

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
5 February 2009 (05.02.2009)

PCT

(10) International Publication Number
WO 2009/018447 A2

(51) International Patent Classification:
A01N 63/02 (2006.01)

(21) International Application Number:
PCT/US2008/071769

(22) International Filing Date: 31 July 2008 (31.07.2008)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/962,870 31 July 2007 (31.07.2007) US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- without international search report and to be republished upon receipt of that report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(54) Title: DIAGNOSTIC AND TREATMENT METHODS FOR CHARACTERIZING BACTERIAL MICROBIOTA IN SKIN CONDITIONS

(57) Abstract: The present invention relates to methods for characterization of bacterial skin microbiota to provide diagnostic, therapeutic, and preventive measures for alleviating skin conditions. In certain embodiments, the invention relates to characterization of bacterial skin microbiota associated with psoriasis and related diagnostic, therapeutic, and preventive measures for alleviating psoriasis. These methods will be useful for detecting, diagnosing, and monitoring individuals who have or are at risk of certain skin conditions.



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DIAGNOSTIC AND TREATMENT METHODS FOR CHARACTERIZING BACTERIAL MICROBIOTA IN SKIN CONDITIONS

[01] This application claims priority from U.S. Provisional Patent Application Serial No. 60/962,870, filed July 31, 2007, which is herein incorporated by reference in its entirety.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[02] This invention was made in part in the course of research sponsored by the National Institutes of Health (NIH) Grant RO1 GM 63270; the Ellison Medical Foundation; Diane Belfer Program for Microbial Ecology; and a Bernard Levine Scholarship. The U.S. government may have certain rights in this invention.

FIELD OF THE INVENTION

[03] The present invention relates to characterization of microbiota associated with various skin conditions and related diagnostic, therapeutic, and preventive measures for alleviating the skin conditions. In certain embodiments, the invention relates to characterization of microbiota associated with psoriasis and related diagnostic, therapeutic, and preventive measures for alleviating, treating, or preventing psoriasis.

BACKGROUND OF THE INVENTION

[04] Psoriasis is a common dermatosis of unknown cause. It is characterized as a chronic inflammatory condition of human skin. Psoriasis is estimated to affect about 3% of the population in industrialized countries (Baroni, A., et al., 2004. *J. Cutan. Pathol.* 31:35-42.), and is typically characterized by erythrosquamous cutaneous lesions associated with abnormal patterns of keratinocyte growth and differentiation (Lebwohl, M. 2003., *Lancet* 361:1197-1204). The classic symptoms of psoriasis are raised, red patches of skin topped with loose, silvery scales, usually on the knees or elbows.

[05] There are several types of psoriasis. Symptoms for each type may vary in severity and appear in a wide array of combinations. In general, the major symptoms of psoriasis include: Bright red areas of raised patches (plaques) on the skin, often covered with loose, silvery scales. Plaques can occur anywhere, but commonly they occur on the knees,

elbows, scalp, hands, feet, or lower back. Nearly 90% of people with psoriasis have plaque-type psoriasis.

[06] Other manifestations of psoriasis include tiny areas of bleeding when skin scales are picked or scraped off (Auspitz's sign). Some individuals experience mild scaling to thick, crusted plaques on the scalp. Some patients experience itching, especially during sudden flare-ups or when the psoriasis patches are in body folds, such as under the breasts or the buttocks.

[07] Nail disorders are common, especially in severe psoriasis and include the following symptoms: tiny pits in the nails (not found with fungal nail infections); yellowish discoloration of the toenails and possibly the fingernails; separation of the end of the nail from the nail bed; and a buildup of skin debris under the nails.

[08] Other symptoms of psoriasis may include symmetrical plaques on the same areas on both sides of the body (for example, both knees or both elbows).

[09] In certain instances patients experience flare-ups of many raindrop-shaped patches. Called guttate psoriasis, this condition often follows an infection with Group A Beta-hemolytic *Streptococcus pyogenes* (Group A strep; GAS) and is the second most common type of psoriasis. It affects less than 10% of those with psoriasis.

[10] Finally, some psoriasis patients experience joint swelling, tenderness, and pain (psoriatic arthritis). These symptoms may occur in up to 39% of people with psoriasis.

[11] Koebner's phenomenon can occur when a person with psoriasis has an injury (such as a cut, burn, or excess sun exposure) to an area of the skin that is not affected by psoriasis. Psoriasis patches then appear on the injured skin or any other part of the skin from several days to about 2 weeks after the injury.

[12] Inflammatory aspects of the disease involve dermal angiogenesis, infiltration of activated T cells, and increased cytokine levels. One of these cytokines, IL-15, triggers inflammatory cell recruitment, angiogenesis, and production of other inflammatory cytokines, including IFN- γ , TNF- α , and IL-17, which are all upregulated in psoriatic lesions. Although psoriasis has an unknown etiology, certain trigger factors, including physical

trauma and GAS infections as described above, have been hypothesized to provoke clinical manifestations of psoriasis (Schon, M. P., and W. H. Boehncke. 2005. *N. Engl. J. Med.* 352:1899-1912). Fungal organisms, including *Candida albicans* (Waldman, A. et al., 2001. *Mycoses*; 44:77-81) and *Malassezia furfur* (Baroni, A., et al., 2004. *J. Cutan. Pathol.* 31:35-42.), have also been associated with the development of psoriatic skin lesions, and differences have been observed in the *Malassezia* species distributions in healthy subjects and patients with psoriasis (Gupta, A. K., et al., 2001. *Med. Mycol.* 39:243-251.; Hernandez Hernandez, F., et al., 2003. *Rev. Iberoam. Micol.* 20:141-144.; Prohic, A. 2003. *Croat*; 11:10-16.). Recent studies have also begun to characterize bacterial populations of human skin by using culture-independent molecular techniques (Dekio, I., et al., (2005) *J. Med. Microbiol.*; 54(12):1231-1238.

[13] The human skin has been considered to harbor a complex microbial ecosystem (Fredricks, DN. (2001); *J Investig Dermatol Symp Proc* 6, 167–169), with transient, short-term resident and long-term resident biota, based on the consistency with which they are isolated. *Staphylococcus*, *Micrococcus*, *Corynebacterium*, *Brevibacteria*, *Propionibacteria*, and *Acinetobacter* species, among others, are regularly cultivated from normal skin. *Staphylococcus aureus*, *Streptococcus pyogenes*, (GAS) and *Pseudomonas aeruginosa* may be transient colonizers, especially in pathological conditions. Environmental factors, such as temperature, humidity, and light exposure, and host factors, including gender, genotype, immune status, and cosmetic use, all may affect microbial composition, population size, and community structure.

[14] Knowledge of the human skin biota, chiefly through cultivation-based studies, is considerably limited in assessing compositions of complex microbial communities. In contrast, broad-range PCR primers targeted to highly conserved regions makes possible the amplification of small subunit rRNA genes (16S rDNA) sequences from all bacterial species (Zoetendal, EG, Vaughan, EE & de Vos, WM. (2006) *Mol Microbiol* 59, 1639–1650), and the extensive and rapidly growing 16S rDNA database facilitates identification of sequences to the species or genus level (Schloss, PD & Handelsman, J. (2004) *Microbiol Mol Biol Rev* 68, 686–691). Such techniques are increasingly used for identifying bacterial species in complex environmental niches (Smit, E, Leeflang, P, Gommans, S, van den, BJ, van Mil, S & Wernars, K. (2001) *Appl Environ Microbiol* 67, 2284–2291), including the human

mouth, esophagus, stomach, intestine, feces, and vagina, and for clinical diagnosis (Harris, KA & Hartley, JC. (2003) *J Med Microbiol* 52, 685–691; Saglani, S, Harris, KA, Wallis, C & Hartley, JC. (2005) *Arch Dis Child* 90, 70–73).

[15] Although certain fungal associations and genetic and immunological features of skin conditions such as psoriasis have been examined, the role of bacterial microbiota in psoriasis has not been understood. Thus, there remains a need for methods for diagnosing, treating and preventing skin conditions such as psoriasis, particularly based on characterizing and altering bacterial microbiota to alleviate the condition. Until the present studies, little has been known about the species composition in cutaneous skin samples, and in particular there has been no comparison between bacterial species composition in normal skin and in psoriatic lesions.

SUMMARY OF THE INVENTION

[16] The present invention provides methods for characterizing and determining differences between bacterial populations in healthy or normal skin and in diseased skin, including in psoriatic lesions. Embodiments of the present invention relate to a bacterial signature or marker for psoriasis.

[17] In certain embodiments, the invention relates to determining that at least one *Propionibacterium* species is underrepresented (i.e., found in low amounts or proportions) in diseased or affected skin, when compared with the amount of at least one *Propionibacterium* species found in healthy skin. In certain embodiments, the invention relates to determining the amount of at least one *Propionibacterium* species; wherein a low amount of at least one *Propionibacterium* species indicates psoriasis. In certain embodiments, the diseased or affected skin is a psoriatic lesion. In certain embodiments, the species is *Propionibacterium acnes* (*P. acnes*). In certain embodiments, the invention relates to determining that a low amount of at least one *Propionibacterium* species in psoriatic skin lesions when compared with the amount found in unaffected or healthy skin is a marker for psoriasis.

[18] In further embodiments, the invention relates to diagnostic methods utilizing the amount of at least one *Propionibacterium* species in psoriatic skin lesions compared with

the amount of at least one *Propionibacterium* species found in healthy skin as a marker for psoriasis.

[19] In still further embodiments, the invention relates to determining a stage of psoriasis utilizing the proportion of *Propionibacterium* species in psoriatic skin lesions compared with the proportion of *Propionibacterium* found in healthy skin.

[20] In additional embodiments, the invention relates to altering or replacing *Propionibacterium* species in the skin of patients in need of such treatment, including in psoriatic skin lesions of the patients. In further embodiments, the invention relates to altering or replacing *Propionibacterium acnes* in the skin of patients in need of such treatment, including in psoriatic lesions of the patients.

[21] In additional embodiments, the invention relates to agents and methods for promoting growth of *Propionibacterium* species in the skin of psoriatic patients in need of such treatment. In additional embodiments, the invention relates to agents and methods for promoting growth of *Propionibacterium* species prophylactically in the skin of patients in need of such treatment. In certain embodiments, the *Propionibacterium* species is *Propionibacterium acnes*.

[22] In additional embodiments, the invention relates to methods for treating psoriasis comprising administering an effective amount of at least one *Propionibacterium* species to affected skin in a patient in need of such treatment. In certain embodiments, at least one *Propionibacterium* species includes live *Propionibacterium* cells, killed or inactivated cells, or an extract from the cells. In additional embodiments, the cells may be derived from cells grown under ordinary circumstances or grown to induce increased production of particular constituents.

[23] In additional embodiments, the invention relates to methods for monitoring effectiveness of therapies for psoriasis by measuring changes in the density or proportion of *Propionibacterium* species in the skin of psoriatic patients including in psoriatic skin lesions of patients. In certain embodiments, the *Propionibacterium* species is *Propionibacterium acnes*.

[24] In yet further embodiments, the invention relates to determining the proportion of at least one non-Group A *Streptococcus* species (NGS) in affected or diseased skin of patients, including in psoriatic skin lesions of patients.

[25] In certain embodiments, the invention relates to determining that at least one NGS species is overrepresented (i.e., found in an elevated amount) in psoriatic skin lesions, when compared with the amount of at least one NGS found in healthy or unaffected skin. In certain embodiments, the invention relates to determining that a high proportion of NGS in psoriatic skin lesions when compared with healthy skin, is a marker for psoriasis.

[26] In additional embodiments, the invention relates to inhibiting the growth of or lowering the amount of at least one NGS in the skin of psoriatic patients including in psoriatic skin lesions of patients. In certain embodiments, inhibiting or lowering the amount of at least one NGS includes antibiotic treatment and/or chemical and physical means of inhibiting or lowering the amount of at least one NGS. In certain embodiments, inhibiting or lowering the amount of at least one NGS includes chemical and/or physical means of inhibiting or lowering the amount of at least one NGS.

[27] In further embodiments, the invention relates to diagnostic methods utilizing the proportion of at least one NGS species in psoriatic lesions compared with healthy skin as a marker for psoriasis.

[28] In still further embodiments, the invention relates to determining a stage of psoriasis utilizing the proportion of at least one NGS species in psoriatic lesions compared with healthy skin.

[29] In additional embodiments, the invention relates to methods for monitoring therapies for psoriasis by measuring changes in the density or amount of at least one NGS species in the skin of psoriatic patients including in psoriatic lesions of patients.

[30] In additional embodiments, the invention relates to methods for determining the amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient; wherein a low amount of at least one *Propionibacterium* species in a psoriatic lesion indicates psoriasis.

[31] In additional embodiments, the invention relates to methods for monitoring treatment of psoriasis comprising: determining an amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient; wherein a low amount of at least one *Propionibacterium* species in a psoriatic lesion indicates psoriasis and wherein an increase in the amount of at least one *Propionibacterium* species in a psoriatic lesion indicates treatment progress.

[32] In yet additional embodiments, the invention relates to methods for diagnosing psoriasis comprising: determining a ratio of a non-Group A *Streptococcus* species (NGS) to a *Propionibacterium* species (gS/P ratio) in a psoriatic skin lesion in a patient; and wherein a raised gS/P ratio indicates psoriasis.

[33] In additional embodiments, the invention relates to vaccine compositions and vaccinations for suppressing at least one NGS species in the skin of patients in need of such treatment. In certain embodiments, the invention relates to vaccine compositions and vaccinations for prophylactically reducing the incidence of psoriasis in patients in need of such treatment.

[34] In additional embodiments, the invention relates to methods for diagnosing and monitoring treatment of psoriasis by determining the ratio of non-Group A *Streptococcus* species (NGS) to *Propionibacterium* species to (gS/P ratio) (*i.e.*, (S) standing for non-Group A *Streptococcus* species and (P) standing for *Propionibacterium* and (g) standing for genus) in psoriatic lesions compared with the ratio found in healthy skin. In certain embodiments, the *Propionibacterium* species is *Propionibacterium acnes*.

[35] In additional embodiments, the invention relates to methods for determining a raised gS/P ratio for diagnosing and monitoring treatment of psoriasis in patients in need of such treatment.

[36] In additional embodiments, the invention relates to methods for treating or preventing psoriasis by lowering the gS/P ratio.

[37] In additional embodiments, the invention relates to vaccine compositions and related methods for lowering the gS/P ratio in the skin in patients in need of such treatment. In certain embodiments, the invention relates to vaccine compositions and related methods

for prophylactically lowering the gS/P ratio in the skin and reducing the incidence of psoriasis in patients in need of such treatment.

[38] In additional embodiments, the invention relates to a method for treating psoriasis in a patient comprising administering an effective amount of inactivated or killed *Propionibacterium* cells to the patient in need of such treatment. In further embodiments, the invention relates to a method for treating psoriasis in a patient comprising administering an effective amount of killed or inactivated *Propionibacterium acnes* cells to the patient in need of such treatment. In yet additional embodiments, the invention relates to a method for treating psoriasis in a patient comprising administering an effective amount of an extract from *Propionibacterium* to the patient in need of such treatment. In certain embodiments, the *Propionibacterium* is *Propionibacterium acnes*.

[39] In additional embodiments, the invention relates to methods for diagnosing a skin disease comprising: a. determining the amount of at least one desired bacterial species in a skin sample suspected of being diseased from a patient; b. determining the amount of at least one desired bacterial species in a healthy skin sample from the patient; c. comparing the amounts in part a) and b); and d. wherein an altered amount of the at least one desired bacterial species in a skin sample suspected of being diseased when compared with a healthy skin sample indicates a skin disease. In certain embodiments, the skin disease is selected from the group consisting of atopic dermatitis, acne, alopecia, seborrhea, dandruff, and pemphigus. In certain embodiments, the determining comprises performing quantitative polymerase chain reaction (qPCR). In additional embodiments, amplified target DNA from the qPCR reaction is characterized by fluorescent emission detected by binding of one or more of a labeled probe selected from the group consisting of SEQ ID NO:6 and SEQ ID NO:8 to the amplified target DNA.

[40] In yet additional embodiments, the invention relates to a kit for determining a bacterial signature comprising at least one nucleic acid selected from the group consisting of SEQ ID NO:6 and SEQ ID NO:8. In yet further embodiments, the invention relates to an isolated nucleic acid fragment comprising SEQ ID NO:6 or SEQ ID NO:8.

BRIEF DESCRIPTION OF THE DRAWINGS

[41] FIG. 1 shows a flow diagram of exemplary methods for determining skin microbiota.

[42] FIG. 2 A-B show samplings of the ten most common genera of bacteria found in human skin based on 16S rDNA clone analysis. Fig. 2A shows percentages of bacteria from skin samples from healthy individuals and from normal skin of patients with psoriasis. Fig. 2B shows percentages of bacteria from skin samples from psoriatic lesions from patients with psoriasis.

[43] FIG. 3 A-B are representations of the ten most common species of bacteria found in human skin based on 16S rDNA clone analysis. Fig. 3A shows percentages of bacteria from skin samples from healthy individuals and from normal skin of patients with psoriasis. Fig. 3B shows percentages of bacteria from skin samples from psoriatic lesions from patients with psoriasis.

[44] FIG. 4 shows the distribution of 3,963 16S rDNA clones from normal and psoriatic samples, by phylum.

[45] FIG. 5 shows the standard curve with the *Streptococcus* genus probe (SEQ ID NO:8) using cloned 16S rDNA.

[46] FIG. 6 shows detection of specific 16S rDNA in single and multiplex qPCR reactions.

DETAILED DESCRIPTION

[47] The present invention relates generally to characterizing skin microbiota under various conditions and comparing normal and diseased skin microbiota in order to determine a microbial signature for the desired condition. The microbiota is determined utilizing a broad range molecular approach. While any number of suitable molecular techniques may be utilized, particularly useful molecular techniques to identify bacteria and archaea include PCR from a desired sample, cloning of microbial ribosomal 16S rRNA (16S rDNA), sequencing and analysis. In contrast to techniques involving cultivation of microorganisms from skin samples, this molecular approach, based on sequencing the 16S

rRNA gene conserved in all bacteria, permits analysis of variable regions that allow identification of bacterial species and inferences about phylogenetic relationships with known bacteria. Figure 1 is a schematic showing exemplary methods for determining skin microbiota.

[48] Assessing microbial populations in human skin using molecular techniques involving the ribosomal operon provides for comparisons between the populations of bacteria present in healthy (or uninvolved skin) and diseased skin, such as skin affected by psoriasis (e.g., psoriatic lesions). This process is applicable to a variety of skin conditions including, but not limited to atopic dermatitis, acne, alopecia, seborrhea, dandruff, and pemphigus.

[49] Determining the bacterial profiles in skin affected by a condition compared with the bacterial profile of healthy or unaffected skin, provides the ability to develop diagnostic, treatment, and preventive measures for the condition.

[50] In accordance with the present invention, there may be numerous tools and techniques within the skill of the art, such as those commonly used in molecular immunology, cellular immunology, pharmacology, and microbiology. *See, e.g.*, Sambrook *et al.* (2001) *Molecular Cloning: A Laboratory Manual*. 3rd ed. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York; Ausubel *et al.* eds. (2005) *Current Protocols in Molecular Biology*. John Wiley and Sons, Inc.: Hoboken, NJ; Bonifacino *et al.* eds. (2005) *Current Protocols in Cell Biology*. John Wiley and Sons, Inc.: Hoboken, NJ; Coligan *et al.* eds. (2005) *Current Protocols in Immunology*, John Wiley and Sons, Inc.: Hoboken, NJ; Coico *et al.* eds. (2005) *Current Protocols in Microbiology*, John Wiley and Sons, Inc.: Hoboken, NJ; Coligan *et al.* eds. (2005) *Current Protocols in Protein Science*, John Wiley and Sons, Inc.: Hoboken, NJ; and Enna *et al.* eds. (2005) *Current Protocols in Pharmacology*, John Wiley and Sons, Inc.: Hoboken, NJ.

[51] In accordance with the present invention there may be employed conventional molecular biology, microbiology, protein expression and purification, antibody, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. *See, e.g.*, Sambrook, Fritsch and Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (Cold Spring Harbor Laboratory Press, New

York:1989); *DNA Cloning: A Practical Approach*, Volumes I and II (Glover ed.:1985); *Oligonucleotide Synthesis* (Gait ed.:1984); *Nucleic Acid Hybridization* (Hames & Higgins eds.:1985); *Transcription And Translation* (Hames & Higgins, eds.:1984); *Animal Cell Culture* (Freshney, ed.:1986); *Immobilized Cells And Enzymes* (IRL Press:1986); Perbal, *A Practical Guide To Molecular Cloning* (1984); Ausubel *et al.*, eds. *Current Protocols in Molecular Biology*, (John Wiley & Sons, Inc.:1994); and Harlow and Lane. *Antibodies: A Laboratory Manual* (Cold Spring Harbor Laboratory Press: 1988).

[52] Common abbreviations correspond to units of measure, techniques, properties or compounds as follows: "min" means minutes, "h" means hour(s), "μL" means microliter(s), "mL" means milliliter(s), "mM" means millimolar, "M" means molar, "mmole" means millimole(s), "kb" means kilobase, and "bp" means base pair(s). "Polymerase chain reaction" is abbreviated PCR; "Reverse transcriptase polymerase chain reaction" is abbreviated RT-PCR; and "Sodium dodecyl sulfate" is abbreviated SDS.

[53] "Amplification" of DNA as used herein denotes the use of polymerase chain reaction (PCR) to increase the concentration of a particular DNA sequence within a mixture of DNA sequences. For a description of PCR see Saiki *et al.*, Science 1988, 239:487.

[54] A "polynucleotide" or "nucleotide sequence" is a series of nucleotide bases (also called "nucleotides") in a nucleic acid, such as DNA and RNA, and means any chain of two or more nucleotides. A nucleotide sequence typically carries genetic information, including the information used by cellular machinery to make proteins and enzymes. These terms include double or single stranded genomic and cDNA, RNA, any synthetic and genetically manipulated polynucleotide, and both sense and anti-sense polynucleotides (although only sense stands are being represented herein). This includes single- and double-stranded molecules, *i.e.*, DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases, for example thio-uracil, thio-guanine and fluoro-uracil.

[55] The nucleic acids herein may be flanked by natural regulatory (expression control) sequences, or may be associated with heterologous sequences, including promoters, internal ribosome entry sites (IRES) and other ribosome binding site sequences, enhancers, response

elements, suppressors, signal sequences, polyadenylation sequences, introns, 5'- and 3'-non-coding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, and internucleotide modifications such as, for example, those with uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.) and with charged linkages (*e.g.*, phosphorothioates, phosphorodithioates, etc.). Polynucleotides may contain one or more additional covalently linked moieties, such as, for example, proteins (*e.g.*, nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (*e.g.*, acridine, psoralen, etc.), chelators (*e.g.*, metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. The polynucleotides may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the polynucleotides herein may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

[56] The term "nucleic acid hybridization" refers to anti-parallel hydrogen bonding between two single-stranded nucleic acids, in which A pairs with T (or U if an RNA nucleic acid) and C pairs with G. Nucleic acid molecules are "hybridizable" to each other when at least one strand of one nucleic acid molecule can form hydrogen bonds with the complementary bases of another nucleic acid molecule under defined stringency conditions. Stringency of hybridization is determined, *e.g.*, by (i) the temperature at which hybridization and/or washing is performed, and (ii) the ionic strength and (iii) concentration of denaturants such as formamide of the hybridization and washing solutions, as well as other parameters. Hybridization requires that the two strands contain substantially complementary sequences. Depending on the stringency of hybridization, however, some degree of mismatches may be tolerated. Under "low stringency" conditions, a greater percentage of mismatches are tolerable (*i.e.*, will not prevent formation of an anti-parallel hybrid). See *Molecular Biology of the Cell*, Alberts *et al.*, 3rd ed., New York and London: Garland Publ., 1994, Ch. 7.

[57] Typically, hybridization of two strands at high stringency requires that the sequences exhibit a high degree of complementarity over an extended portion of their

length. Examples of high stringency conditions include: hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% SDS, 1 mM EDTA at 65°C, followed by washing in 0.1x SSC/0.1% SDS at 68°C (where 1x SSC is 0.15M NaCl, 0.15M Na citrate) or for oligonucleotide molecules washing in 6xSSC/0.5% sodium pyrophosphate at about 37°C (for 14 nucleotide-long oligos), at about 48°C (for about 17 nucleotide-long oligos), at about 55°C (for 20 nucleotide-long oligos), and at about 60°C (for 23 nucleotide-long oligos)). Accordingly, the term “high stringency hybridization” refers to a combination of solvent and temperature where two strands will pair to form a “hybrid” helix only if their nucleotide sequences are almost perfectly complementary (see *Molecular Biology of the Cell*, Alberts *et al.*, 3rd ed., New York and London: Garland Publ., 1994, Ch. 7).

[58] Conditions of intermediate or moderate stringency (such as, for example, an aqueous solution of 2×SSC at 65°C; alternatively, for example, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% SDS, 1 mM EDTA at 65°C, and washing in 0.2 x SSC/0.1% SDS at 42°C) and low stringency (such as, for example, an aqueous solution of 2×SSC at 55°C), require correspondingly less overall complementarity for hybridization to occur between two sequences. Specific temperature and salt conditions for any given stringency hybridization reaction depend on the concentration of the target DNA and length and base composition of the probe, and are normally determined empirically in preliminary experiments, which are routine (see Southern, *J. Mol. Biol.* 1975; 98: 503; Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 2, ch. 9.50, CSH Laboratory Press, 1989; Ausubel *et al.* (eds.), 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3).

[59] As used herein, the term “standard hybridization conditions” refers to hybridization conditions that allow hybridization of sequences having at least 75% sequence identity. According to a specific embodiment, hybridization conditions of higher stringency may be used to allow hybridization of only sequences having at least 80% sequence identity, at least 90% sequence identity, at least 95% sequence identity, or at least 99% sequence identity.

[60] Nucleic acid molecules that “hybridize” to any desired nucleic acids of the present invention may be of any length. In one embodiment, such nucleic acid molecules are at

least 10, at least 15, at least 20, at least 30, at least 40, at least 50, and at least 70 nucleotides in length. In another embodiment, nucleic acid molecules that hybridize are of about the same length as the particular desired nucleic acid.

[61] As used herein, the term "isolated" means that the referenced material is removed from the environment in which it is normally found. Thus, an isolated biological material can be free of cellular components, *i.e.*, components of the cells in which the material is found or produced. Isolated nucleic acid molecules include, for example, a PCR product, an isolated mRNA, a cDNA, or a restriction fragment. Isolated nucleic acid molecules also include, for example, sequences inserted into plasmids, cosmids, artificial chromosomes, and the like. An isolated nucleic acid molecule is preferably excised from the genome in which it may be found, and more preferably is no longer joined to non-regulatory sequences, non-coding sequences, or to other genes located upstream or downstream of the nucleic acid molecule when found within the genome. An isolated protein may be associated with other proteins or nucleic acids, or both, with which it associates in the cell, or with cellular membranes if it is a membrane-associated protein.

[62] "Treating" or "treatment" of a state, disorder or condition includes:

(1) preventing or delaying the appearance of clinical symptoms of the state, disorder, or condition developing in a person who may be afflicted with or predisposed to the state, disorder or condition but does not yet experience or display clinical symptoms of the state, disorder or condition; or

(2) inhibiting the state, disorder or condition, *i.e.*, arresting, reducing or delaying the development of the disease or a relapse thereof (in case of maintenance treatment) or at least one clinical symptom, sign, or test, thereof; or

(3) relieving the disease, *i.e.*, causing regression of the state, disorder or condition or at least one of its clinical or sub-clinical symptoms or signs.

[63] The benefit to a subject to be treated is either statistically significant or at least perceptible to the patient or to the physician.

[64] An "immune response" refers to the development in the host of a cellular and/or antibody-mediated immune response to a composition or vaccine of interest. Such a response usually consists of the subject producing antibodies, B cells, helper T cells, suppressor T cells, regulatory T cells, and/or cytotoxic T cells directed specifically to an antigen or antigens included in the composition or vaccine of interest.

[65] As used herein, the term "vaccine" refers to a composition comprising a cell or a cellular antigen, and optionally other pharmaceutically acceptable carriers, administered to stimulate an immune response in an animal, most preferably a human, specifically against the antigen and preferably to engender immunological memory that leads to mounting of a protective immune response should the subject encounter that antigen at some future time. Vaccines often include an adjuvant.

[66] A "therapeutically effective amount" means the amount of a compound that, when administered to an animal for treating a state, disorder or condition, is sufficient to effect such treatment. The "therapeutically effective amount" will vary depending on the compound, the disease and its severity and the age, weight, physical condition and responsiveness of the animal to be treated.

[67] The compositions of the invention may include a "therapeutically effective amount" or a "prophylactically effective amount" of an antibody or antigen-binding portion of the invention. A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount of an antibody or antibody portion may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody or antibody portion to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the antibody or antibody portion are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount will be less than the therapeutically effective amount.

[68] While it is possible to use a composition provided by the present invention for therapy as is, it may be preferable to administer it in a pharmaceutical formulation, e.g., in admixture with a suitable pharmaceutical excipient, diluent or carrier selected with regard to the intended route of administration and standard pharmaceutical practice. Accordingly, in one aspect, the present invention provides a pharmaceutical composition or formulation comprising at least one active composition, or a pharmaceutically acceptable derivative thereof, in association with a pharmaceutically acceptable excipient, diluent and/or carrier. The excipient, diluent and/or carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof.

[69] The compositions of the invention can be formulated for administration in any convenient way for use in human or veterinary medicine. The invention therefore includes within its scope pharmaceutical compositions comprising a product of the present invention that is adapted for use in human or veterinary medicine.

[70] In a preferred embodiment, the pharmaceutical composition is conveniently administered as an oral formulation. Oral dosage forms are well known in the art and include tablets, caplets, gelcaps, capsules, and medical foods. Tablets, for example, can be made by well-known compression techniques using wet, dry, or fluidized bed granulation methods.

[71] Such oral formulations may be presented for use in a conventional manner with the aid of one or more suitable excipients, diluents, and carriers. Pharmaceutically acceptable excipients assist or make possible the formation of a dosage form for a bioactive material and include diluents, binding agents, lubricants, glidants, disintegrants, coloring agents, and other ingredients. Preservatives, stabilizers, dyes and even flavoring agents may be provided in the pharmaceutical composition. Examples of preservatives include sodium benzoate, ascorbic acid and esters of p-hydroxybenzoic acid. Antioxidants and suspending agents may be also used. An excipient is pharmaceutically acceptable if, in addition to performing its desired function, it is non-toxic, well tolerated upon ingestion, and does not interfere with absorption of bioactive materials.

[72] Acceptable excipients, diluents, and carriers for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington: The Science and

Practice of Pharmacy. Lippincott Williams & Wilkins (A.R. Gennaro edit. 2005). The choice of pharmaceutical excipient, diluent, and carrier can be selected with regard to the intended route of administration and standard pharmaceutical practice.

[73] As used herein, the phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are "generally regarded as safe", *e.g.*, that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopoeia or other generally recognized pharmacopeias for use in animals, and more particularly in humans.

[74] "Patient" or "subject" refers to mammals and includes human and veterinary subjects.

[75] The dosage of the therapeutic formulation will vary widely, depending upon the nature of the disease, the patient's medical history, the frequency of administration, the manner of administration, the clearance of the agent from the host, and the like. The initial dose may be larger, followed by smaller maintenance doses. The dose may be administered as infrequently as weekly or biweekly, or fractionated into smaller doses and administered daily, semi-weekly, etc., to maintain an effective dosage level. In some cases, oral administration will require a higher dose than if administered intravenously. In some cases, topical administration will include application several times a day, as needed, for a number of days or weeks in order to provide an effective topical dose.

[76] The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, olive oil, sesame oil and the like. Water or aqueous solution saline solutions and aqueous dextrose and glycerol solutions are preferably employed as carriers, particularly for injectable solutions. Alternatively, the carrier can be a solid dosage form carrier, including but not limited to one or more of a binder (for compressed pills), a glidant, an encapsulating agent, a flavorant, and a colorant. Suitable

pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

[77] As used herein, the term "adjuvant" refers to a compound or mixture that enhances the immune response to an antigen. An adjuvant can serve as a tissue depot that slowly releases the antigen and also as a lymphoid system activator that non-specifically enhances the immune response (Hood et al., *Immunology, Second Ed.*, 1984, Benjamin/Cummings: Menlo Park, California, p. 384). Often, a primary challenge with an antigen alone, in the absence of an adjuvant, will fail to elicit a humoral or cellular immune response. Adjuvants include, but are not limited to, complete Freund's adjuvant, incomplete Freund's adjuvant, saponin, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil or hydrocarbon emulsions, keyhole limpet hemocyanins, and potentially useful human adjuvants such as N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine, and BCG (*bacille Calmette-Guerin*). Preferably, the adjuvant is pharmaceutically acceptable.

[78] In the case of the present invention, parenteral routes of administration are also possible. Such routes include intravenous, intra-arteriole, intramuscular, intradermal, subcutaneous, intraperitoneal, transmucosal, intranasal, rectal, vaginal, or transdermal routes. If desired, inactivated therapeutic formulations may be injected, e.g., intravascular, intratumor, subcutaneous, intraperitoneal, intramuscular, etc.

[79] In a preferred embodiment, the route of administration is topical. Although there are no physical limitations to delivery of the formulation, topical delivery is preferred because of its ease and convenience, and because topical formulations readily accommodate additional mixtures commonly in the form of a cream, ointment, lotion, salve, or as a component added to a bath.

[80] Typical topical formulations or products occur in a variety of forms, including solids, liquids, suspensions, semisolids (such as creams, gels, pastes or "sticks"), powders or finely dispersed liquids such as sprays or mists. Examples of topical products commonly classified as "cosmetics" include skin care products such as creams, lotions, moisturizers

and "treatment cosmetics" such as exfoliants and/or skin cell renewal agents; toners and astringents; pre-moistened wipes and washcloths; tanning lotions; bath products such as oils; as well as powders and sprays; skin colorant and make-up products such as foundations, blushes, rouges, eye shadows and liners, lip colors and mascaras; lip balms and sticks; hair care and treatment products such as shampoos, conditioners, colorants, dyes, bleaches, straighteners and permanent wave products; baby products such as baby lotions, oils, shampoos, powders and wet wipes. Examples of topical products commonly classified as "topical drugs" are many and varied, and include over-the-counter and/or prescription products such as antiperspirants, insect repellents, sunscreens and sunburn treatments, anti-acne agents, antibiotics, topical respiratory agents, ocular drugs such as eyedrops and saline solutions, therapeutic retinoids, anti-dandruff agents, external analgesics such as capsaicin products, topical contraceptives, topical drug delivery systems, gastrointestinal agents such as suppositories, enemas and hemorrhoid treatments, reproductive system agents such as vaginal treatments, and many other products with therapeutic or other effects. Other topical products include hand, facial and body soaps and detergents and other forms of skin cleansers, as well as solvents, propellants, polishes, lubricants, adhesives, waxes and others which are either applied topically or are topically exposed to the body during normal use.

[81] In the present invention, the terms normal, unaffected, or healthy skin refer to skin that does not demonstrate signs of psoriasis or any other recognized skin condition. Normal, unaffected, healthy skin may be used to refer to the skin from a patient with psoriasis, that is, does not exhibit symptoms of psoriasis. Furthermore, samples of normal, unaffected, or healthy skin are taken from individuals who have not been treated with any antibiotics for at least one month prior to sampling.

[82] A psoriatic lesion is an area of skin that exhibits any of the signs of psoriasis including raised, red patches of skin topped with loose, silvery scales, often on the knees or elbows, and other extensor surfaces, but can be present anywhere.

[83] As used herein, promoting the growth of *Propionibacterium* and agents that promote growth of *Propionibacterium* are ones that result in a desired amount of at least one *Propionibacterium* species in a desired location. In particular embodiments, the growth

is promoted in the skin area corresponding to the psoriatic lesion of a patient. Agents that promote growth of *Propionibacterium* species may include pre-biotics that favor the metabolism of *Propionibacterium* species over that of competing organisms in the skin. In certain embodiments, an effective amount of *Propionibacterium* species is applied to the skin area corresponding to the psoriatic lesion of a patient in order to promote growth of at least one *Propionibacterium* species. The active ingredient may be live *Propionibacterium* cells, killed or inactivated cells, or an extract from the cells. Each of these forms may be derived from cells grown under ordinary circumstances or grown to induce increased production of particular constituents.

[84] As used herein, inhibiting the growth of NGS may include using any agents, antibiotics, chemical, or physical means, or combinations thereof to inhibit the growth or eliminate NGS organisms. At the highest level, antibiotics can be classified as either bactericidal or bacteriostatic. Bactericidal agents kill bacteria directly whereas bacteriostatics prevent them from dividing. However, these classifications are based on laboratory behavior; in practice, both of these are capable of ending a bacterial infection, or suppressing bacterial growth. Examples of suitable antibiotics for inhibiting the growth of, or killing, or preventing growth of NGS species include agents listed in Table 1:

TABLE 1

Types of antimicrobial agents that can be used to suppress NGS.

Generic Name	Brand Names
Loracarbef	Lorabid
Ertapenem	Invanz
Imipenem/Cilastatin	Primaxin
Meropenem	Merrem
Cefadroxil	Duricef
Cefazolin	Ancef
Cephalexin	Keflex

Generic Name	Brand Names
Loracarbef	Lorabid
Cefaclor	Ceclor
Cefamandole	Mandole
Cefoxitin	Mefoxin
Cefprozil	Cefzil
Cefuroxime	Ceftin
Cefixime	
Cefdinir	Omnicef
Cefditoren	
Cefoperazone	Cefobid
Cefotaxime	Claforan
Cefpodoxime	
Ceftazidime	Fortum
Ceftibuten	
Ceftizoxime	
Ceftriaxone	Rocephin
Cefepime	Maxipime
Teicoplanin	
Vancomycin	Vancocin
Azithromycin	Zithromax, Sumamed, Zitrocin
Clarithromycin	Biaxin
Dirithromycin	
Erythromycin	
Roxithromycin	
Troleandomycin	
Aztreonam	
Amoxicillin	Novamox
Ampicillin	
Azlocillin	
Carbenicillin	

Generic Name	Brand Names
Loracarbef	Lorabid
Cloxacillin	
Dicloxacillin	
Flucloxacillin	
Mezlocillin	
Nafcillin	
Penicillin	
Piperacillin	
Ticarcillin	
Bacitracin	
Colistin	
Polymyxin B	
Ciprofloxacin	Cipro, Ciplox
Enoxacin	
Gatifloxacin	Tequin
Levofloxacin	Levaquin
Lomefloxacin	
Moxifloxacin	Avelox
Norfloxacin	
Ofloxacin	Ocuflox
Trovafoxacin	Trovan
Mafenide	
Prontosil (archaic)	
Sulfacetamide	
Sulfamethizole	
Sulfanilimide (archaic)	
Sulfasalazine	
Sulfisoxazole	
Trimethoprim	
Trimethoprim-Sulfamethoxazole (Co-trimoxazole) (TMP-SMX)	Bactrim

Generic Name	Brand Names
Loracarbef	Lorabid
Demeclocycline	
Doxycycline	Vibramycin
Minocycline	Minocin
Oxytetracycline	
Tetracycline	Sumycin
Chloramphenicol	Chloromycetin
Clindamycin	Cleocin
Ethambutol	
Fosfomycin	
Fusidic acid	
Furazolidone	
Isoniazid	
Linezolid	Zyvox
Metronidazole	Flagyl
Mupirocin	
Nitrofurantoin	Macrochantin, Macrobid
Platensimycin	
Pyrazinamide	
Quinupristin/Dalfopristin	Syncercid
Rifampin	
Spectinomycin	
Telithromycin	Ketek

[85] However, other chemical formulations including astringents, antiseptics, pre-biotics, and physical means such as occlusive dressings with particular impregnations (of any suitable chemical formulation or antimicrobial agent) could also be useful as means for suppressing NGS. In certain embodiments, it may be useful to utilize at least one chemical which acts as a skin "exfoliant" such as retinoids (e.g. tretinoin, retinol and retinal), carboxylic acids including α -hydroxy acids (e.g. lactic acid, glycolic acid), β -hydroxy acids (e.g. salicylic acid), α -keto acids, acetic acid and trichloroacetic acid, 1-pyrrolidone-5-carboxylic acid, capryloyl salicylic acid, α -hydroxy decanoic acid, α -hydroxy octanoic acid,

gluconolactone, methoxypropyl gluconamide, oxalic acid, malic acid, tartaric acid, mandelic acid, benzylic acid, gluconic acid, benzoyl peroxide or phenol.

[86] As described herein, characterizing and comparing the bacterial microbiota of normal/healthy skin with that of diseased skin, such as psoriatic lesions provide a microbial signature useful in diagnosing, treating, and preventing psoriasis. Because human skin is extensive and variable in its characteristics, typically a single site, the volar forearm was sampled in order to maximize homogeneity and allow analysis of bilateral conservation.

[87] In certain embodiments, the invention provides a kit comprising useful probes or primers for analyzing skin microbiota in any of the methods described herein. In certain embodiments, the kits may be packaged in association with instructions teaching a method of using the primers or probes according to one or more of the methods described herein. The kit can also optionally contain any useful buffers, controls, or other reagents that are useful in PCR or qPCR reactions or any of the methods described herein. Additionally, in certain embodiments, the invention relates to any one or more of the isolated nucleic acid probes or primers for amplifying or detecting desired bacteria from a sample, as described herein. Such primers and/or probes are useful in PCR and qPCR reactions for determining the bacterial biota of superficial skin.

[88] Initial studies providing molecular analysis of normal human forearm superficial skin bacterial biota were described. (Gao, Z. et al., 2007, *Proc Natl Acad Sci USA*, 104(8):2927-2932). For the initial 1,221 clones analyzed, 182 SLOTUs (species-level operational taxonomic units) belonging to 8 phyla were identified, estimated as 74.0% (95% CI: 64.8% ~ 77.9%) of the SLOTUs in this ecosystem; an average of 48.0 ± 12.2 SLOTU were found in each subject. Three phyla, Actinobacteria, Firmicutes, and Proteobacteria, accounted for 94.6% of the clones. Most (85.3%) of the bacterial sequences corresponded to known and cultivated species, but 98 (8.0%) clones, comprising 30 phylotypes, had <97% similarity to prior database sequences. Only 6 (6.6%) of the 91 genera and 4 (2.2%) of the 182 SLOTUs, respectively, were found in all six subjects.

[89] Analysis of 817 clones obtained 8 to 10 months later from four subjects, showed new phyla (2), genera (28), and SLOTU (65). Only four (3.4%) of the 119 genera

(*Propionibacteria*, *Corynebacteria*, *Staphylococcus*, and *Streptococcus*) were observed in each subject tested twice, but these represented 54.4% of all clones. These results show that the bacterial biota in normal skin is highly diverse, with few well-conserved and well-represented genera, but otherwise low-level interpersonal consensus (Gao *et al.* PNAS 2007; 104; 2927-32).

Materials And Methods.

Subjects.

[90] Specimens from superficial skin were obtained from the left and right forearms of six healthy subjects (three males and three females); second samples were obtained 8–10 months later from four of these subjects. The mean age of the subjects was 38 years of age (range, 21–54 years of age); all were in good health and had not received any antibiotics for at least one month. The study was approved by the New York University Institutional Review Board, and all subjects provided written informed consent.

[91] From each healthy subject, at least two samples were obtained from the left and right forearms and, for four subjects, another sample was obtained from each forearm 8-10 months after the first. From each patient with psoriasis, at least three skin samples, including unaffected skin and two or three samples from psoriatic lesions, were studied. Lesions differing in the extent of erythema, swelling, and scaling were chosen. No patient had ever received therapy for psoriasis. Samples were obtained in a DNA-free clean room by rubbing the skin using two sterile cotton swabs soaked in ST solution (0.15 M NaCl with 0.1% Tween 20). The head of each swab was aseptically cut from the handle, placed into a microcentrifuge tube containing 100 µl of ST solution, centrifuged for 5 min, and then removed. To detect possible contamination, negative controls were prepared using cotton swabs in ST solution without any contact with skin and then subjected to the above-mentioned procedures.

Specimen Processing.

[92] DNA was extracted from the swabs in a PCR-free clean-room by using the DNeasy Tissue Kit (Qiagen, Chatsworth, CA); because Gram-positive bacteria are more resistant to lysis than Gram-negative organisms, the manufacturer's protocol for genomic DNA isolation from Gram-positive bacteria was followed. Samples were eluted in 100 µl of

AE buffer, and to eliminate bacterial or DNA contamination, the enzymatic lysis buffer was passed through a micro-centrifuge filter (MW threshold 30,000 daltons; Amicon, Bedford, MA) at $747 \times g$ for 20 min.

DNA isolation.

[93] DNA was extracted from the swabs in a PCR-free clean-room by using the DNeasy Tissue Kit (Qiagen, Chatsworth, CA) utilizing the steps described below.

1. Bacterial cells were harvested from the swabs in a microcentrifuge tube by centrifuging for 10 min at $5000 \times g$ (7500 rpm). The supernatant was discarded.

2. The bacterial pellet was resuspended in $180 \mu\text{l}$ enzymatic lysis buffer (20 mM Tris.Cl, pH 8.0; 2mM sodium EDTA; 1.2% Triton®X-100; 20mg/ml lysozyme).

3. The pellet suspension was incubated for at least 30 min at 37°C .

4. $25 \mu\text{l}$ proteinase K and $200 \mu\text{l}$ Buffer AL was added and mixed by vortexing.

5. The sample was incubated at 70°C for 30 min.

6. $200 \mu\text{l}$ ethanol (100%) was added to the sample, and mixed thoroughly by vortexing.

7. The mixture from step 6 was transferred by pipette into the DNeasy Minispin column (Qiagen, Valencia, CA) placed in a 2 ml collection tube and centrifuged at $\geq 6000 \times g$ (8000 rpm) for 1 min. The flow-through and collection tube were discarded.

8. The DNeasy Minispin column was placed in a new 2 ml collection tube, $500 \mu\text{l}$ Buffer AW1 was added, and the column was centrifuged for 1 min at $\geq 6000 \times g$ (8000 rpm). The flow-through and collection tube were discarded.

9. The DNeasy Mini spin column was placed in a new 2 ml collection tube, $500 \mu\text{l}$ Buffer AW2 was added, and the column was centrifuged for 3 min at $20,000 \times g$ (14,000 rpm) to dry the DNeasy membrane. The flow-through and collection tube were discarded.

10. The DNeasy Mini spin column was placed in a clean 1.5 ml or 2 ml microcentrifuge tube, and $100 \mu\text{l}$ Buffer AE was pipette directly onto the DNeasy

membrane. The column was incubated at room temperature for 5 min, and then centrifuged for 1 min at $\geq 6000 \times g$ (8000 rpm) to elute.

16S rDNA PCR Amplification.

[94] Universal bacterial 16S rDNA PCR primers 8F (forward primer 5'-AGA GTT TGA TYM TGG CTC AG (SEQ ID NO:1)) and 1510R (reverse primer 5'-TAC GGY TAC CTT GTT ACG ACT T (SEQ ID NO:2)) were used to amplify the approximately 1.5 kb region corresponding to positions 8 to 1513 of the *Escherichia coli* 16S rDNA gene by using a 30-cycle PCR (as described in Pei, Z., et al., (2004) *Proc Natl Acad Sci USA* 101, 4250–4255; Edwards, U., et al., (1989) *Nucleic Acids Res* 17, 7843–7853; and Nagashima, K. et al., (2003) *Appl Environ Microbiol* 69, 1251–1262). To each 5 μ l of the suspension of extracted template DNA was added 45 μ l of a PCR mixture containing 5 μ l of 10 $\times$ PCR buffer (Qiagen, Valencia, CA), 2.5 mM MgCl₂, 200 μ M each dNTP, 20 pmol of each primer, and 5 units of TaqDNA polymerase. PCR was performed for 2 min at 94°C, followed by 30 amplification cycles of 45 s at 94°C, 30 s at 52°C, and 90 s at 72°C, with a final cycle for 20 min at 72°C. The results of PCR amplification were examined by electrophoresis on 1% agarose gels.

16S rDNA Clone Libraries.

[95] The PCR products were separated from free PCR primers by using a PCR purification kit (Qiagen, Valencia, CA), ligated with the pGEM-T-Easy vector (Promega, Madison, WI), used to transform *E. coli* DH5 α competent cells, and clones analyzed. Putatively positive clones were screened by PCR with Sp6/T7 primers. The cloned inserts underwent sequence analysis using PCR primers 8F (forward primer 5'-AGA GTT TGA TYM TGG CTC AG (SEQ ID NO:1)) and 27R (reverse primer 5'-CGA CAI CCA TGC AIC ACC T (SEQ ID NO:3)), corresponding to position 8 to 1064 of the *E. coli* 16S rDNA (complete *E. coli* 16S rDNA shown in SEQ ID NO:4; which corresponds with GenBank Accession No. J01859). Each sequence was manually edited in conjunction with its chromatogram with Sequencher, adjusting for quality. DNA sequences of ≈ 980 bases were obtained initially to determine either identity or approximate phylogenetic position. For those clones containing inserts of ambiguous phylogenetic status, nearly full-length 16S bacterial rDNA sequences ($\approx 1,400$ bp) were obtained, using the additional primer, 1510R

(reverse primer 5'-TAC GGY TAC CTT GTT ACG ACT T (SEQ ID NO:2). For identification of closest relatives, the newly determined sequences were compared with those available in the Ribosomal Database Project (RDP) II (release 9.39) (Maidak, B.L., et al., (2001) *Nucleic Acids Res* 29, 173–174.) and GenBank (www.ncbi.nlm.gov) databases, by using the standard nucleotide-nucleotide BLAST program to ascertain their closest relatives.

Elimination of Contaminating Sequences.

[96] Because reagents used in DNA extraction and PCRs may contain bacteria or their genomic DNA, and under certain experimental conditions these contaminating DNA molecules may become detectable after PCR amplification, a reagent control was utilized that included all DNA extraction and PCR reagents but without the skin sample, which was examined in parallel using the identical procedures as for the skin sample DNA. After electrophoresis and ethidium bromide staining, preparations from these controls did not generate any visible bands, but the agarose gel at the expected location of the signal was excised, ligated to pGEM-T Easy Vector (Promega) and transformed. Clones derived from these reagent controls underwent sequence analysis, and sequences of known species and unknown species were identified. For a more conservative data analysis, the species found in both control and skin samples were excluded.

Sequence Deposition.

[97] All sequences that are not classifiable by using the current 16S database at RDP II were deposited in the GenBank database (Accession Nos. DQ130020-DQ130049 and DQ847437-DQ847450, and corresponding to SEQ ID NO:10 to SEQ ID NO:53).

Statistical Methods.

[98] Double principal coordinate analysis (DPCoA) uses phylotype differences to derive the dissimilarity matrix of samples and calculate the sample diversity. In this analysis, the dissimilarities between different phylotypes are calculated based on the sum of distance to the common ancestor of two phylotypes on phylotype tree. To facilitate the visualization of sample dissimilarity and diversity, the first two orthogonal principal axes were obtained based on the sample dissimilarity, and were plotted to show the distribution of samples in a two- dimensional space. The diversity information can be decomposed into

within- and between- samples diversity values. This allowed the use of a "pseudo F" statistic (the ratio of within-cluster diversity and between-cluster diversity) to examine possible clustering phenomena, and significance was evaluated by permutation tests. The *P* test also was used to assess for significant differences between samples.

Phylogenetic Analysis

[99] All sequences were examined for chimerism by using Chimera Detection at Ribosomal database Project (RDP) II (release 8.1) and Bellerophon (Huber, T. et al., (2004) *Bioinformatics* 20, 2317–2319). In total, only three clones were removed from the phylogenetic analysis. The remaining sequences were compared with those of RDP II (release 9.39) (Maidak, BL. et al., (2001) *Nucleic Acids Res* 29, 173–174.) and in GenBank to identify SLOTUs, as reported (Pei, Z., et al., (2004) *Proc Natl Acad Sci USA* 101, 4250–4255.). The sequences were aligned with NAST at Greengenes (<http://greengenes.lbl.gov/cgi-bin/nph-index.cgi>), (DeSantis, T.Z. Jr., et al., (2006) *Nucleic Acids Res* 34, W394–W399.). Misalignments were manually curated in ARB (Ludwig, W., et al., (2004) *Nucleic Acids Res* 32, 1363–1371.), and then hypervariable regions were masked by using MASK COLUMNS at Greengenes. The phylogenetic trees were generated by using MEGA 3.1 (Kumar, S., et al., (2004) *Brief Bioinform* 5, 150–163.). Evolutionary distances were calculated with the Jukes–Cantor algorithm (Jukes, TH & Cantor, CR. (1969) in *Mammalian Protein Metabolism* ed. Munro, HN. (Academic, New York,) pp. 21–132.). The statistical strength of the Neighbor-Joining method was assessed by bootstrap resampling (1,000 replicates) (Saitou, N & Nei, M. (1987) *Mol Biol Evol* 4, 406–425.).

Statistical Analyses.

[100] The total number of SLOTUs that may be present in the sampled human skin and its associated confidence interval were calculated by using a nonparametric richness estimator, Chao1, as described by Hughes, J.B., et al., (2001) *Appl Environ Microbiol* 67, 4399–4406). DPCoA (Pavoine, S. et al., (2004) *J Theor Biol* 228, 523–537) and the *P* test (Lozupone, C., et al., (2006) *BMC Bioinformatics* 7, 371; and Martin, AP. (2002) *Appl Environ Microbiol* 68, 3673–3682) were used to evaluate sample diversity and the relationships among samples.

Example 1. Ratio of the genus *Streptococcus* to *Propionibacterium*

[101] Figures 2A-B show samplings of the ten most common genera of bacteria found in human skin based on 16S rDNA clone analysis performed on samples as described above. Figure 2A shows the percentages of bacteria from skin samples from healthy individuals and from normal skin of patients with psoriasis (n=2,649 clones). These results show that the skin from healthy persons and the normal skin of patients with psoriasis exhibit a gS/P ratio of 0.4. (i.e., ratio of genus *Streptococcus* to *Propionibacterium* = 0.4).

[102] Figure 2B shows the results of skin samples from lesions of patients with psoriasis (n=1,314 clones). These results show that the skin from psoriatic lesions exhibit a gS/P ratio of 5.0 (i.e., ratio of *Streptococcus* to *Propionibacterium*=5.0).

Example 2. Ratio of *Streptococcus mitis* to *Propionibacterium acnes* (sS/P)

[103] Figure 3 shows the percent of clones of the 10 most common bacterial species found in human skin, based on 16S rDNA clones. Fig. 3A shows the results of skin samples from healthy persons and normal skin of patients with psoriasis (n=2,649 clones). These results show that the skin from healthy persons and the normal skin of patients with psoriasis exhibit an sS/P ratio of 0.2 (i.e., ratio of the species *Streptococcus mitis* to *Propionibacterium acnes* = 0.2).

[104] Figure 3B shows the results of skin samples from lesions of patients with psoriasis (n=1,314 clones). These results show that the skin from psoriatic lesions exhibit an sS/P ratio of 2.5 (i.e., ratio of the species *Streptococcus mitis* to *Propionibacterium acnes* =2.5). The bars in the graphs are labeled and correspond to the following bacterial species: *Propionibacterium acnes* (A1, B7); *Corynebacterium tuberculostearicum* (A2, B1); *Staphylococcus hominis* (A5, B2); *Streptococcus mitis* (A4, B3); *Staphylococcus epidermidis* (A8, B9); *Enhydrobacter aerosaccus* (A3); *Staphylococcus capitis* (A6); *Staphylococcus caprae* (A7); *Dermacoccus* AF409025 (A9); *Corynebacterium mucifaciens* (A10); *Corynebacterium simulans* (B4); *Rothia mucilaginosa* (B5); *Staphylococcus aureus* (B6); *Streptococcus salivarius* (B8); *Flavobacteriaceae* DQ337018 (B10).

Example 3. Characterization of the presence of 16s rDNA from bacterial genera found in skin samples from healthy individuals (or normal skin from psoriatic patients) and in skin samples from psoriatic lesions from psoriatic patients.

[105] The presence of 16S rDNA from *Propionibacterium*, *Streptococcus*, *Staphylococcus* and *Corynebacterium* found in healthy (e.g., no obvious signs of disease or skin condition) skin samples from six individuals was determined as shown in Table 2.

Table 2

Presence of 16S rDNA from four genera found in skin samples from six healthy individuals

Samples ^a	No. of clones	Percent				
		<i>Propionibacterium</i>	<i>Streptococcus</i>	<i>Staphylococcus</i>	<i>Corynebacterium</i>	Any of the 4
AT	208	10.6	7.7	3.4	1.4	23.1
BT	204	12.3	5.9	2.9	7.4	28.5
CT	202	12.4	5.9	16.8	26.2	61.3
DT	204	14.7	2.0	18.6	44.6	79.9
ET	203	23.2	10.8	15.8	21.2	71.0
FT	200	59.5	2.5	9.5	13.5	85.0
AT2	203	2.0	2.5	2.0	1.0	7.5
CT2	206	37.9	32.0	1.9	1.5	73.3
ET2	202	9.9	7.9	8.4	7.4	33.6
FT2	206	28.6	3.9	29.6	18.9	81.0
Mean ± SD	203.8 ± 2.3	21.1 ± 17.0	8.1 ± 8.9	10.9 ± 9.2	14.3 ± 13.9	54.4 ± 28.4

[106] ^a Samples from each participant at one sampling time (2 sites).

[107] The presence of 16S rDNA from *Propionibacterium*, *Streptococcus*, *Staphylococcus* and *Corynebacterium* found in psoriatic lesions of skin samples from patients with psoriasis was determined as shown in Table 3.

TABLE 3

Presence of 16S rDNA from four genera found in skin samples from Psoriatic Patients

Samples ^a	No. of clones	Percent				
		<i>Propionibacterium</i>	<i>Streptococcus</i>	<i>Staphylococcus</i>	<i>Corynebacterium</i>	Any of the 4
1PT	207	14.0	15.0	24.2	18.8	72.0
2PT	299	1.3	2.3	23.7	8.7	36.0
3PT	200	1.0	22.5	1.5	38.5	63.5
4PT	204	0	31.4	5.9	2.0	39.3
6PT	203	1.0	12.3	35.5	5.4	54.2
8PT	201	0	8.0	19.4	62.7	90.1
Mean ± SD	219.0 ± 39.3	2.9 ± 5.5	15.3 ± 10.4	18.4 ± 12.6	22.7 ± 23.6	59.3 ± 20.5

[108] The presence of 16S rDNA from four bacterial genera found in the lesions from six patients with psoriasis is shown, by lesion in Table 4.

TABLE 4

Presence of 16S rDNA from four genera found in the lesions from six patients with psoriasis, by lesion

Sample	No. of Clones	Percent				
		Propionibacterium	Streptococcus	Staphylococcus	Corynebacterium	Any of the 4
1P1	103	23.3	10.7	21.4	9.7	65.1
1P2	104	4.8	19.2	26.9	27.9	78.8
2P1	99	0	2.0	16.2	3.0	21.2
2P2	100	3.0	2.0	27.0	8.0	40.0
2P3	100	1.0	3.0	28.0	15.0	47.0
3P1	102	2.0	0	2.0	74.5	78.5
3P2	98	0	45.9	1.0	1.0	47.9
4P1	100	0	52.0	3.0	0	55.0
4P2	104	0	11.5	8.7	3.8	24.0
6P1	102	1.0	12.7	17.6	5.9	37.2
6P2	101	1.0	11.9	53.5	5.0	71.4
8P1	101	0	3.0	36.6	46.5	86.1
8P2	100	0	13.0	2.0	79.0	94.0
Mean±SD	101.1±1.8	2.8±6.3	14.4±16.4	18.8±15.8	21.5±27.7	57.5±23.6

[109] The presence of 16S rDNA from five species found in samples of normal skin from healthy persons and from samples from patients with psoriasis is shown in Table 5.

TABLE 5

Presence of 16S rDNA from five species found in samples of normal skin from healthy persons and from patients with psoriasis

Sample	No. of Clones	Percent					
		Pa ^a	Ct ^b	Sh ^c	Sm ^d	Se ^e	Any of the 5
AL	105	17.1	0	0	0	0	17.1
AR	103	3.9	2.9	1.0	3.9	0	11.7
BL	103	14.6	2.9	1.0	4.9	0	23.4
BR	101	9.9	0	0	5.9	1.0	16.8
CL	103	12.6	8.7	2.9	0	1.9	26.1
CR	99	12.1	10.1	2.0	1.0	8.1	33.3
DL	101	11.9	14.9	4.0	1.0	0	31.8
DR	103	15.5	13.6	1.9	0	10.7	41.7
EL	100	32.0	5.0	0	1.0	1.0	39.0
ER	103	9.7	5.8	0	10.7	2.9	29.1
FL	102	45.1	7.8	5.9	2.9	6.9	68.6
FR	98	65.3	5.1	1.9	1.0	3.1	76.4
AL2	100	0	0	0	0	0	0
AR2	103	3.9	0	1.9	0	1.0	6.8
CL2	101	53.5	0	0	9.9	0	63.4
CR2	105	22.9	1.0	1.0	23.8	0	48.7
EL2	103	6.8	0	0	6.8	0	13.6
ER2	99	12.1	5.1	0	5.1	1.0	23.3
FL2	102	23.5	7.8	6.9	0	3.9	42.1
FR2	104	32.7	12.5	1.0	0	3.8	50.0
Mean±SD	101.9±2.0	20.3±17.4	5.2±4.9	1.6±2.0	3.9±5.8	2.3±3.1	33.1±20.7
1PN	102	4.9	20.6	7.8	2.0	2.0	37.3
2PN	100	0	1.0	9.0	0	15.0	25.0
3PN	103	52.4	12.6	0	1.0	0	66.0
4PN	102	1.0	1.0	22.5	2.0	1.0	27.5
6PN	103	11.7	7.8	15.5	1.0	1.9	37.9
8PN	101	0	26.7	0	1.0	0	27.7
Mean±SD	101.8±1.2	11.7±20.4	11.6±10.5	9.1±8.8	1.2±0.8	3.3±5.8	36.9±15.2
Mean±SD	101.9±1.8	18.3±18.1	6.7±6.9	3.3±5.4	3.3±5.2	2.5±3.8	34.1±19.4

^a: *Propionibacterium acnes*

^b: *Corynebacterium tuberculostrictum*

^c: *Staphylococcus hominis*

^d: *Streptococcus mitis*

^e: *Staphylococcus epidermidis*

Summary of Results

[110] The microbial biota of the normal and psoriatic skin were compared using broad-range 16S rDNA PCR for archaea and bacteria. From 6 patients, 19 cutaneous samples were obtained, of which 13 were from diseased skin and 6 from the normal skin. From each sample, approximately 100 cloned PCR products were analyzed. Using 98% sequence

identity as a species boundary, 1,841 (95.6%) clones were similar to known bacterial 16S rDNA, representing 6 phyla, 86 genera, or 189 species-level operational taxonomic units (SLOTUs); 84 (4.4%) clones were <98% identical to known 16S rDNA, probably representing novel species. No archaeal 16S rDNA were detected. *Firmicutes* was the most abundant and diversified phylum representing 38.3% of the SLOTUs and 46.0% of the clones from psoriatic skin, compared with 34.7% of the SLOTUs and 38.8% of the clones from the normal skin. The psoriatic skin samples showed 19.6 ± 6.4 genera, significantly more than detected in normal skin samples (11.5 ± 3.9) ($P=0.008$). The samples from psoriatic lesions yielded 52 new genera not observed in normal skin samples. These results show that psoriasis is associated with substantial alteration of the cutaneous bacterial biota.

Phylogenetic analysis.

[111] The 16S clone libraries from the six patients with psoriasis yielded 1,314 and 611 sequences for the lesions and normal skin samples, respectively. According to the RDP-II database, these could be grouped to 8 phyla, 94 genera, and 212 species-level operational taxonomic units (SLOTUs) at 98% identity. In total, 1,841 cloned sequences were similar to those of known bacterial isolates, and represented 189 SLOTUs. A total of 84 (4.4%) clones were <98% identical to current GenBank entries, and these clones were grouped into 5 phyla, 16 genera, and 23 novel phylotypes. In 20 skin samples from 6 healthy subjects, the inventors previously detected 247 SLOTUs, which belonged in 10 phyla (Gao, 2007, PNAS). The number of species per skin sample was not significantly different between the healthy subjects and those with psoriasis. A single representative of one additional bacterial phylum, *Planctomycetes*, was detected in one sample from a patient with psoriasis. *Planctomycetes*, a phylum comprised of aquatic bacteria, is found in fresh, brackish, and marine water samples. Overall, the bacteria detected from the 39 human skin specimens from this and the prior studies comprise 366 different SLOTUs.

Distribution at the phylum level.

[112] The distribution of bacterial phyla was determined in samples of healthy and diseased skin. *Firmicutes* and *Actinobacteria*, the dominant phyla in both groups, were found in each sample, as shown in Figure 4. Five other phyla (*Proteobacteria*, *Bacteroidetes*, *Fusobacteria*, *Planctomycetes* and *TM7*) were found in the samples from

diseased skin. The most numerous and diverse phylum populating the psoriatic lesions was *Firmicutes* (46.0%), significantly ($P < 0.001$) overrepresented compared to the samples from healthy persons. In contrast, *Actinobacteria*, the most prevalent (48.0%) and diverse phylum in the samples from normal skin of the patients, was significantly ($P < 0.001$) lower (37.4%) in the samples from psoriatic lesions.

Table 6.

The five most common species found in different groups of skin specimens.

Species	Percent of total clones (rank) ^e			
	NNT1 ^a	NNT2 ^b	PNT ^c	PPT ^d
<i>Propionibacterium acnes</i>	20.6(1)	19.5(1)	11.8(1)	2.5(7)
<i>Corynebacterium tuberculostearicum</i>	6.4(2)	3.3(6)	11.6(2)	11.4(1)
<i>Staphylococcus hominis</i>	1.6(12)	1.3(11)	9.2(4)	9.1(2)
<i>Streptococcus mitis</i>	2.7(6)	5.8(3)	1.1(15)	5.6(3)
<i>Enhydrobacter aerosaccus</i>	2.8(5)	12.5(2)	0.2(58)	0.8(32)
<i>Staphylococcus capitis</i>	1.0(20)	0.6(29)	11.5(3)	1.1(19)
<i>Staphylococcus caprae</i>	3.5(3)	2.1(9)	2.9(7)	1.8(11)
<i>Staphylococcus epidermidis</i>	2.9(4)	1.2(12)	3.3(6)	2.2(9)
<i>Corynebacterium simulans</i>	0.7(31)	0.2(51)	4.4(5)	3.4(4)
<i>Demacoccus AF409025</i>	0.1(116)	5.8(3)	0	1.4(17)
<i>Rothia mucilaginosa</i>	1.5(15)	0.2(51)	0.3(40)	3.0(5)
<i>Staphylococcus haemolyticus</i>	0.2(81)	3.5(5)	1.1(15)	0.4(51)
Five most common species	36.2	47.1	48.5	32.5

^aNNT1: 12 samples from six healthy persons, reported in a prior study (Gao Z. et al., PNAS, 2007).

^bNNT2: Eight samples from four of six healthy people 8-10 months later.

^cPNT: Six samples from normal skin of six patients with psoriasis.

^dPPT: 13 samples from psoriatic lesions from six patients with psoriasis.

^eBold indicates most common 5 bacterial species; number in parentheses indicates rank order of that species in the samples.

Table 7.

The 10 most common genera detected in human skin samples.

Genus	Percent of clones (%)			
	Normal subjects ^a		Psoriatic subjects	
	Time 1 (n = 1,221) ^a	Time 2 (n = 817)	Normal (n = 611)	Lesions (n = 1314) ^b
<i>Corynebacterium</i>	19.0	7.2	29.1	21.2
<i>Staphylococcus</i>	11.1	10.5	31.8	18.1
<i>Propionibacterium</i>	22.0	19.7	12.4	2.8
<i>Streptococcus</i>	5.8	11.6	3.4	14.3

<i>Enhydrobacter</i>	2.8	12.5	0.2	0.8
<i>Acinetobacter</i>	3.7	3.8	1.0	1.6
<i>Dermacoccus</i>	0.8	6.2	0	1.4
<i>Pseudomonas</i>	2.7	1.0	2.5	1.4
<i>Rothia</i>	1.8	0.4	0.5	3.7
<i>Micrococcus</i>	0.5	2.7	0.2	2.2
Percent	70.2	75.6	81.1	67.5

^a From (Gao Z., et al., Proc. Natl. Acad. Sci. U. S. A)

^b Number of clones studied.

Distribution at the genus level.

[113] In total, 166 genera were detected in the 39 samples from human skin. The data in Table 6 and Table 7 include the frequency of 10 of the most common genera in healthy and diseased samples. Only 20 genera were found in all 4 groups of specimens (NNT1, NNT2, PNT and PPT), but none of the genera was found in every sample. *Corynebacterium*, *Staphylococcus*, *Streptococcus*, and *Propionibacterium* were the four dominant genera in the samples from both normal skin and from the lesions of patients with psoriasis, accounting for 76.7% and 57.5% of all clones, respectively. Clones representing the genus *Streptococcus* were detected significantly more frequently ($15.2 \pm 10.4\%$) from psoriatic lesion samples ($p < 0.05$) than from the uninvolved skin samples of the patients ($3.4 \pm 2.5\%$). In contrast, *Propionibacterium* species represented $21.1 \pm 18.2\%$ of the total clones in the samples from the healthy subjects, significantly higher than in lesions from patients with psoriasis ($2.9 \pm 5.5\%$) ($P < 0.05$). For the patients with psoriasis, clones representing *Propionibacterium* were detected more frequently in samples from healthy skin ($12.3 \pm 21.6\%$) than from lesions ($2.9 \pm 5.5\%$), but the difference was not significant ($P = 0.33$).

Distribution at the SLOTU level.

[114] Table 6 also shows the four most prevalent bacterial species in each of the different groups, accounting for 29.6~44.0 % of the total clones in that group. *Propionibacterium acnes* was the most prevalent species in the samples from the healthy subjects and from the unaffected skin of the patients with psoriasis (also shown in Figure 3A and Table 4). Representation of *P. acnes* was much lower in the samples from the lesions of the patients with psoriasis than in the samples from normal persons ($P < 0.05$); the normal skin from psoriasis patients showed intermediate levels ($12.3 \pm 21.6\%$).

Staphylococcus aureus, long regarded as being associated with psoriasis (Skov L, & Baadsgaard O., 2000) was found in only 1.1% and 2.8% of the clones from the unaffected and diseased samples of the patients, respectively.

Analysis of clustering.

[115] 39 samples of 16S rDNA clone library profiles from human skin were compared by using Unifrac distance metric. The results showed that the samples from same person had a tendency to cluster closer than samples from different individuals.

Double principal coordinate analysis (DPCoA) of the samples from human skin.

[116] Similarities in SLOTU distributions between skin samples were evaluated using DPCoA. Four hypotheses concerning the grouping of samples were tested. First, analysis using all 39 samples of human skin from 12 persons (6 healthy persons and 6 patients with psoriasis) showed that those from the same subject were more similar to each other than to samples from other subjects ($P < 0.001$). The same result was confirmed for the newly analyzed 19 samples from the six patients with psoriasis ($P = 0.006$). Second, in analysis of the 19 samples from the patients with psoriasis, those obtained from psoriatic lesions were not significantly different than those from unaffected skin from the same patient, although there was an overall trend ($P = 0.062$). Third, the samples of diseased skin from the patients ($n = 13$) were clustered together, compared to samples of normal skin from healthy subjects ($n = 20$) ($P = 0.001$). Fourth, the samples obtained from unaffected skin from the patients ($n = 6$) were not significantly different from those from normal skin of healthy subjects ($n = 20$) ($P = 0.12$).

[117] **Additional quantitations with a universal probe in combination with a genus-specific probe for *Propionibacterium* sp.**

[118] **Methods:** A universal probe (G-16) (ACTGCTGCCTCCCGTA) (SEQ ID NO:5) for quantitation of all bacteria and a genus-specific probe (Pro-17) (AAGTCAACCCGTATCGAAAG) (SEQ ID NO:6) for *Propionibacterium* sp. were designed, targeting eubacterial 16S rDNA. qPCR reactions were performed using universal primers that can amplify an ~1500bp fragment. Serial dilution of cloned PCR products was used to build standard curves. The method was evaluated for the specificity of the

probe and quantification of bacteria in samples from healthy persons. **Results:** The Pro-17 genus-specific probe recognized cloned DNA representing 4 species within the genus *Propionibacterium* that had been previously detected in human skin, but not other common skin genera, including *Streptococcus*, *Staphylococcus*, *Corynebacterium*, *Rothia*, *Micrococcus*, *Kocuria*, or *Gemella sp.* Based on standard curves, as few as 10^2 genomes per reaction were detected. Examination of two samples showed $\sim 10^3$ - 10^4 total bacterial genomes/swabbed area.

[119] **Conclusion:** The qPCR assay is a reproducible, sensitive, rapid, and reliable method for the detection and relative quantitation of bacteria that populate human skin.

[120] Table 8. Most common genera detected in normal human skin samples compared with those detected in psoriatic lesions and normal skin from psoriatic patients.

[121] Using analysis of ribosomal genes from clone libraries, provided initial evidence that four genera, *Corynebacterium*, *Streptococcus*, *Staphylococcus*, and *Propionibacterium*, were most common in normal human skin, with significant differences in their prevalences in samples from healthy subjects, the normal skin of patients with psoriasis and the psoriatic lesions from the same patients (Table 8).

TABLE 8

Genus	Percent of clones (%)		
	Psoriatic subjects		Normal ^b subjects (n=1,221)
	Lesions (n=1,314) ^a	Normal (n=611)	
<i>Propionibacterium</i>	2.8	12.4	22.0
<i>Streptococcus</i>	14.3	3.4	5.8
<i>Corynebacterium</i>	21.2	29.1	19.0
<i>Staphylococcus</i>	18.1	31.8	11.1
Percent	57.5	76.8	57.9

^a Number of clones studied

^b From (Gao Z., et al., *Proc. Natl. Acad. Sci. U.S.A.*, 2007; 104, 2927-32.)

[122] Certain embodiments of the present invention relate to a system for detecting and accurately quantifying the total population size of bacteria and genera *Corynebacterium*, *Streptococcus*, *Staphylococcus* and *Propionibacterium sp.* in skin samples using qPCR.

Methods

[123] Using a computer algorithm for generating and estimating the phylogenetic range of 16S rRNA oligonucleotide probes in conjunction with the RDP-II database (PRIMROSE software package 1.1.7), the 16S rDNA sequences were scanned for conserved regions. A universal probe (G-16) (SEQ ID NO:5) for quantitation of all bacteria and a genus-specific probe (Pro-17)(SEQ ID NO:6) for *Propionibacterium sp.* were designed, targeting eubacterial 16S rDNA. qPCR reactions were performed using universal primers 8F (SEQ ID NO:1) and 1510R (SEQ ID NO:2) that can amplify an ~1500bp fragment. Serial dilution of cloned 16S rDNA PCR products was used to build standard curves. The method was evaluated for the specificity of the probe and quantification of bacteria in samples from healthy persons.

Results

Comparison of two bacterial universal probes by q-PCR

[124] To increase the sensitivity of quantification of q-PCR, two universal probes were compared, based on Blast search in the RDP (**Table 9A-B**) and by q-PCR (**Table 10**). The probes G16 (SEQ ID NO:5) and Probe 1 (ACTGAGACACGGTCCA) (SEQ ID NO:7) were tested separately with their respective serial qPCR standard dilution series and two PCR products from human skin. The PCR efficiency was equally high for both independent assays (between 90% and 100%).

Table 9A.

Sensitivity of two universal probes (Probe 1 and G-16) for detection of bacterial species potentially found on human skin, based on RDP-II

Probe designation	Percent of sequences with DNA identity to probe				
	Eubacteria (n=273,300)	Deinococcus- Thermus (n=615)	Thermo- microbia (n=17)	Cyano- bacteria (n=8,110)	Proteo- bacteria (n=110,912)
Probe1 ^a	18.51	0	0	7.77	26.91
G-16 ^b	71.85	86.18	11.76	53.08	

^a ACTGAGACACGGTCCA (SEQ ID NO:7) (Ott SJ. *et al.* J Clin Microbiol 2004; 42:2566-72).

^b ACTGCTGCCTCCCTA (SEQ ID NO:5).

Table 9B.

Sensitivity of two universal probes (Probe 1 and G-16) for detection of bacterial species potentially found on human skin, based on RDP-II

Probe designation	Percent of sequences with DNA identity to probe					
	Firmicutes (n=63,582)	Actino- bacteria (n=26,307)	Plancto- mycetes (n=2,569)	Bactero- idetes (n=27,586)	Fuso- bacteria (n=984)	TM7 (n=389)
Probe1 ^a	11.37	0.71		32.48	0.20	41.6
G-16 ^b	81.70	80.27	1.01	78.64	90.24	75.0

^a ACTGAGACACGGTCCA (SEQ ID NO:7) (Ott SJ. *et al.* J Clin Microbiol. 2004; 42:2566-72).

^b ACTGCTGCCTCCCGTA (SEQ ID NO:5).

Table 10.**Sensitivity of two universal probes for detection of bacterial species in the skin by q-PCR**

Samples	Given Copies (/ul)	G16		Probe 1	
		Ct	Calc Copies	Ct	Calc Copies
Standard	997,00,000	9.0	1,004,414,926	8.0	1,378,120,258
Standard	99,700,000	12.4	112,648,565	11.6	111,860,467
Standard	9,970,000	15.8	12,841,402	15.6	6,844,984
Standard	997,000	20.0	842,066	18.7	774,867
Standard	99,700	24.1	65,042	22.2	67,474
Standard	9,970	27.5	7,339	24.2	16,829
Standard	997	29.8	1,677	28.2	1,055
MPL (unknown)		14.2	34,271,325	14.4	15,908,244
MPLx0.1 (unknown)		18.2	2,807,271	18.0	1,293,676
MPR (unknown)		15.7	13,380,869	16.5	3,657,015
MPRx0.1 (unknown)		20.6	605,339	20.5	228,549
Positive control		12.8	84,021,150	12.0	87,223,386
No template control					
Negative control					

Characteristics of the Probe G16 qPCR assay

[125] The 16S rDNA copies from 2 swab samples of skin were measured with this universal probe. The Ct (threshold cycle) values and the related cell numbers were determined by qPCR. The Ct value is the cycle when the fluorescence detected is significantly higher than the baseline value. The Ct value of each qPCR depends on the initial template amount (copy number) of the target sequence and is inversely proportional to the log of this copy number. As shown in **Table 11**, it was possible to determine the copy number of the tested samples from the standard curves (PCR efficiencies were >90%, $R > 0.99$) using the probe G16. The lower qualitative detection limit was in the range of a few copies of the marker per reaction volume (RV) demonstrated by the fact that the standard containing 25 marker copies per RV was detectable. Based on standard curves, the probe could detect as few as 40 marker copies per reaction volume.

Table 11.

The copies of 16S rDNA from 2 skin samples calculated by qPCR assays using probe 16G (SEQ ID NO:5)

Samples	Ct	Template Conc	Calc Conc	% Var
Standard	6.5	250,200,000	377,123,533	50.7%
Standard	9.4	25,020,000	52,628,711	110.3%
Standard	14.2	2,502,000	2,124,093	15.1%
Standard	20.1	250,200	40,708	83.7%
Standard	23.6	2,502	3,802	52.0%
Standard	27.8	250	229	8.5%
Standard	30.3	25	41	64.2%
GR3(Unknown)	26.6		494	
GL3(Unknown)	22.8		6,564	
Positive Control	25.9		791	
No template control				
Negative control				

Sensitivity and specificity of the genus-specific probe (Pro-17) (SEQ ID NO:6)

[126] The specificity of the *Propionibacterium* sp. probe was determined by comparing cloned 16S rDNA PCR products from *Propionibacterium* sp. ($n=4$) and other common skin genera ($n=7$), including *Streptococcus*, *Staphylococcus*, *Corynebacterium*, *Rothia*, *Gemella*, *Micrococcus*, and *Kocuria* species. For sensitivity assays, serial dilution of cloned 16S rDNA PCR products from *Propionibacterium acnes* was used to build standard curves for enumeration of unknown samples. The results showed that the Pro-17 genus-specific probe (SEQ ID NO:6) recognized cloned DNA representing 4 species within the genus *Propionibacterium* that had been previously detected in human skin, but not seven other common skin genera tested. A standard curve (PCR efficiencies were 87%, $R > 0.99$) was created by 10-fold dilutions of 16S rDNA PCR products with genus-specific probe Pro-17 (SEQ ID NO:6).

Detection using the all-bacteria probe and *Propionibacterium* species probe from skin swabs.

[127] In order to test the performance of the q-PCR assay on clinical samples, 4 skin swabs were collected from one healthy person. All samples were positive for the all-bacteria probe and for *Propionibacterium* species, indicating that qPCR can be performed on clinical samples following a rapid and inexpensive DNA extraction procedure. These results are shown in Table 12.

Table 12.

Quantitation of all-bacteria species and *Propionibacterium* sp. from four skin swabs

Samples	All-bacteria species		Propionibacterium species	
	Ct	Number of copies	Ct	Number of copies
GR	26.6	37,099	39.6	24
GL	28.6	11,541	36.1	107
GRN	27.8	17,728	34.5	210
GLN	25.5	69,415	38.6	31

Conclusions:

1. The qPCR assay is a sensitive, rapid, and reliable method for the detection and relative quantitation of bacteria that populate human skin.
2. Universal probe 16G (SEQ ID NO:5) is more sensitive to detect the bacteria found in human skin than Probe 1 (SEQ ID NO:7).
3. The q-PCR assays using a genus-specific probe allow detection of all known *Propionibacterium* sp. that are found in the skin samples.
4. The probe is specific to the genus *Propionibacterium* sp; no significant cross-reaction of the genus-specific probe among the different common genera was seen.
5. Based on standard curves, as few as 4×10^1 genomes per reaction volume could be detected. Examination of the samples from skin swabs showed $\sim 10^3$ - 10^5 total bacterial and $\sim 10^1$ - 10^2 *Propionibacterium* sp. 16S rDNA copies/swabbed area.

Design of Additional genus-specific probes in combination with New Universal 16S rDNA probe.

[128] A new universal 16S rDNA probe for quantitation of all eubacterial and two new genus-specific probes (*Propionibacterium* and *Streptococcus* sp.) were designed. qPCR reactions were performed using universal primers that can amplify an ~ 800 bp rDNA fragment and the genus-specific probes were combined in multiplex reactions. The method was evaluated for the specificity of the probes and quantitation of bacteria in samples from one healthy person and one patient with psoriasis (uninvolved skin and psoriatic lesions). The genus-specific probes were shown to be sensitive and specific using cloned DNA representing species from genera previously detected in human skin. Each of the tested

human specimens yielded positive results with the universal eubacterial probe and both genus-specific probes.

[129] Three samples of healthy skin showed *Streptococcus* to *Propionibacterium* ratios of 0.001 to 0.011 (median 0.004), whereas three samples from the psoriasis lesions showed 0.160 ~ 2.000 (median 0.646). These results demonstrated that the qPCR assay is a sensitive, rapid, and reliable method for the detection and relative quantitation of bacteria that populate human skin. *Propionibacterium sp.* appears to predominate in samples from healthy skin, but was substantially underrepresented in the samples from psoriasis lesions.

[130] The results described herein show the development of a system to accurately quantify the total population size of bacteria and the ratio of *Streptococcus* to *Propionibacterium* in skin samples from healthy persons and patients with psoriasis using quantitative real-time-PCR (qPCR).

Methods

[131] Using a computer algorithm for generating and estimating the phylogenetic range of 16S rRNA oligonucleotide probes in conjunction with the RDP-II database (PRIMROSE software package 1.1.7), ten 16S rDNA sequences belonging to different phyla were scanned for conserved regions.

[132] A universal probe (G-16) (SEQ ID NO:5) for quantitation of all eubacteria and the genus-specific probes for *Propionibacterium sp.* (SEQ ID NO:6) and for *Streptococcus sp.* (AGATGGACCTGCGTTGT) (SEQ ID NO:8) were designed, targeting the specific eubacterial 16S rDNA. qPCR reactions were performed using universal primers (8F, SEQ ID NO:1) and U785R, (GGACTACCVGGGTATCTAAKCC) (SEQ ID NO:9) that can amplify an ~800bp fragment from a large fraction of all eubacteria. Serial dilution of a mixture of equal amounts of 16S rDNA copies from *Propionibacterium acnes* and *Streptococcus mitis* genomic DNA were used to build standard curves.

Results

Standard curves of the qPCR assays

[133] A bacterial universal probe (SEQ ID NO:5) and two genus-specific dual-labeled probes (SEQ ID NO:6 and SEQ ID NO:7) were used to detect and quantify all eubacteria

and *Propionibacterium sp.* and *Streptococcus sp.* from human skin samples. The probe is TaqMan-minor groove binder (MGB) probe (Applied Biosystems, Foster City, CA, USA) labeled with FAM fluorescent dye or VIC fluorescent dye.

[134] A 10-fold dilution of a mix of equal amounts of 16S rDNA copies from *Propionibacterium acnes* and *Streptococcus mitis* genomic DNA was used to build standard curves. The Ct (threshold cycle) values and the related cell numbers were determined by qPCR. The Ct value is the cycle when the fluorescence detected is significantly higher than the baseline value. The Ct value of each qPCR depends on the initial template amount (copy number) of the target sequence and is inversely proportional to the log of this copy number. It was possible to determine the copy number of the tested samples from the standard curves (PCR efficiencies were >90%, R>0.99) using probe G16 (SEQ ID NO:5) (Table 13). The lower qualitative detection limit was in the range of a few copies of the marker per reaction volume (RV), demonstrated by the fact that the standard containing 25 marker copies per RV was detectable. Based on standard curves, the probe was calculated to detect as few as 40 marker copies per reaction volume.

[135] For qPCR, 1 μ l of DNA sample was added to a 25 μ l PCR reaction containing 2.5 μ l 10x PCR buffer (QIAGEN, Valencia, CA), 1.5 mM MgCl₂, 200 μ M each dNTP, 10 pmol of each primer, 5 pmol of each probe, and 1.25 units of Taq polymerase. The PCR reaction was run in a Rotor-Gene 3000 (Corbett Life Science) with an initial hold at 50°C for 2 minutes, then 95°C for 5 minutes, followed by 45 cycles of 95°C for 10 sec, 52°C for 60 sec, and 72°C for 90 sec. During the 52°C steps, the Rotor-Gene stimulates the samples and then acquires fluorescence data on channels appropriate to 6-FAM and JOE/VIC.

Table 13.

Copies of total 16S rDNA from two unknown skin samples calculated by qPCR assays using probe 16G (SEQ ID NO:5)

Samples	Ct ^a	Concentrations		% Variation
		Template	Calculated	
Standard	6.5	2.5 × 10 ⁸	377,123,533	50.7
Standard	9.4	2.5 × 10 ⁷	52,628,711	110.3

Standard	14.2	2.5×10^6	2,124,093	15.1
Standard	20.1	2.5×10^5	40,708	83.7
Standard	23.6	2.5×10^3	3,802	52.0
Standard	27.8	2.5×10^2	229	8.5
Standard	30.3	2.5×10^1	41	64.2
GR3(Unknown)	26.6		494	
GL3(Unknown)	22.8		6,564	
Positive Control	25.9		791	
No template control			0 ^b	
Negative control			0 ^b	

^a CT represents the number of PCR cycles calculated to reach the threshold for positivity.

^b Below the lowest level of detection.

Sensitivity and specificity of the genus-specific probes

[136] The specificity of the two probes (SEQ ID NO:6 and SEQ ID NO:8) were determined by comparing cloned 16S rDNA PCR products from *Propionibacterium sp.* ($n=4$), *Streptococcus sp.* ($n=2$) and other common skin genera 16S rDNA PCR products, including *Staphylococcus*, *Corynebacterium*, *Rothia*, *Gemella*, *Micrococcus*, and *Kocuria* species. The genus-specific probes recognized the cloned DNA representing species within the same genera that had been previously detected in human skin, but not other common skin genera. The sensitivity of the assays was assessed using 10-fold dilutions of the same templates used for the standard curves, corresponding to 3×10^6 through 3×10^1 16S rDNA copies per reaction. The limit of detection for the two genus-specific probes ranged from 10^1 to 10^2 16S rDNA copies per reaction. Figure 5 shows the standard curve created by 10-fold dilutions of 16S rDNA copies with the genus-specific *Streptococcus* probe (SEQ ID NO:8). The probe performed well, with $R > 0.99$ and PCR efficiencies of 80%.

Comparison of the qPCR result in single and multiplex format

[137] To determine whether the two genus-specific probes could be used in multiplex reactions, the detection of 16S rDNA copies from *Propionibacterium acnes* and *Streptococcus mitis* genomic DNA was compared in single and multiplex formats. No significant differences were found when the two genus-specific probes were tested in multiplex compared with the single formats (Figure 6).

Detection of all eubacteria and *Propionibacterium* sp. and *Streptococcus* sp. from skin swabs.

[138] To test the performance of the q-PCR assay on clinical samples, six skin swabs were collected from a healthy person (n=2) and one person with psoriasis (n=4). All samples yielded positive results for the all-eubacterial probe and the two genus-specific probes for *Propionibacterium* and *Streptococcus* species. The results (**Table 14**) show that qPCR can be performed on clinical samples across broad range of DNA concentrations, following a rapid and inexpensive DNA extraction procedure. Three samples of healthy skin showed *Streptococcus* to *Propionibacterium* ratios ranging from 0.001 to 0.011 (median 0.004), whereas 3 samples from psoriasis lesions showed 0.160 ~ 2.000 (median 0.646) (p=0.23; Student's t-test).

Table 14.

Quantitation of all eubacterial species, and *Streptococcus* and *Propionibacterium* species from six skin swabs

Code	Condition	All eubacteria	Streptococcus	Propionibacterium	Ratio of S/P
AL4	Healthy	7.4×10^9	132,204	33,799,641	0.004
AR4	Healthy	1.9×10^9	104,525	120,990,902	0.001
10PN	Uninvolved	3.1×10^4	68	6,245	0.011
10P1	Lesion	3.9×10^4	705	1,091	0.646
10P2	Lesion	5.7×10^9	18	9	2.000
10P3	Lesion	1.8×10^5	609	3,721	0.160

Conclusions

1. The qPCR assay is a sensitive, rapid, and reliable method for the detection and relative quantitation of bacteria that populate human skin.
2. The genus-specific probes (SEQ ID NO:6 and SEQ ID NO:8) recognized cloned DNA representing species within the same genera that had been previously detected in human skin, but not other common skin genera.
3. Based on standard curves, as few as 4×10^1 genomes per reaction volume, using the all eubacteria universal probe (SEQ ID NO:5) could be detected.
4. *Propionibacterium* sp. appears to predominate in the samples from healthy skin, but was substantially underrepresented in the samples from psoriasis lesions.

[139] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims. It is further to be understood that all values are approximate, and are provided for description.

[140] Patents, patent applications, publications, product descriptions, and protocols are cited throughout this application, the disclosures of which are incorporated herein by reference in their entireties for all purposes.

CLAIMS

1. A method for treating psoriasis comprising increasing the amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient in need of such treatment.
2. The method of claim 1, wherein the *Propionibacterium* species is *Propionibacterium acnes*.
3. A method for treating psoriasis comprising administering an effective amount of at least one *Propionibacterium* species to affected skin in a patient in need of such treatment.
4. The method of claim 3, wherein the effective amount of at least one *Propionibacterium* species comprises killed *Propionibacterium* cells.
5. The method of claim 4, wherein the *Propionibacterium* cells are *Propionibacterium acnes*.
6. The method of claim 3, wherein the effective amount of at least one *Propionibacterium* species comprises an extract from *Propionibacterium*.
7. The method of claim 6, wherein the *Propionibacterium* is *Propionibacterium acnes*.
8. The method of claim 3, wherein the *Propionibacterium* species is *Propionibacterium acnes*.
9. A method for promoting growth of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient comprising administering an effective amount of at least one *Propionibacterium* species to the psoriatic skin lesion in a patient in need of such treatment.
10. A method for monitoring treatment of psoriasis comprising:

determining an amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient; wherein a low amount

of at least one *Propionibacterium* species in a psoriatic lesion indicates psoriasis and wherein an increase in the amount of at least one *Propionibacterium* species in a psoriatic lesion indicates treatment progress.

11. A method for monitoring treatment of psoriasis comprising:
 - a. determining an amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient;
 - b. determining the amount of at least one *Propionibacterium* species in a healthy skin sample in the patient;
 - c. comparing the amounts in part a) and b);
 - d. wherein a lower amount of at least one *Propionibacterium* species in a psoriatic lesion when compared with a healthy skin sample indicates psoriasis and wherein an increase in the amount of at least one *Propionibacterium* species in a psoriatic lesion indicates treatment progress.
12. A method for diagnosing psoriasis comprising:

determining the amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient; wherein a low amount of at least one *Propionibacterium* species in a psoriatic lesion indicates psoriasis.
13. A method for diagnosing psoriasis comprising:
 - a. determining the amount of at least one *Propionibacterium* species in a psoriatic skin lesion in a patient;
 - b. determining the amount of at least one *Propionibacterium* species in a healthy skin sample in the patient;
 - c. comparing the amounts in part a) and b); and
 - d. wherein a lower amount of at least one *Propionibacterium* species in a psoriatic lesion when compared with a healthy skin sample indicates psoriasis.
14. A method for diagnosing psoriasis comprising:

- a. determining the amount of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient;
- b. determining the amount of at least one NGS in a healthy skin sample in the patient;
- c. comparing the amounts in part a) and b); and
- d. wherein a higher amount of at least one NGS in a psoriatic skin lesion when compared with a healthy skin sample indicates psoriasis.

15. A method for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient comprising: administering an effective amount of a suitable antibiotic and optionally administering a suitable physical means of inhibiting NGS growth to the patient in need of such treatment.

16. A method for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient comprising: administering an effective amount of a suitable chemical agent.

17. A method for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient comprising: administering an effective amount of a suitable physical treatment.

18. A method for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient comprising: administering an effective amount of a suitable antibiotic and optionally administering a suitable chemical means of inhibiting NGS growth to the patient in need of such treatment.

19. A method for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in a psoriatic skin lesion in a patient comprising: administering an effective amount of a suitable antibiotic and administering a suitable physical and a suitable chemical means of inhibiting NGS growth to the patient in need of such treatment.

20. A vaccine composition for inhibiting the growth of at least one non-Group A *Streptococcus* species (NGS) in the skin of a patient in need of such treatment.

21. A method for diagnosing psoriasis comprising:
 - determining a ratio of a non-Group A *Streptococcus* species (NGS) to a *Propionibacterium* species (gS/P ratio) in a psoriatic skin lesion in a patient; and wherein a raised gS/P ratio indicates psoriasis.
22. A method for diagnosing psoriasis comprising:
 - a. determining a ratio of a non-Group A *Streptococcus* species (NGS) to a *Propionibacterium* species (gS/P ratio) in a psoriatic skin lesion in a patient;
 - b. determining a ratio of a non-Group A *Streptococcus* species (NGS) a *Propionibacterium* species (gS/P ratio) in a healthy skin sample in the patient;
 - c. comparing the amounts in part a) and b); and
 - d. wherein a raised gS/P ratio indicates psoriasis.
23. A method for treating psoriasis comprising lowering the ratio of a non-Group A *Streptococcus* species (NGS) to a *Propionibacterium* species (gS/P ratio) in the skin of a patient in need of such treatment.
24. A vaccine composition for lowering the ratio of a non-Group A *Streptococcus* species (NGS) to a *Propionibacterium* species (gS/P ratio) in the skin of a patient in need of such treatment.
25. A method for treating psoriasis in a patient comprising administering an effective amount of inactivated or killed *Propionibacterium* cells to the patient in need of such treatment.
26. A method for treating psoriasis in a patient comprising administering an effective amount of killed or inactivated *Propionibacterium acnes* cells to the patient in need of such treatment.
27. A method for treating psoriasis in a patient comprising administering an effective amount of an extract from *Propionibacterium* to the patient in need of such treatment.

28. A method for treating psoriasis in a patient comprising administering an effective amount of an extract from *Propionibacterium acnes* to the patient in need of such treatment.

29. A method for diagnosing a skin disease comprising:

- a. determining the amount of at least one desired bacterial species in a skin sample suspected of being diseased from a patient;
- b. determining the amount of at least one desired bacterial species in a healthy skin sample from the patient;
- c. comparing the amounts in part a) and b); and
- d. wherein an altered amount of the at least one desired bacterial species in a skin sample suspected of being diseased when compared with a healthy skin sample indicates a skin disease.

30. The method of claim 28, wherein the skin disease is selected from the group consisting of atopic dermatitis, acne, alopecia, seborrhea, dandruff, and pemphigus.

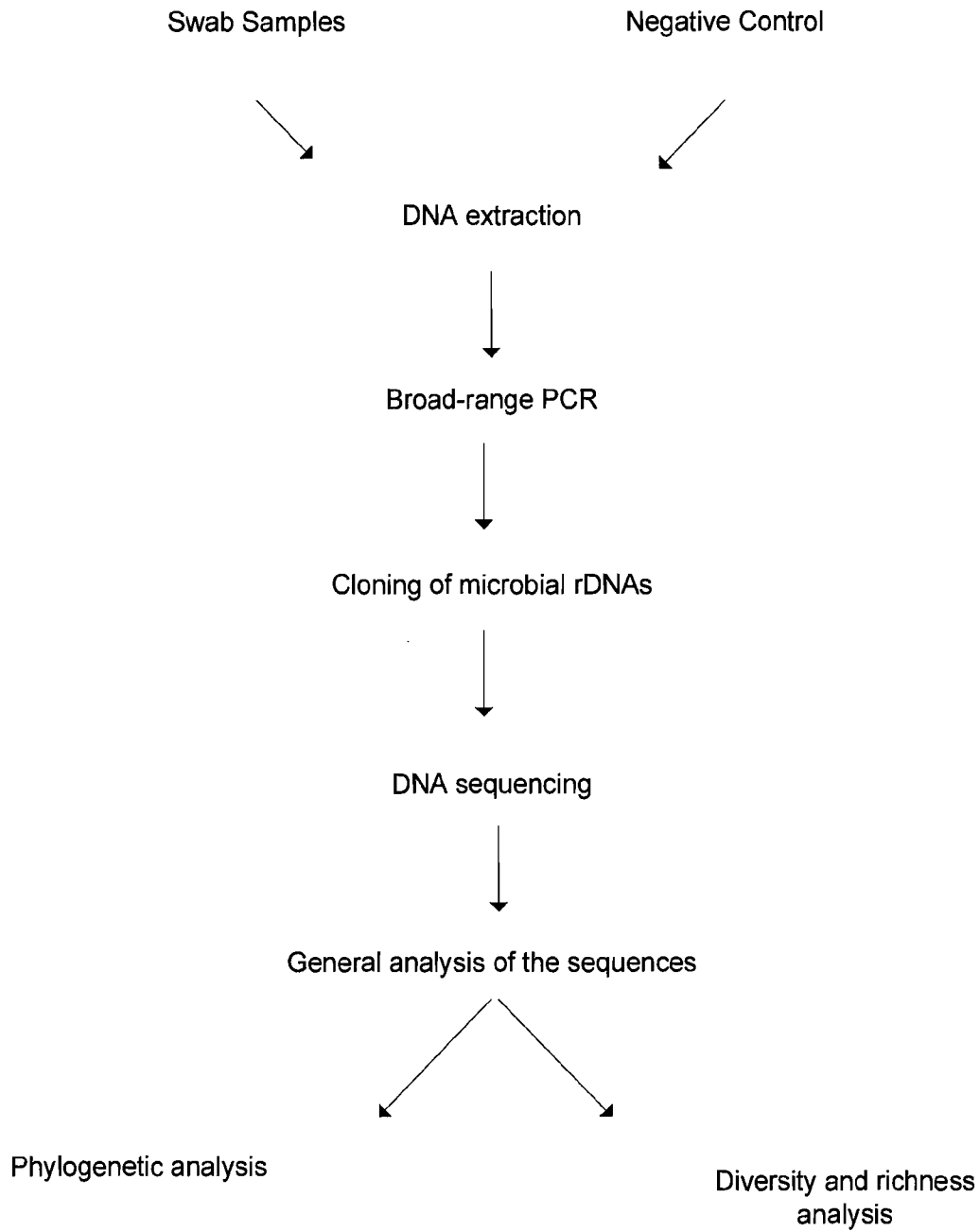
31. The method of claim 29, wherein the determining comprises performing quantitative polymerase chain reaction (qPCR).

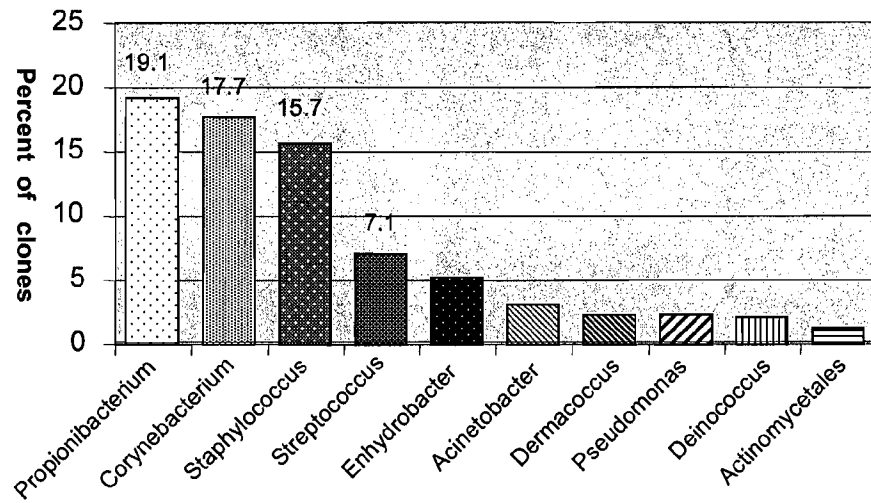
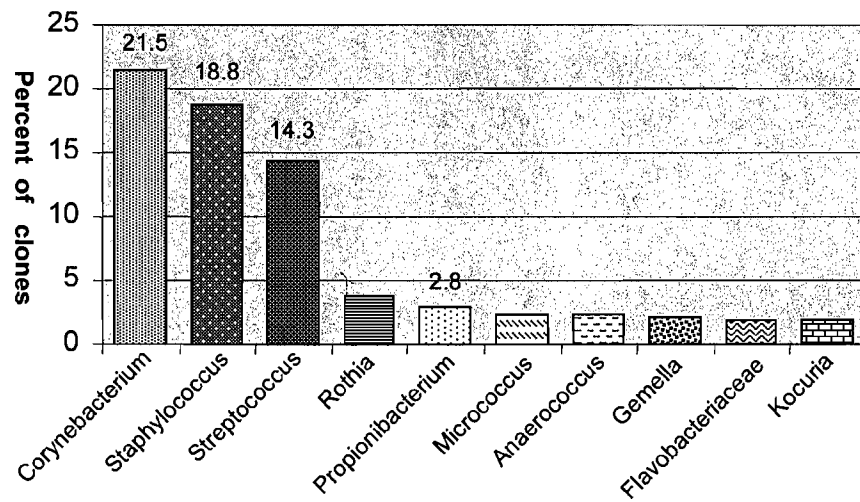
32. The method of claim 31, wherein amplified target DNA from the qPCR reaction is characterized by fluorescent emission detected by binding of one or more of a labeled probe selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:8 to the amplified target DNA.

33. A kit for determining a bacterial signature comprising at least one nucleic acid selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:8.

34. An isolated nucleic acid fragment comprising SEQ ID NO:6 or SEQ ID NO:8.

Methods for Determining Skin Biota

**FIGURE 1**

A**B****Figure 2**

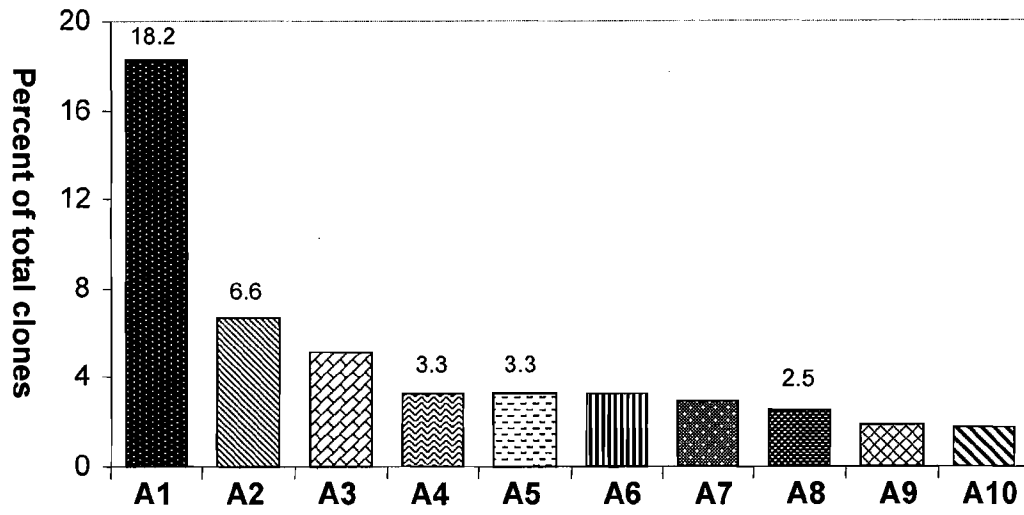
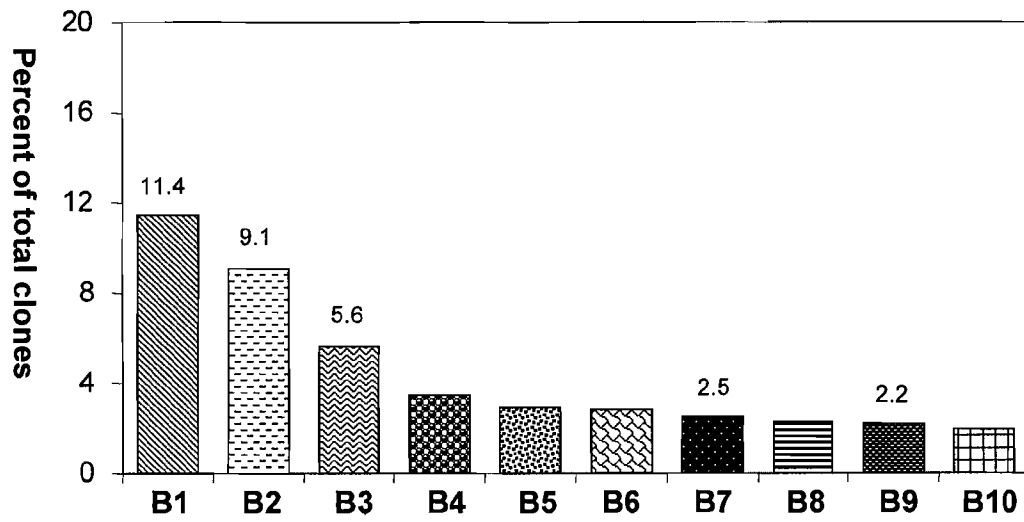
A**B****Figure 3**

FIGURE 4
Distribution of 3,963 16S rDNA clones from
normal and psoriatic samples, by phylum.

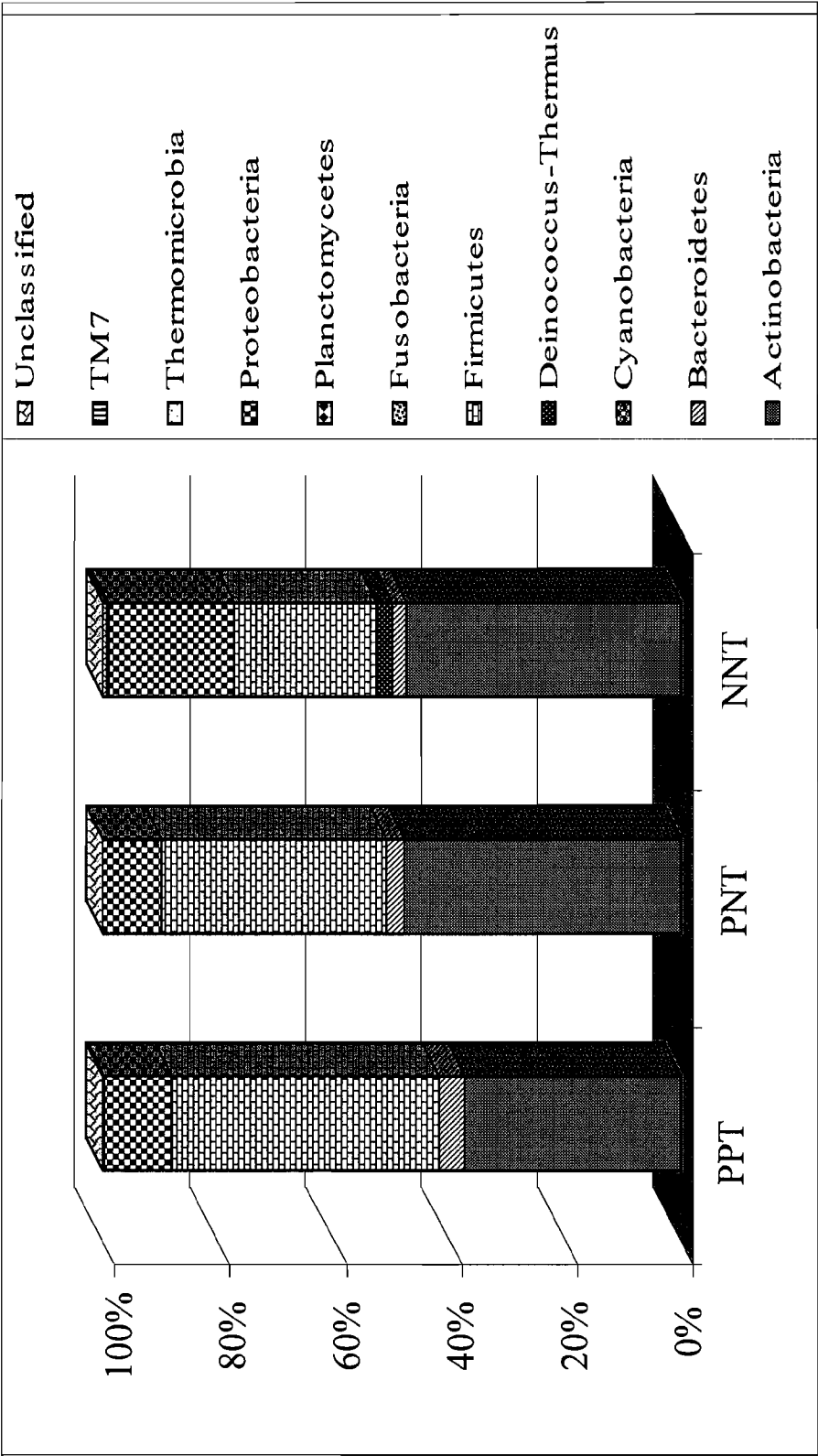
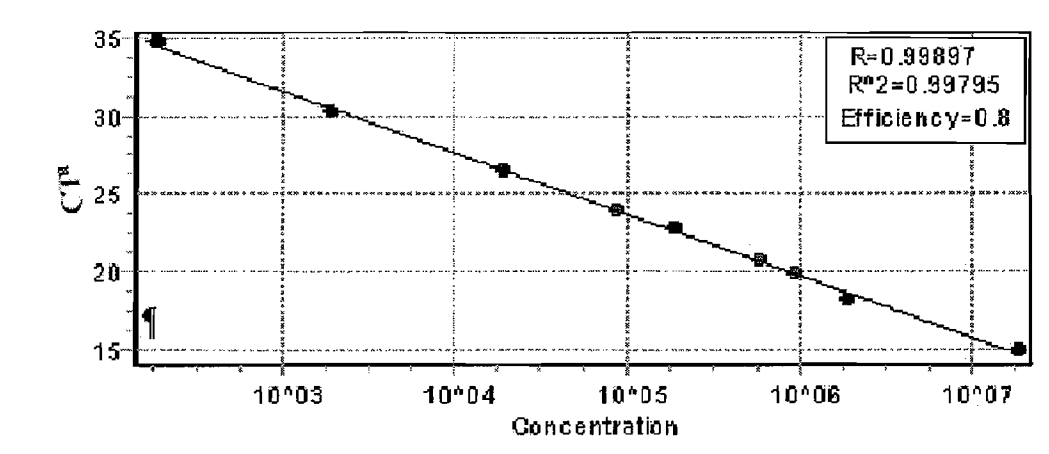


FIGURE 5



^a CT (threshold cycle) corresponds to the minimum number of cycles at which the fluorescence can be detected

Fig. 6 Detection of specific 16S rDNA in single and multiplex qPCR reactions

