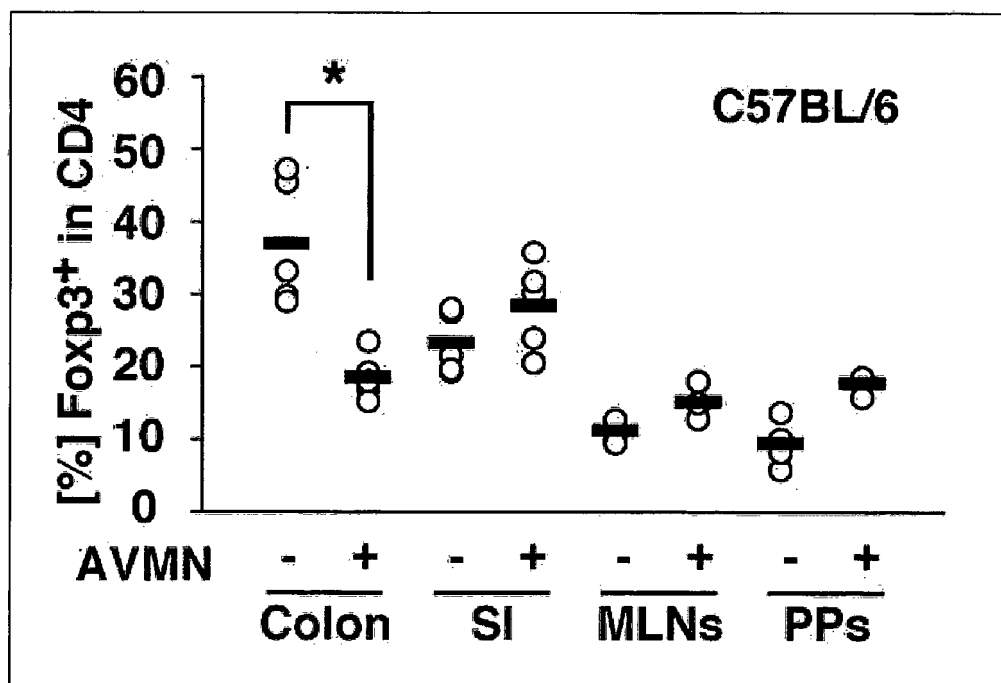
[Fig. 7]



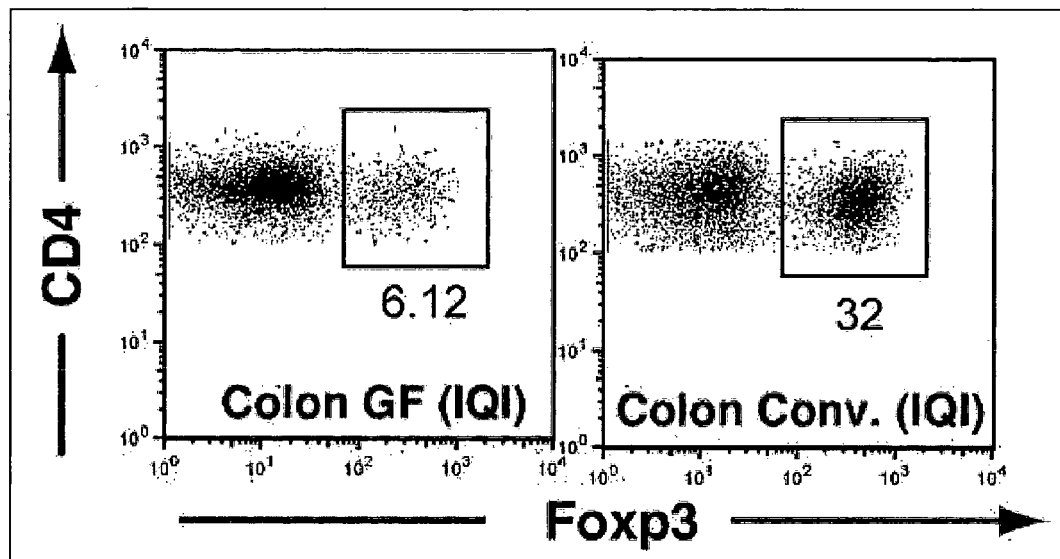
[Fig. 8]



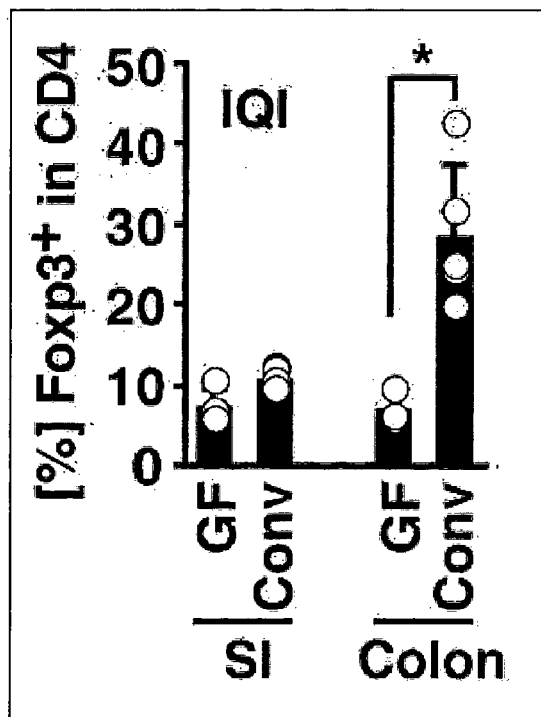
[Fig. 9]



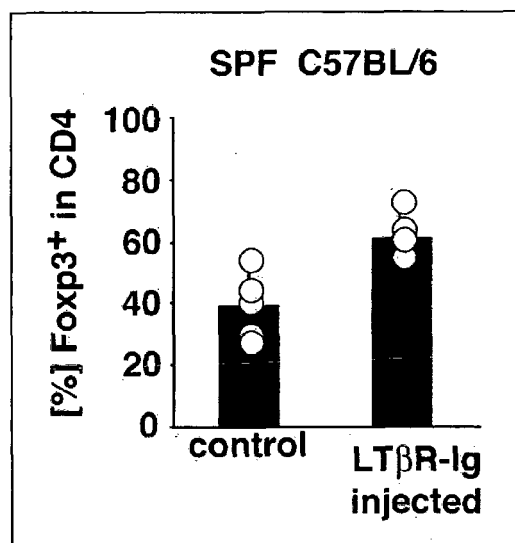
[Fig. 10]



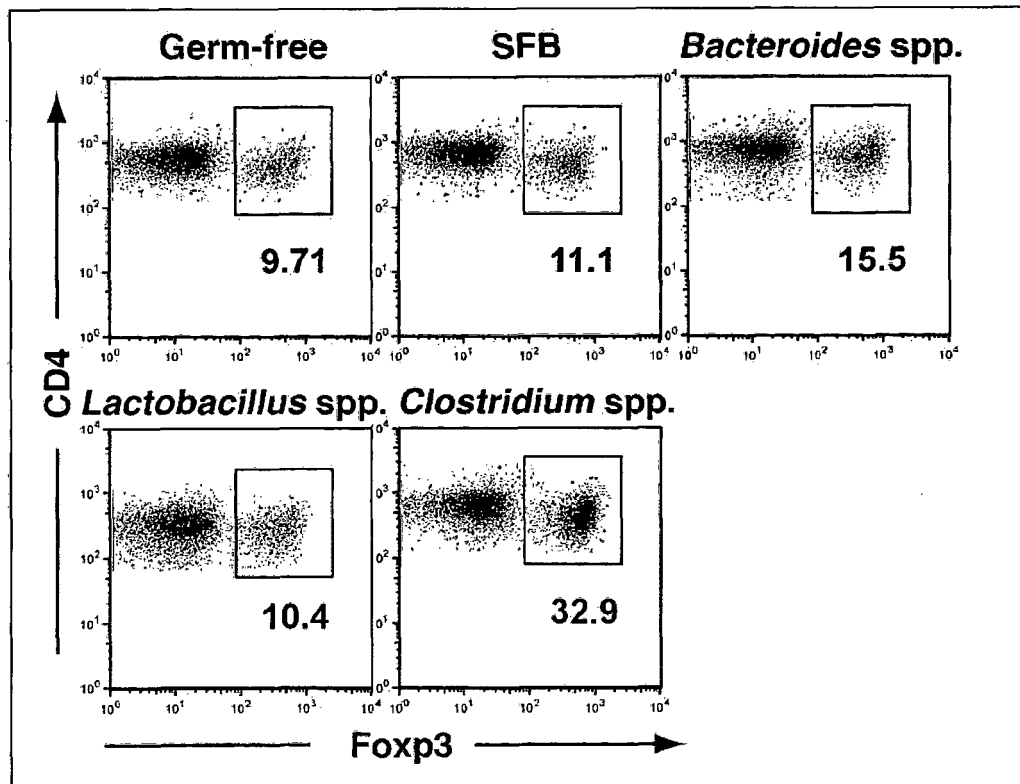
[Fig. 11]



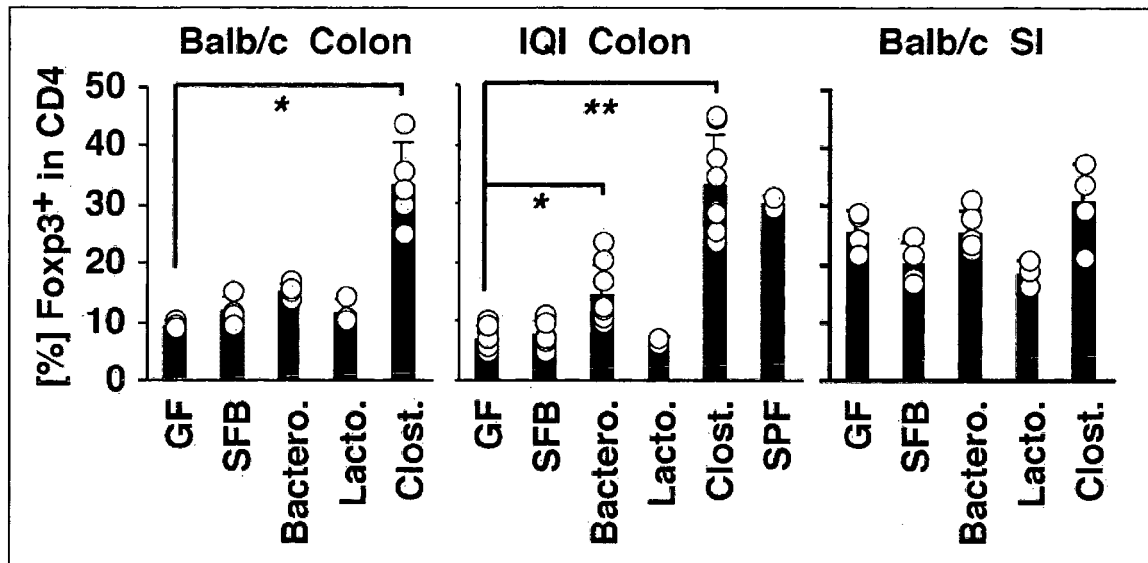
[Fig. 12]



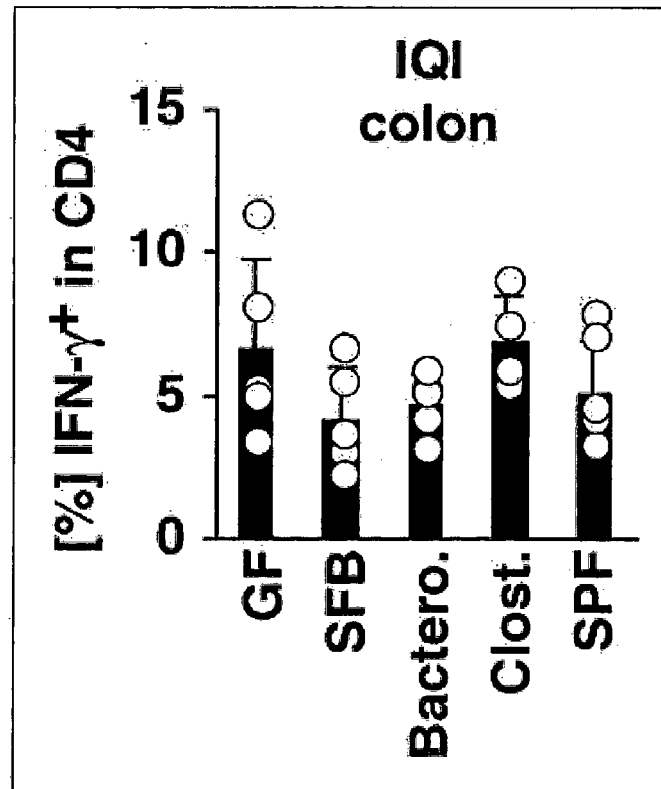
[Fig. 13]



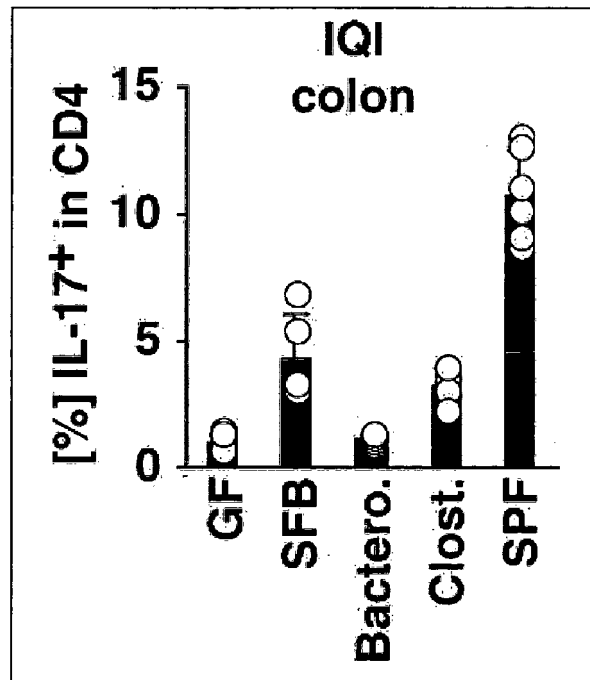
[Fig. 14]



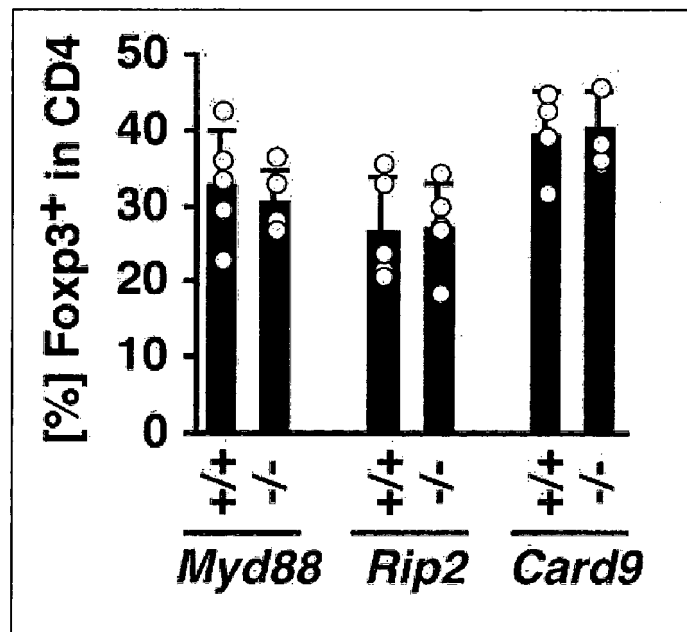
[Fig. 15]



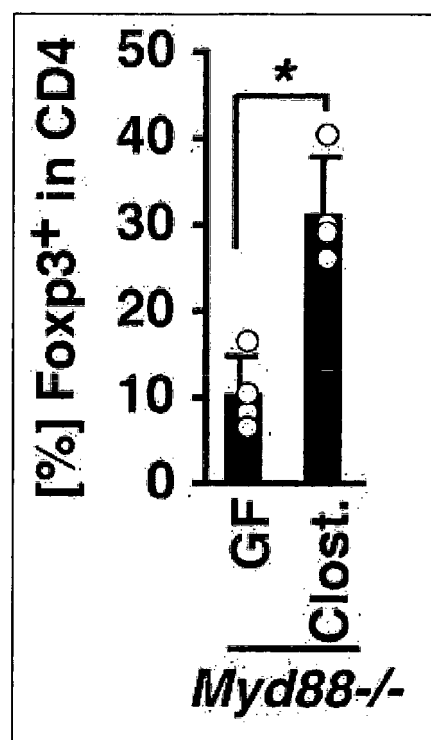
[Fig. 16]



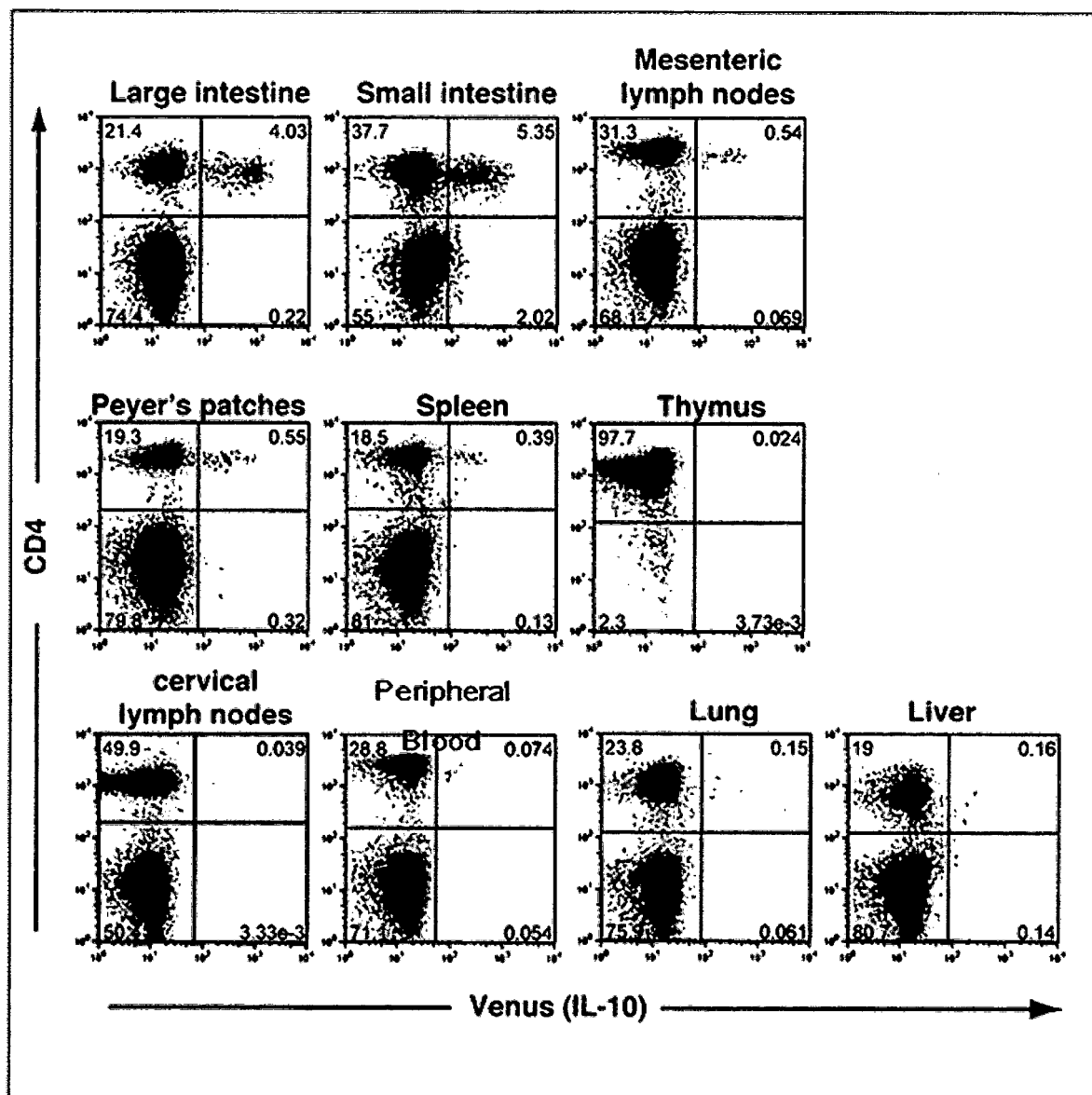
[Fig. 17]



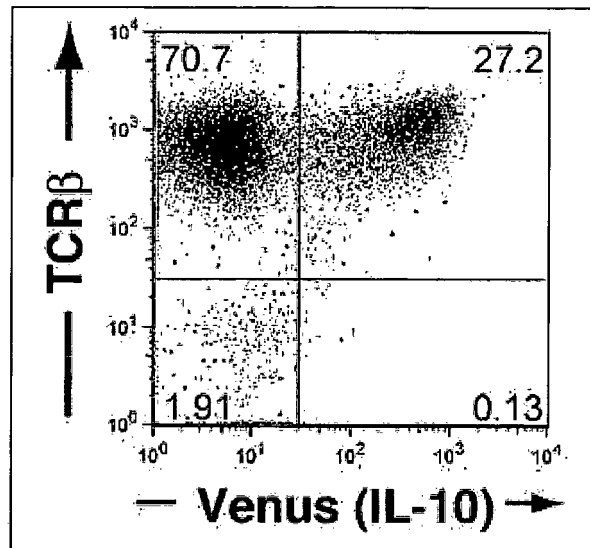
[Fig. 18]



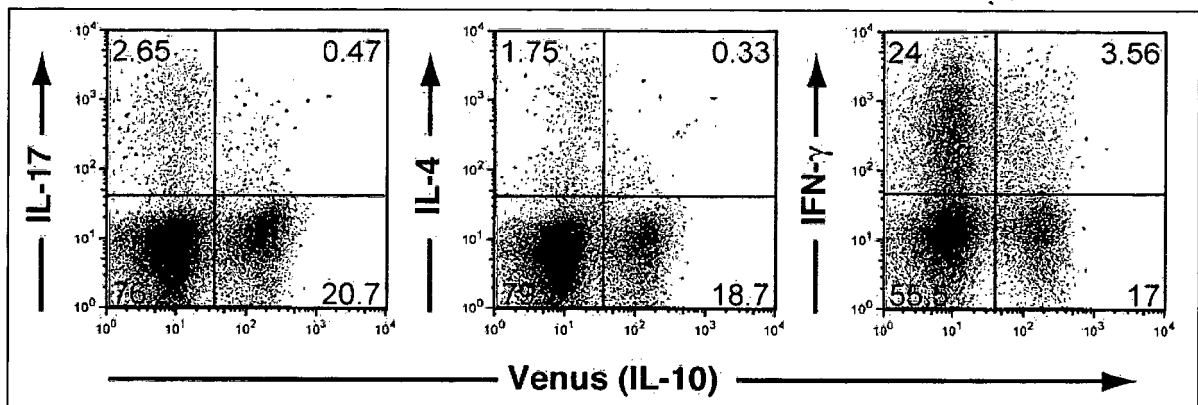
[Fig. 19]



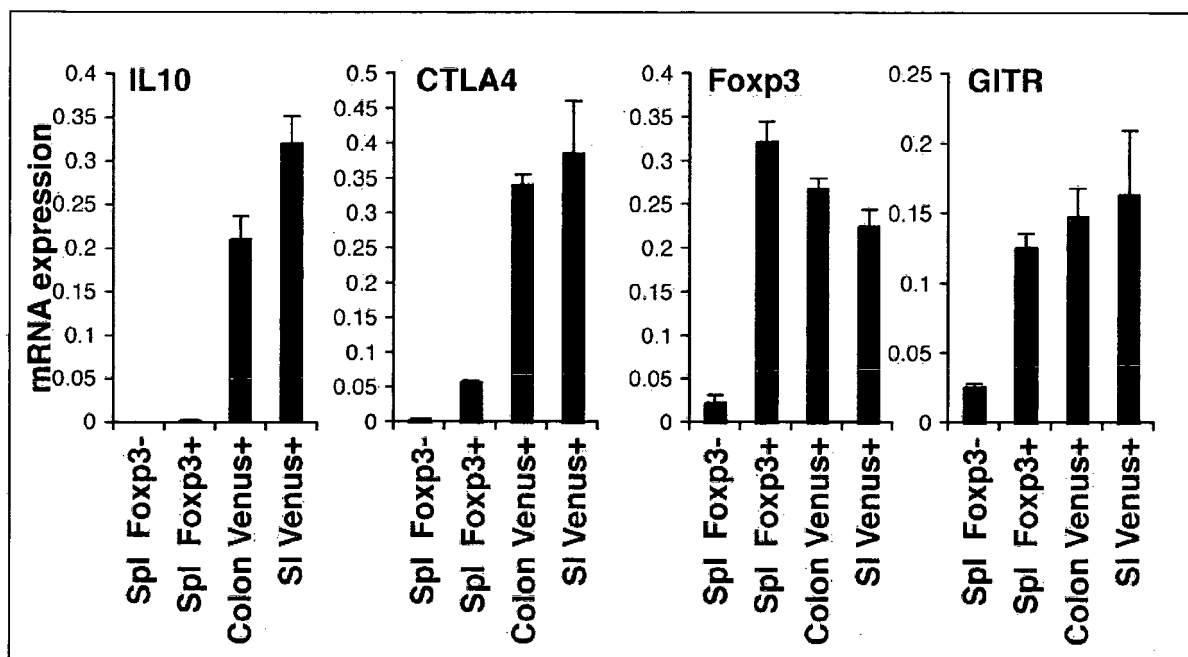
[Fig. 20]



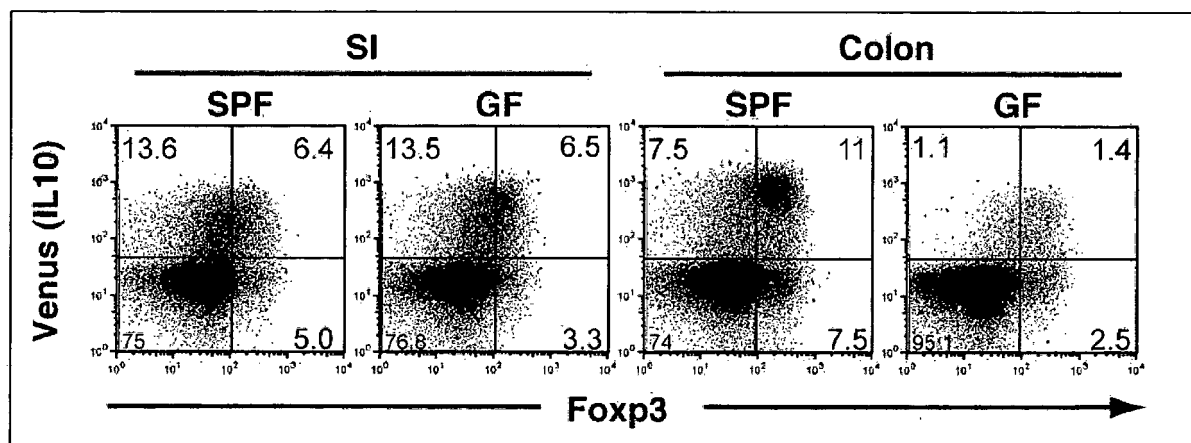
[Fig. 21]



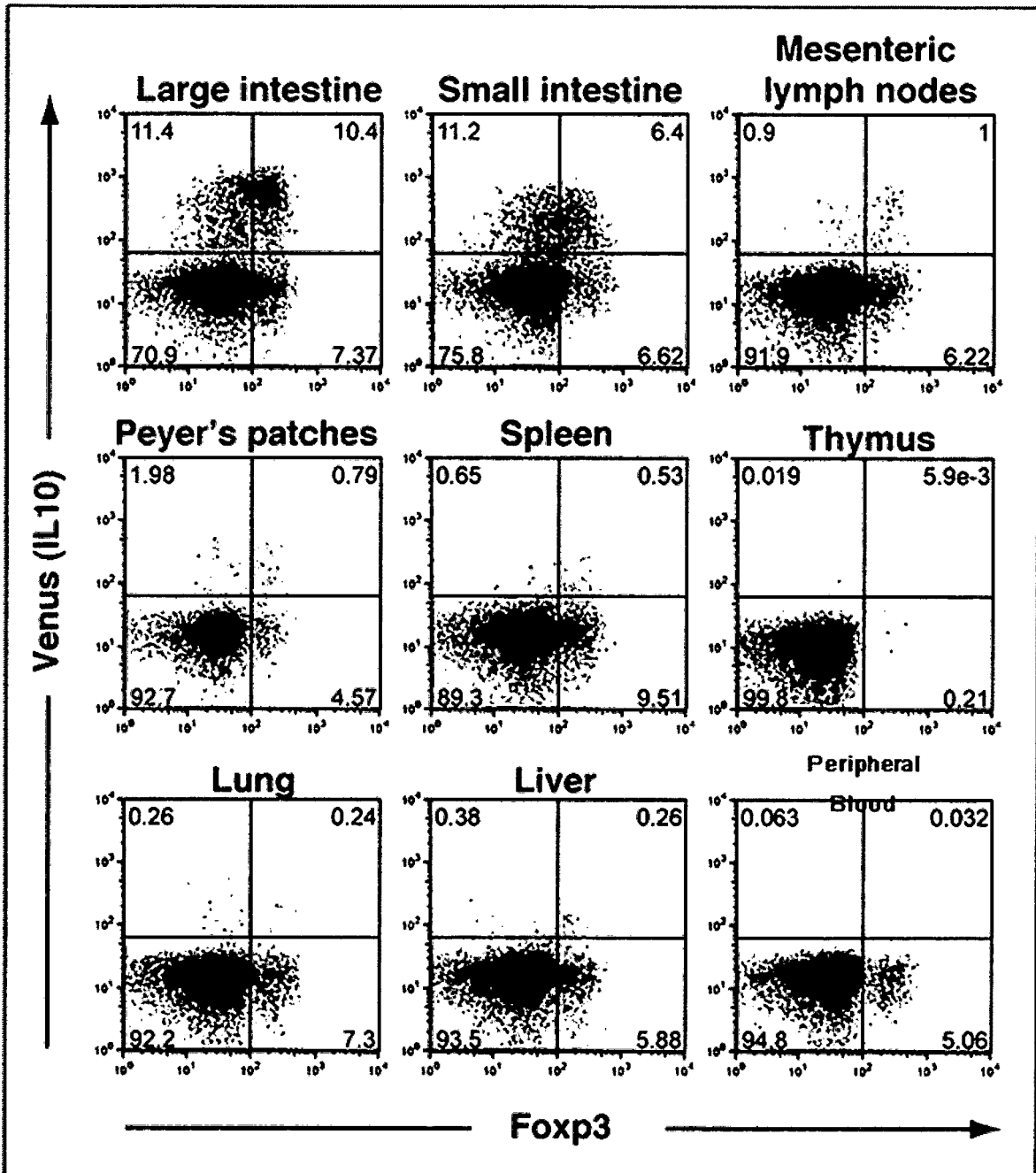
[Fig. 22]



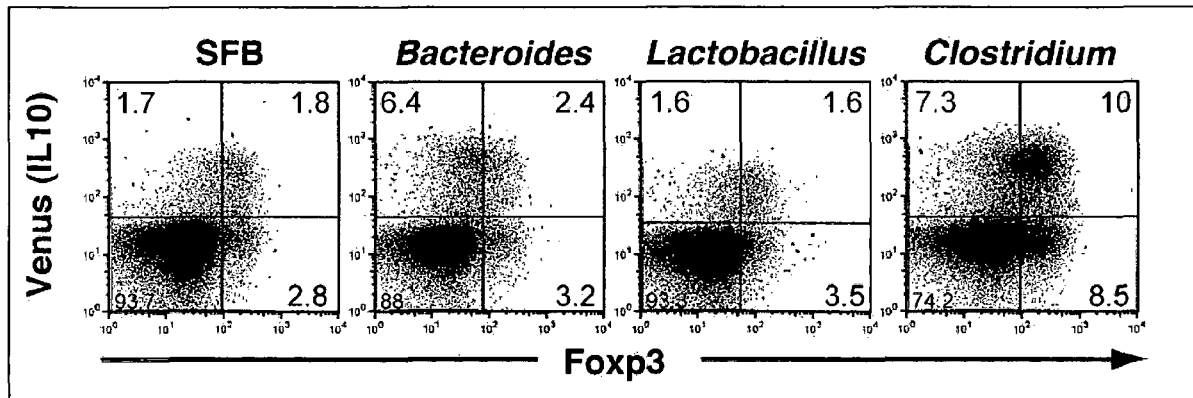
[Fig. 23]



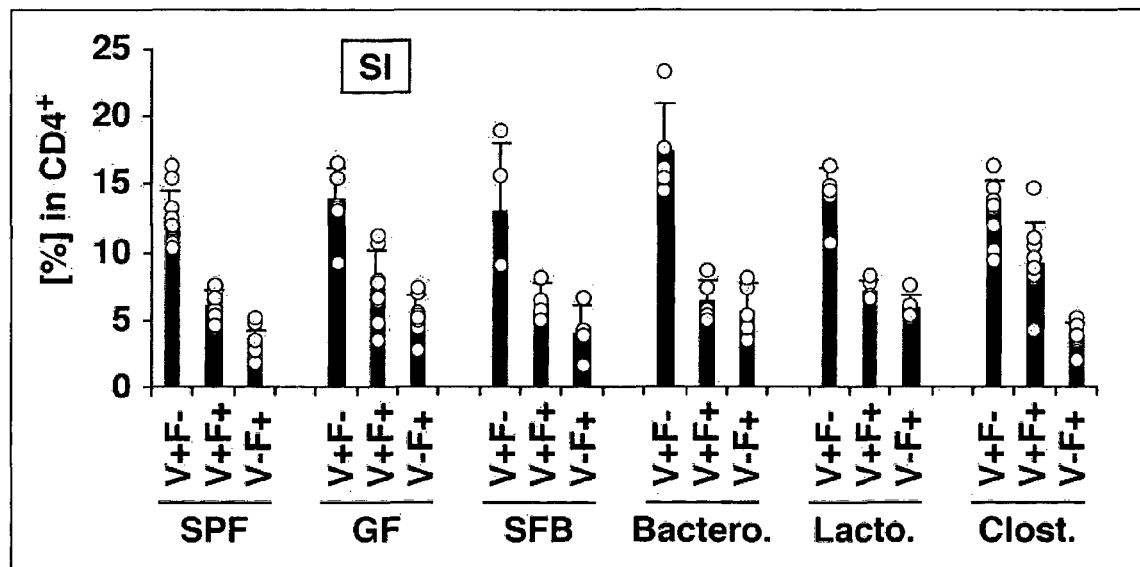
[Fig. 24]



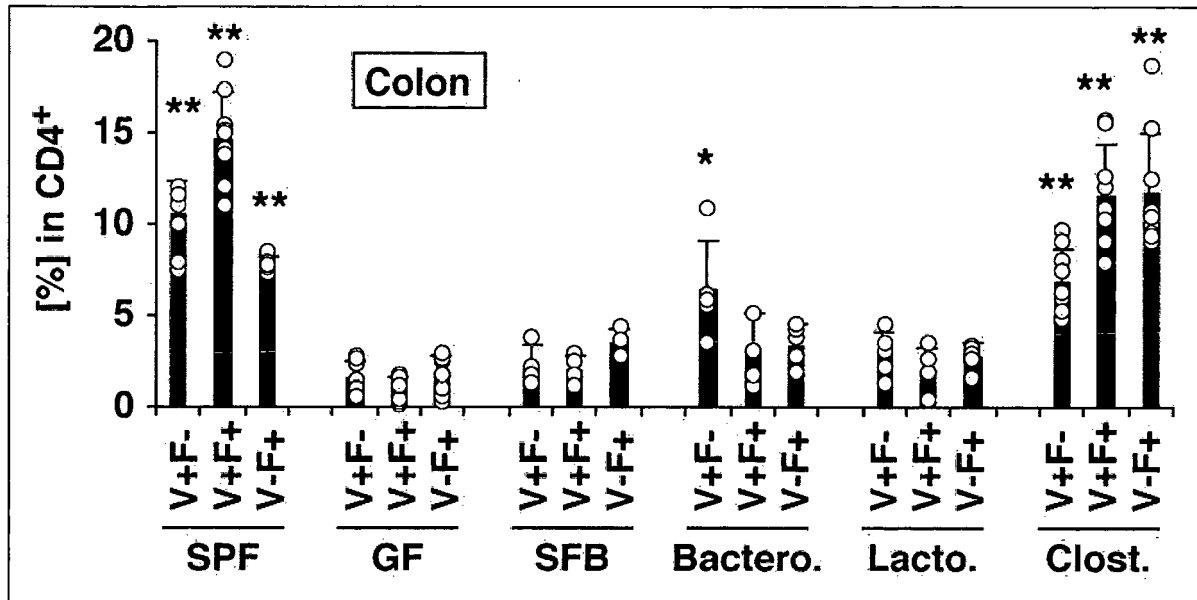
[Fig. 25]



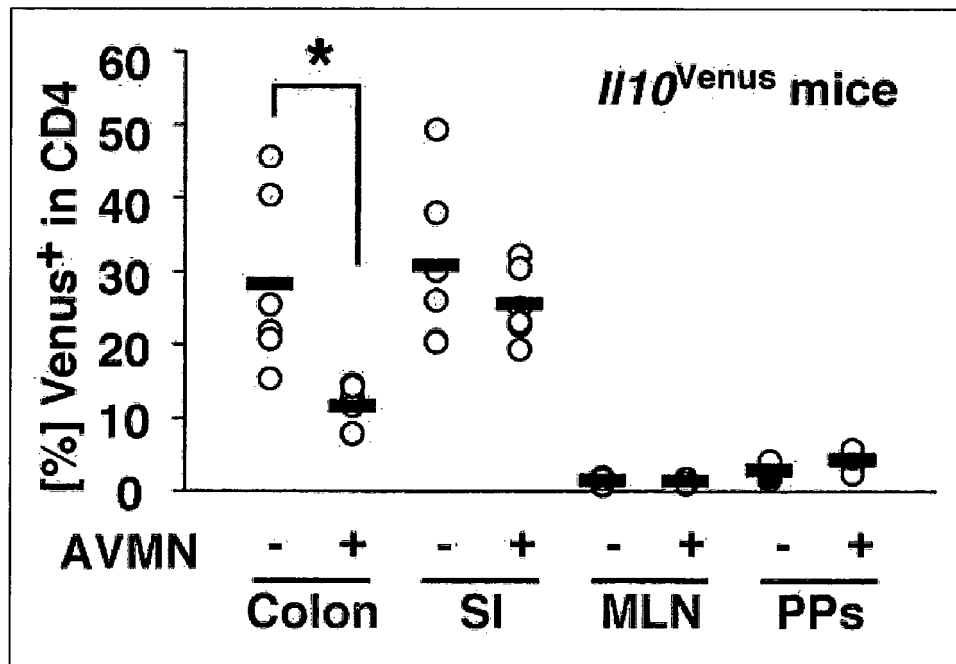
[Fig. 26]



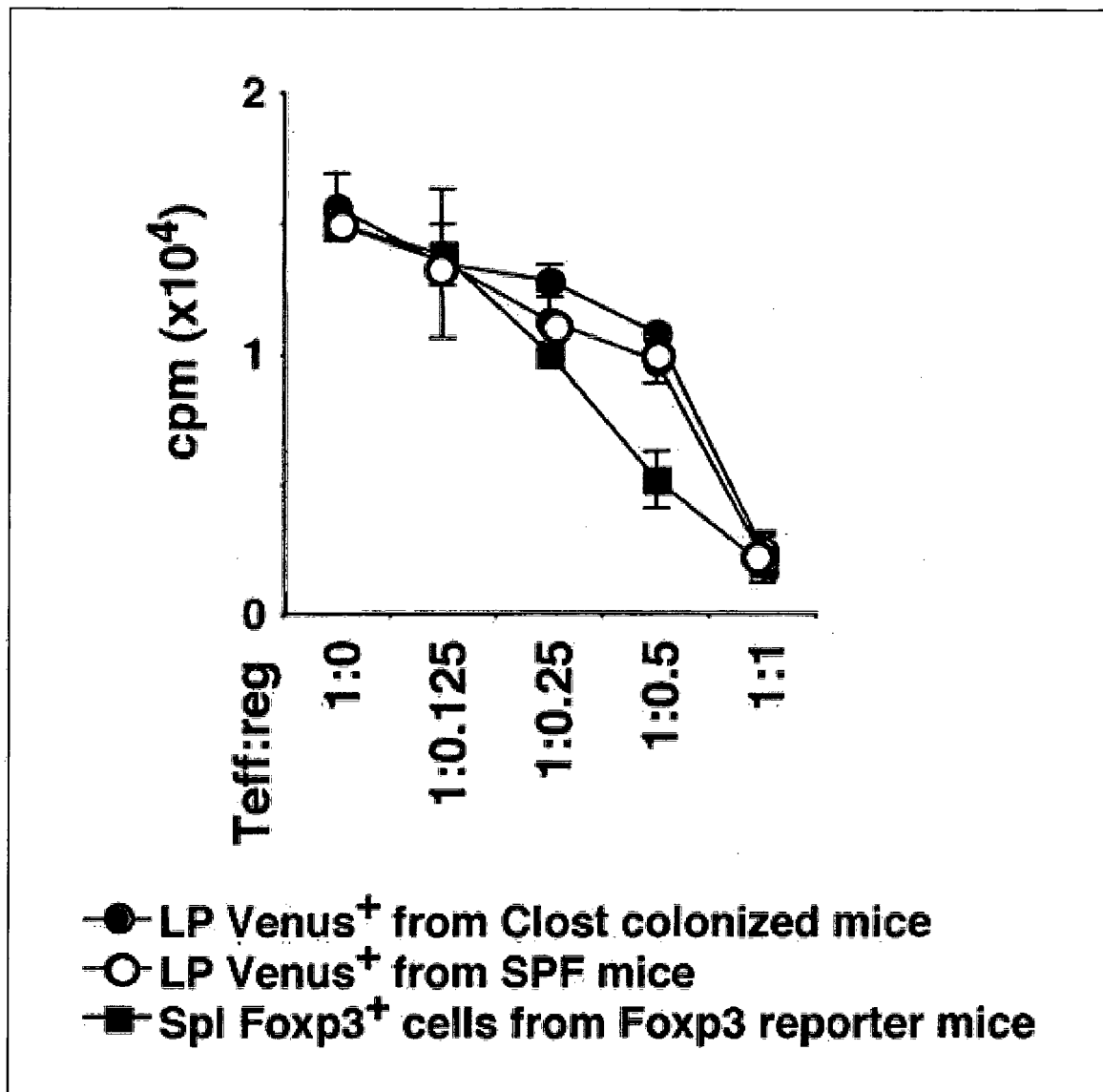
[Fig. 27]



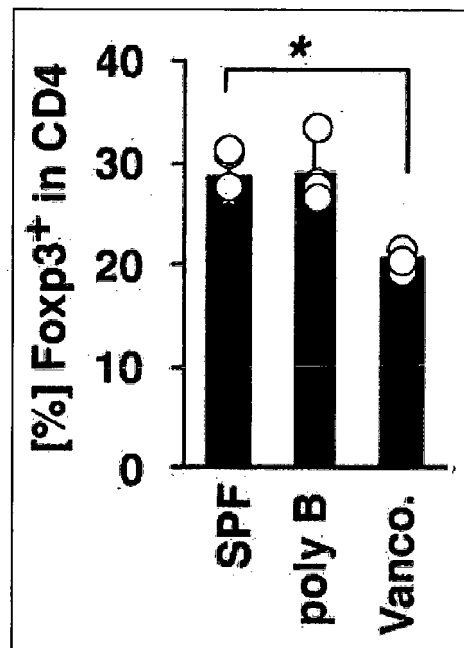
[Fig. 28]



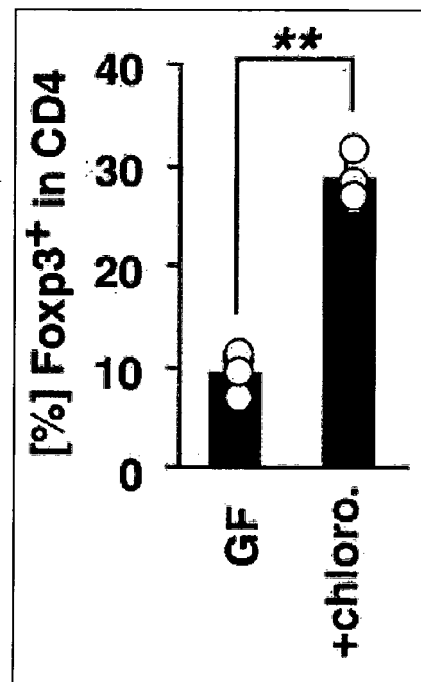
[Fig. 29]



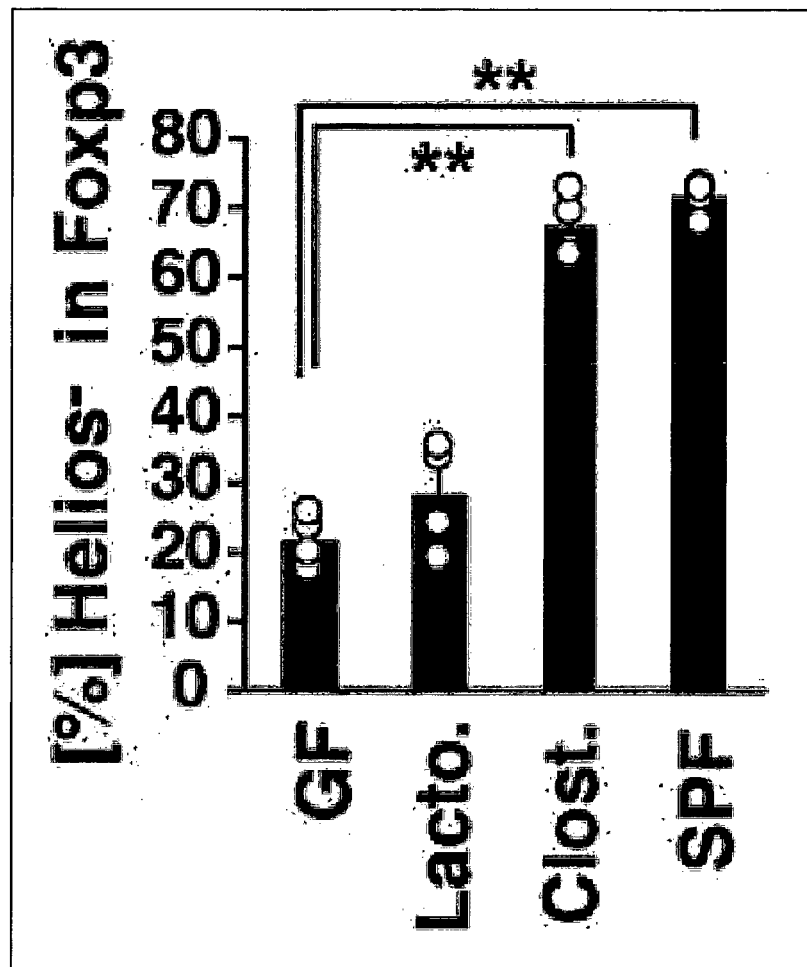
[Fig. 30]



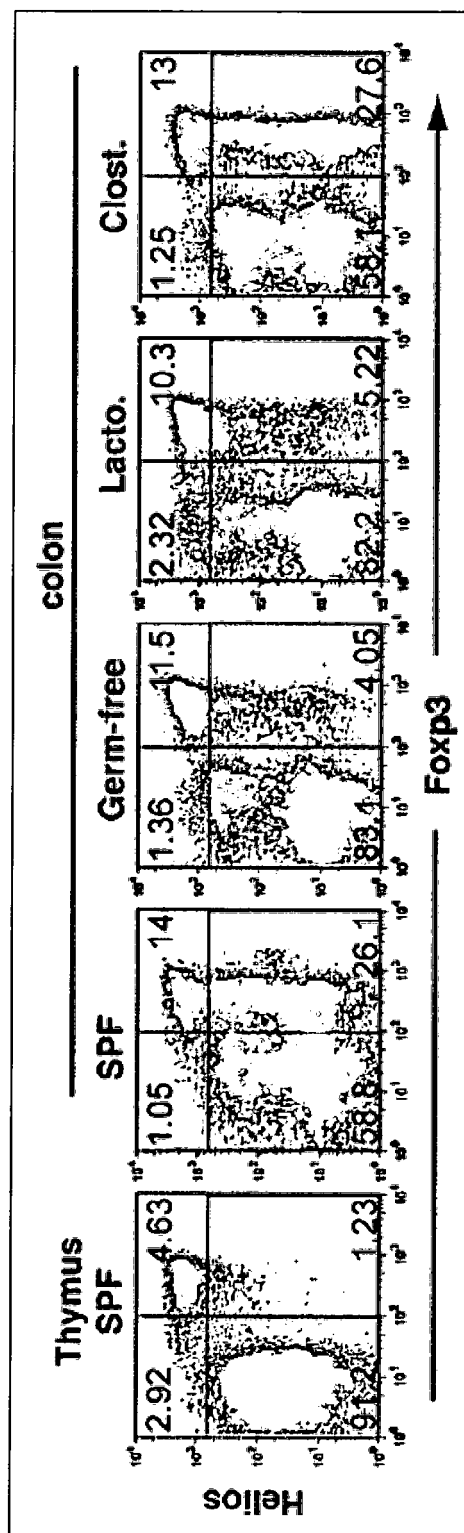
[Fig. 31]



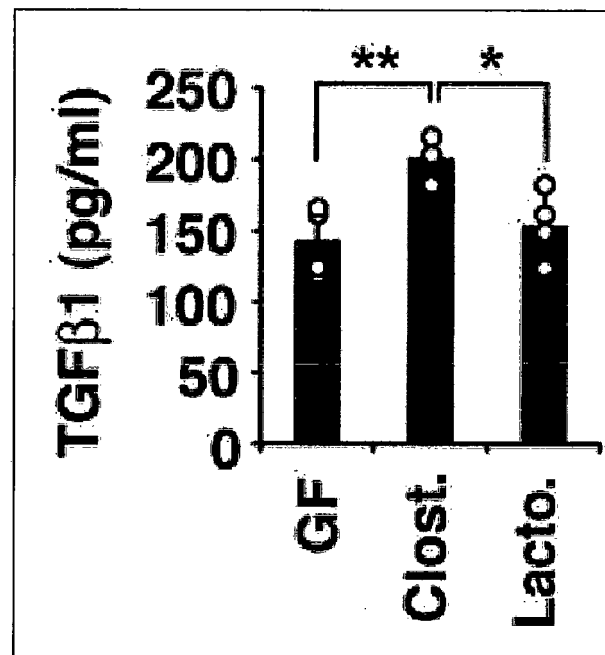
[Fig. 32].



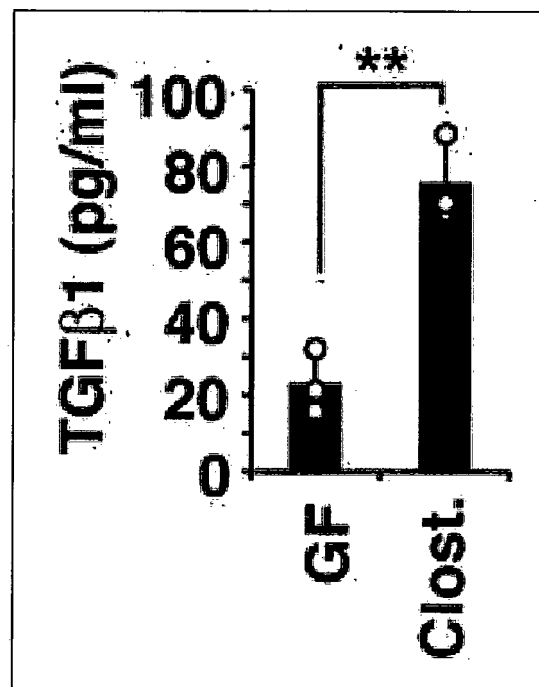
[Fig. 33]



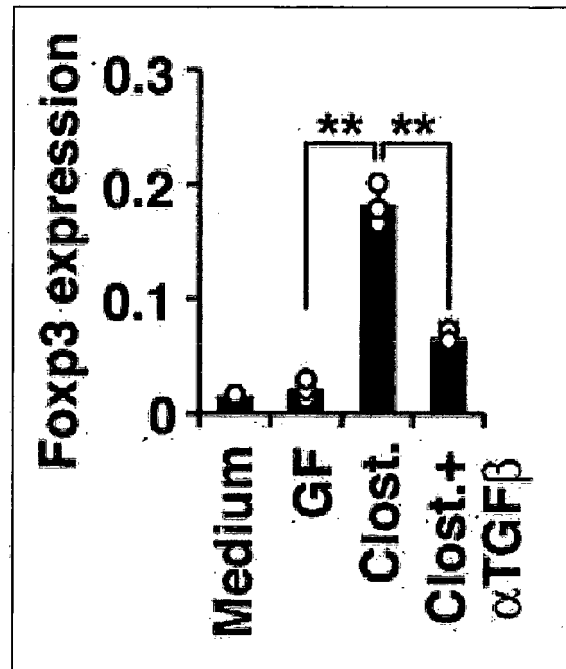
[Fig. 34]



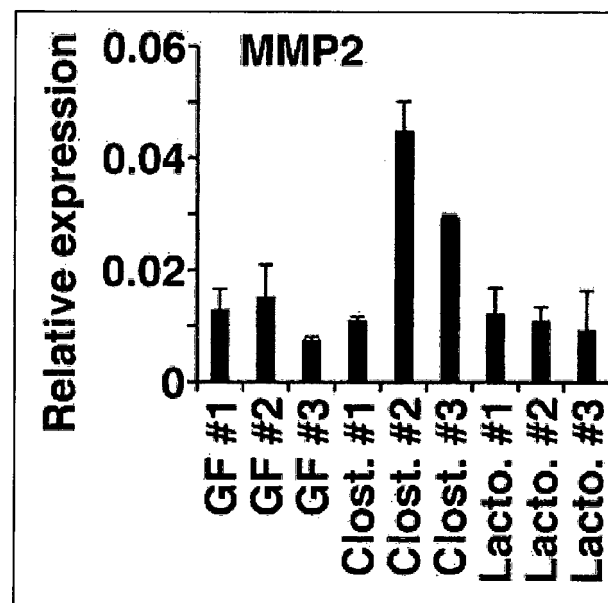
[Fig. 35]



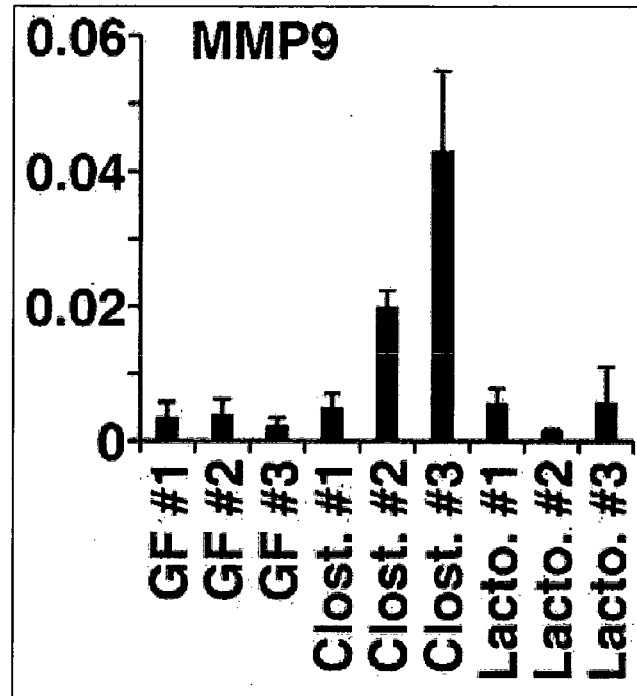
[Fig. 36]



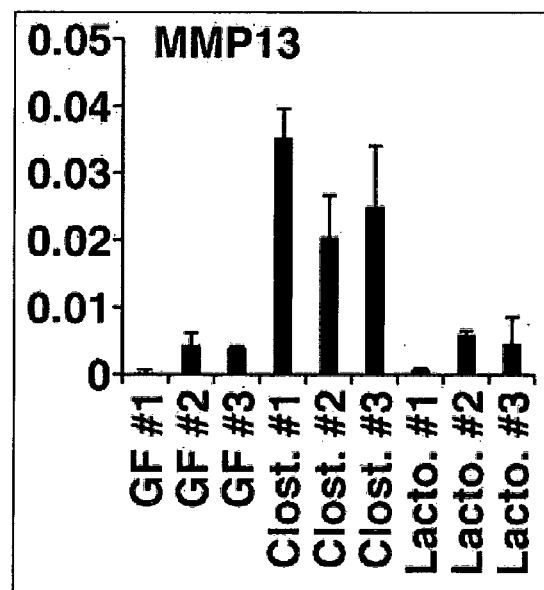
[Fig. 37]



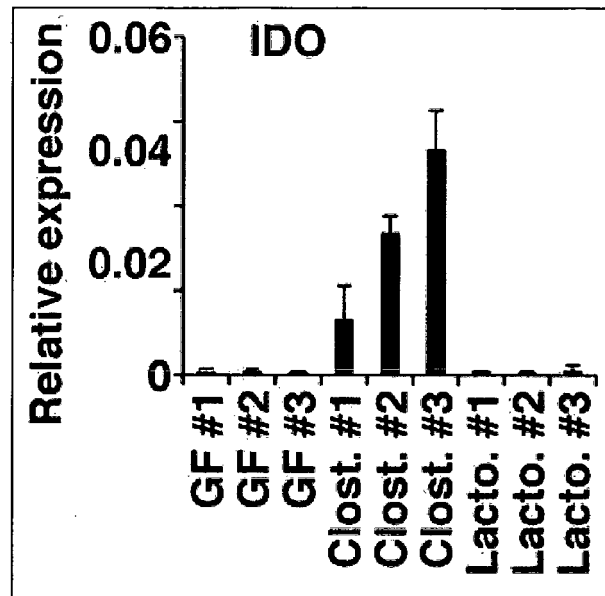
[Fig. 38]



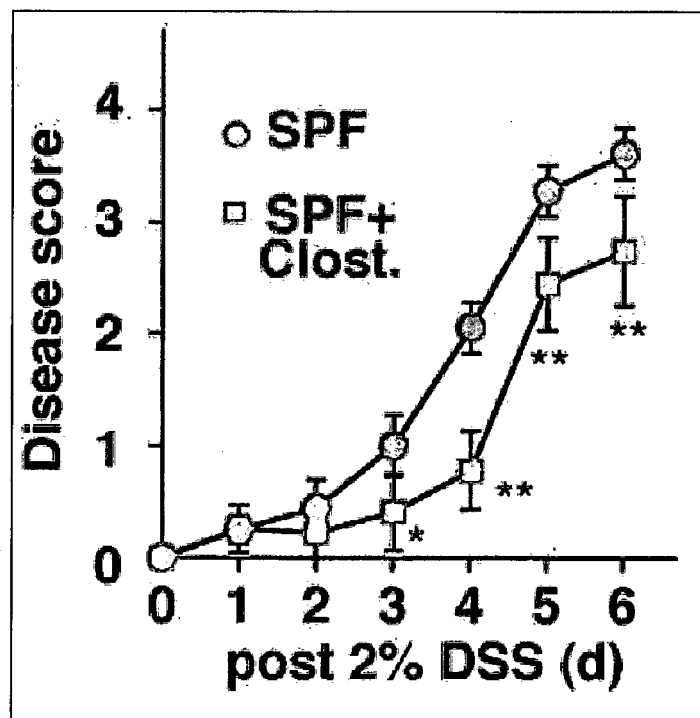
[Fig. 39]



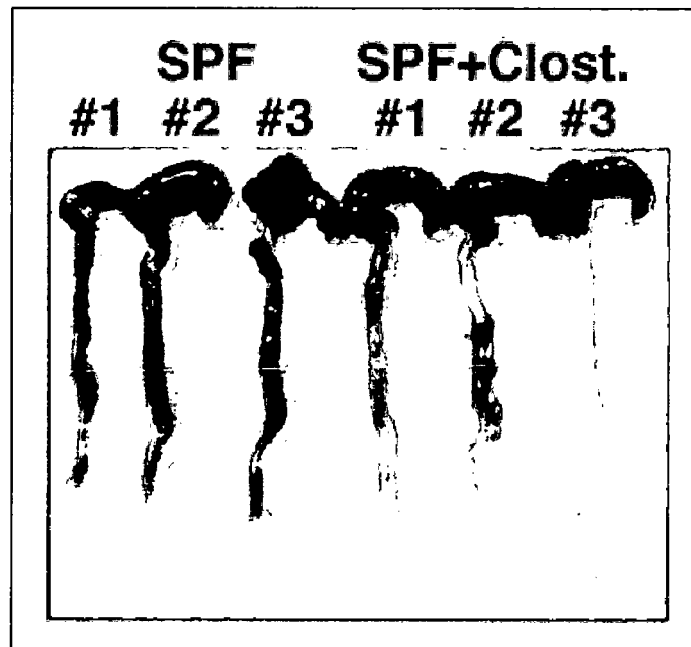
[Fig. 40]



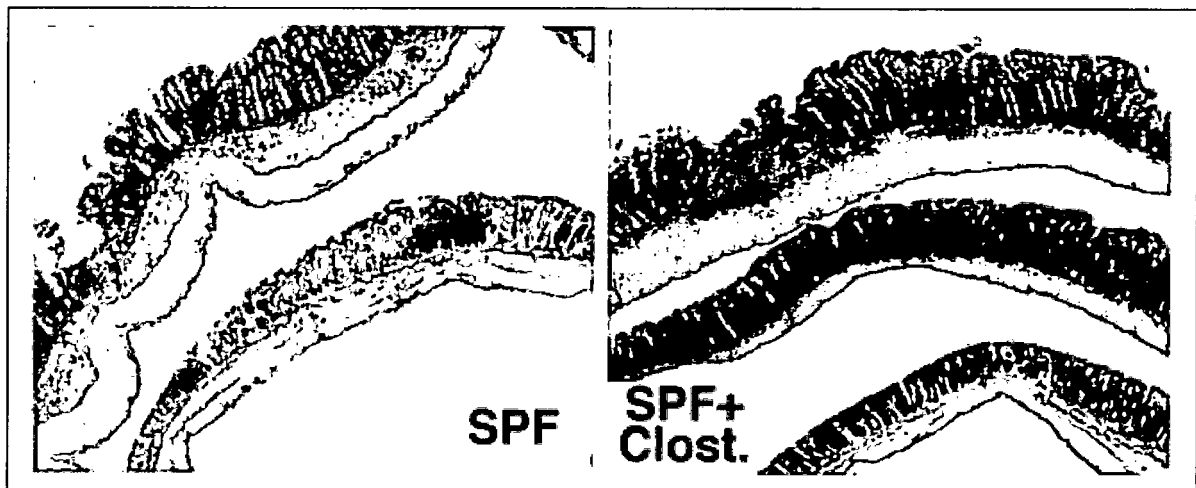
[Fig. 41]



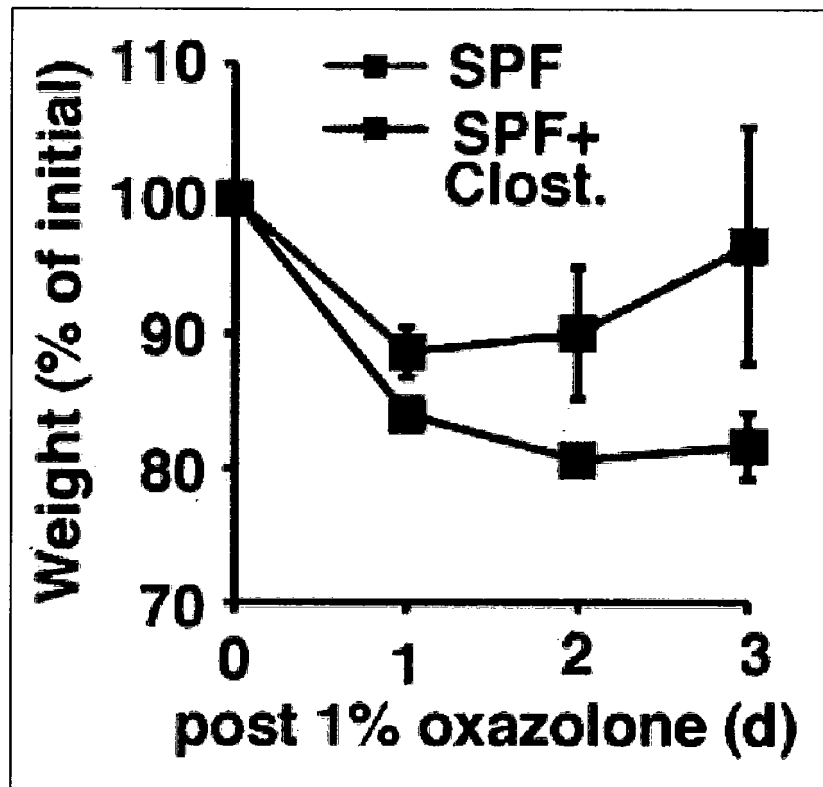
[Fig. 42]



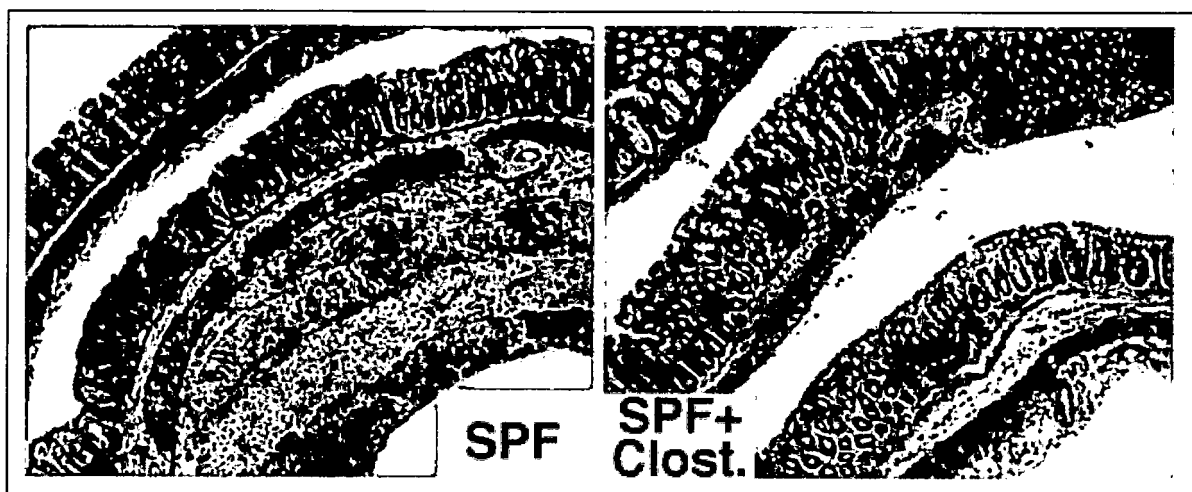
[Fig. 43]



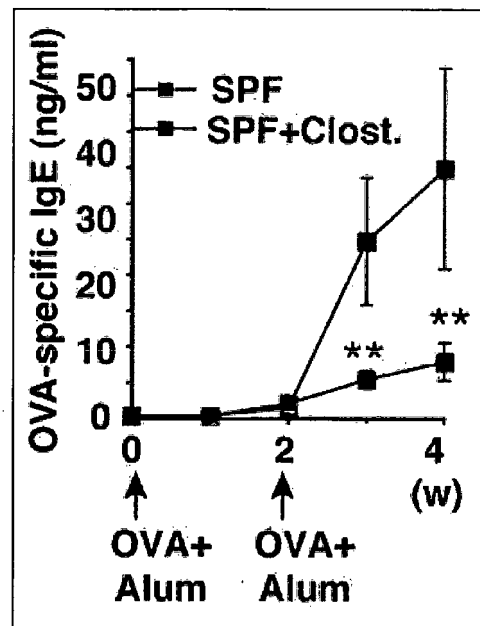
[Fig. 44]



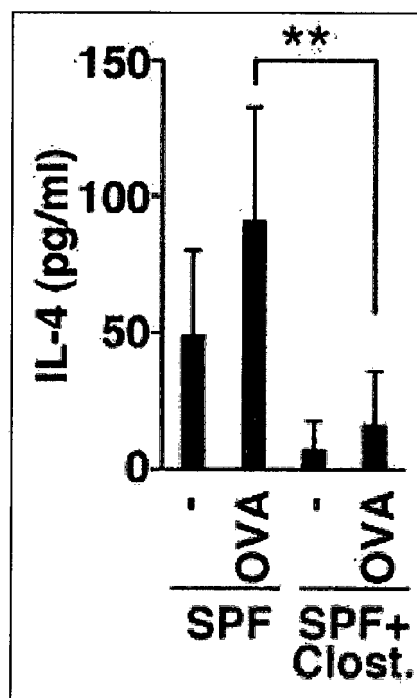
[Fig. 45]



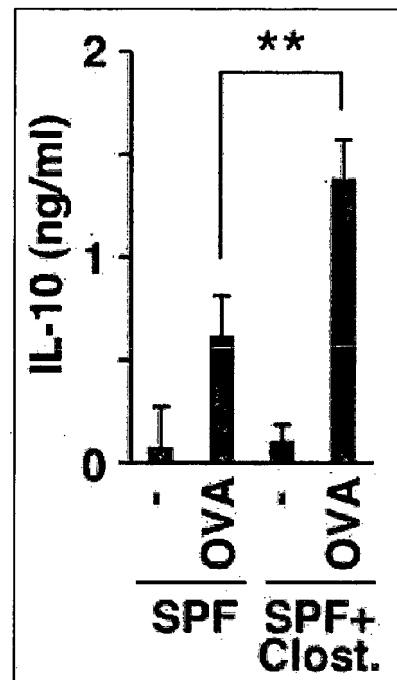
[Fig. 46]



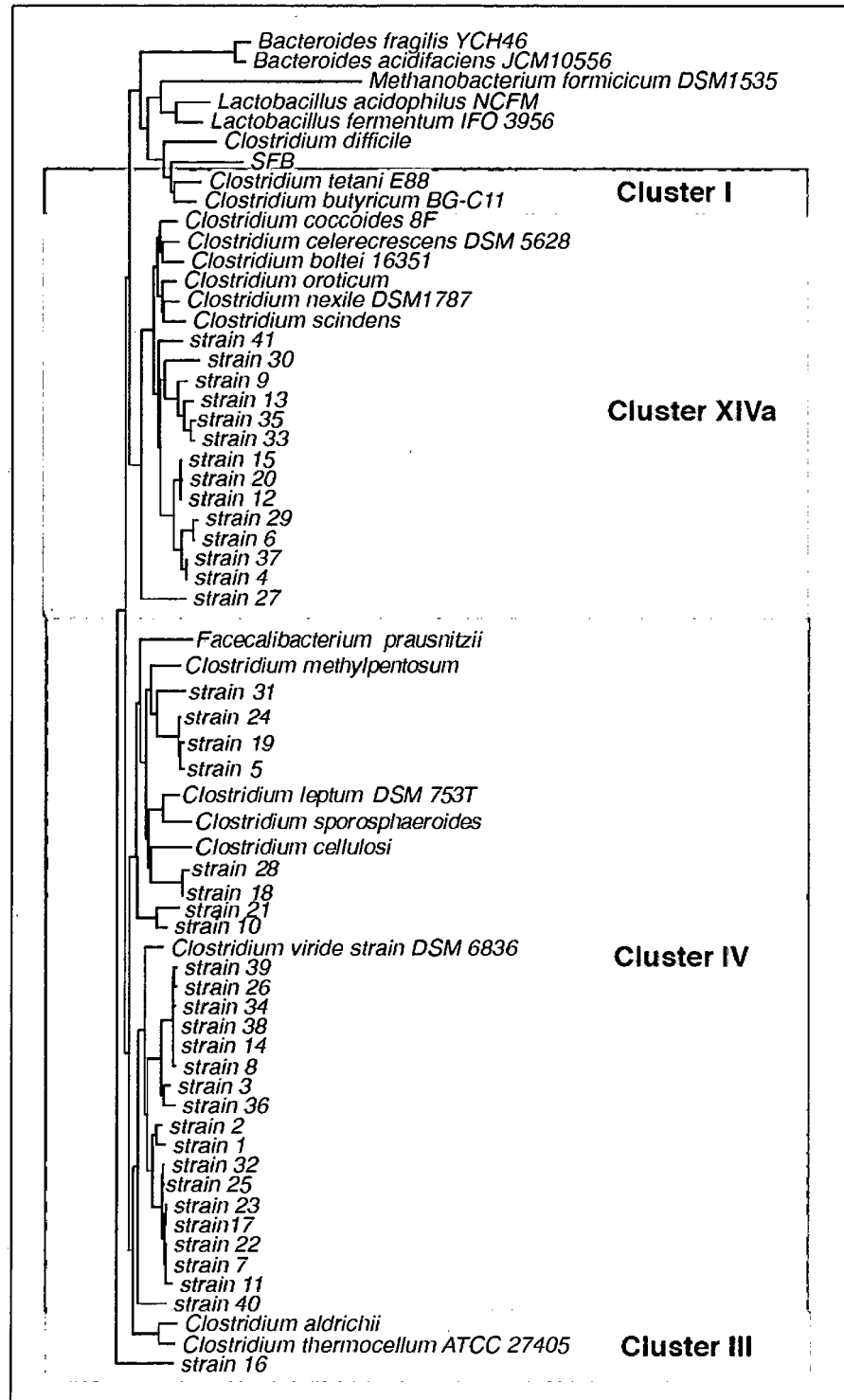
[Fig. 47]



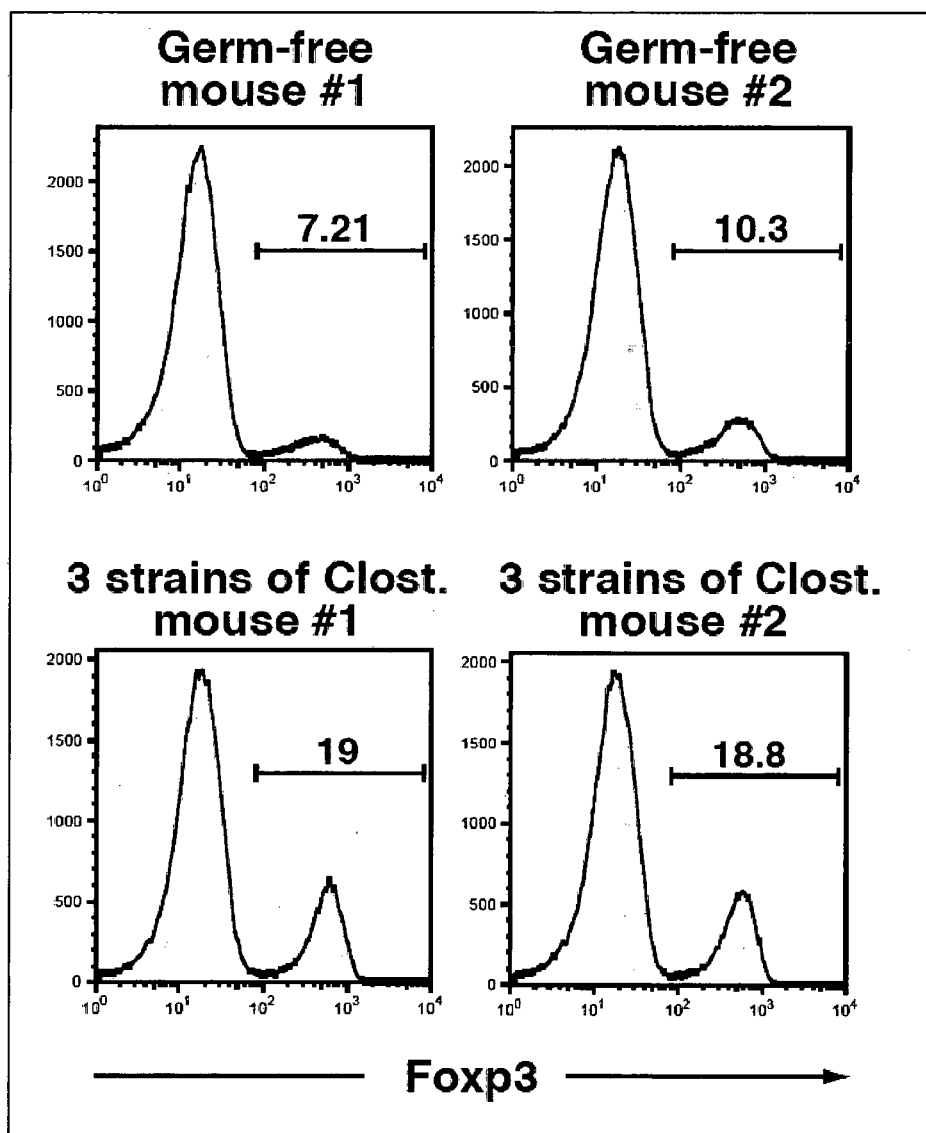
[Fig. 48]



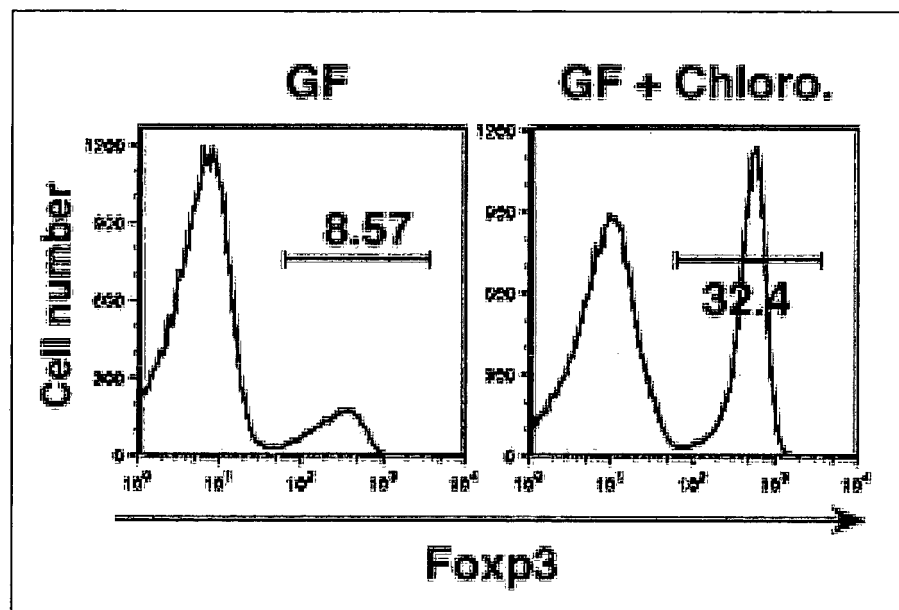
[Fig. 49]



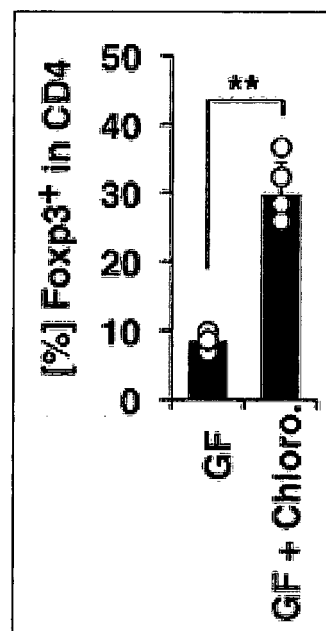
[Fig. 50]



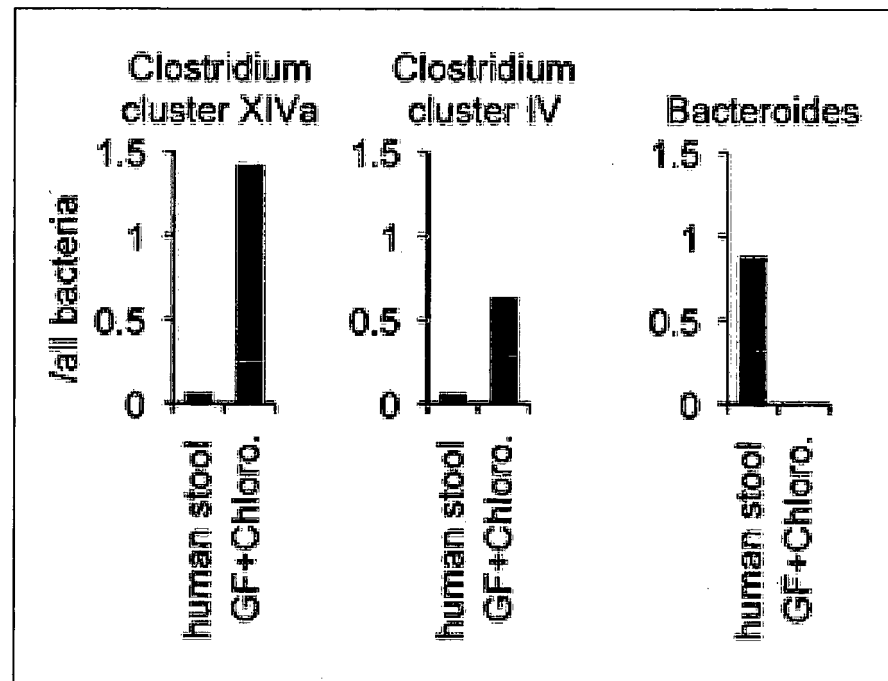
[Fig. 51]



[Fig. 52]



[Fig. 53]



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