Active Beauty
Leadership in Microbiomics for Cosmetics

White Paper
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White paper “Leadership in Microbioms for cosmetics”

1. “The” human microbiome

...or the human “microbiomes”

Human microbiome, previously referred to as human microflora, or human bacterial flora, has been known for decades. Microflora, or as we now call it more precisely microbiota, is in fact the assemblage of microorganisms present in a defined environment. Today what we name microbiome is a little bit more global, and refers to the microorganisms’ community (the microbiota) plus their genes and their surrounding environment. Gathering pivotal information from the genes of a microbiota has been made possible by the tremendous development of genomic technologies over the last two decades, and in particular of a global analysis method called metagenomics, which allows studying all microbiota genes in one experience.  

The human microbiota is composed of a huge diversity of bacteria, yeasts, fungi and other viruses, and their total number is estimated to 10,000 different species. However, the large majority of them are still unknown as they cannot be isolated and studied in laboratory conditions (90% of them at least!). In fact, most of them require very specific living conditions, and in general these are symbiotic conditions with many other microbial partners of the community. Such complex and dynamic systems are very hard, or almost impossible, to reproduce in lab environments, although some models appear.

But if the complexity of a bacterial community is intense, so is our body. As humans and microorganisms co-evolved for millions of years, microbiomes living in and on our body adapted to the variety of our organs. In fact bacterial communities are colonizing all of our pieces, including gut, mouth, nose, vagina, skin... and even blood. But as these organs provide various conditions for bacterial life - such as moisture or dryness, available nutrients, pH and temperature -, these environments have shaped a variety of species communities, each with typical and distinct phenotypes and abundance. This is the reason why, when we talk about human microbiome, we should say human microbiomes.

As an illustration, and this is surely one of the most famous ones, Scientific American edited in 2012 an interactive tool to explore the general patchwork of our microbiomes, showing which were the most abundant microbial families in every area of our body.

In 2008, the National Institutes of Health started the Human Microbiome Project, designed to help understand the health implications of human bacterial flora. During 5 years, a network of not less than 200 researchers labored on deciphering our microbiomes and their link with our health. A total of 250 patents and 370 scientific papers were published, helping the scientific community to better understand our cohabitation with our microbes.

Key numbers arose from these studies, but also a deeper knowledge on host-microbe interactions in general, and in particular those related to diseases. For instance, typical bacterial compositions have been identified between altered lung microbiome and cystic fibrosis, chronic obstructive pulmonary disease, or asthma, and between unbalanced intestinal tract microbiome and individuals with cystic fibrosis and diabetes.

If interactions between microbial communities and host have been demonstrated in several

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2 Human Microbiome Project data, 2013
3 The ecology of the microbiome: Networks, competition, and stability. KZ Coyte et al., Science 2015, 350, 663-666
4 In vitro models of the human microbiota and microbiome. JAK McDonald, Emerging Topics in Life Sciences 2017, 1, 373-384
7 Computational Approaches to Study Microbes and Microbiomes. CS Greene et al., Pac Symp Biocomput. 2016, 21, 557-567
cases, a new axis linking our gut (microbiota) and our brain becomes obvious. In particular, recent studies bring new evidences on the role of gut microbiota in autism spectrum disorders.\(^8,9\) This, of course, paves the way to new treatments promises.

Even more recently, new results on the microbiome gut-brain axis have also shown that gut microbiota could play a role on our sense of smell,\(^10\) when others are looking at the side of nose microbiome.\(^11\)

In conclusion, we discovered during the last decades that not only almost every part of the human body is home to an entire ecosystem of thousands of microorganisms, but also that these were playing an important role in regulating many of our physiological (and psychological?) processes.

Most importantly, we also understood that, in addition to the crucial beneficial role of some defined microbial species that we try to favor using probiotic and prebiotic treatments,\(^12\) it was the **preservation of the whole microbiome equilibrium** that was the primary key.

### 2. Skin microbiota

Among our various microbiomes, the skin microbiota, which at Givaudan we call the *Stratum microbium*\(^9\), is surely the most diverse. With an average surface of 1.8 m\(^2\), our skin is indeed a vast continent with various climates and diversified countries. From deserts (forearms, calves) to jungles (armpits, scalp), our skin provides many niches with **different ecological conditions** (humidity, pH, available nutrients). But skin is also exposed depending on our own environment, lifestyle, and fashion style, to a large variety of **external parameters**, such as outside temperature, UV-exposure, pollution... and contact! This wide variety of skin ecosystems results in many differences in cutaneous microbial composition and abundance depending on the body area, and once again we should talk about skin microbiomes.\(^13,14\)

One of the first descriptions of this **microbiome diversity** on our largest organ was published by Elizabeth Grice and Julia Segre in 2011.\(^15\) Their famous illustration of topographical distribution of bacteria on various skin sites is very explicit, but in fact represents microbial diversity on one individual only.

Later, studies on the skin microbiome have all shown that, if you compare volunteers within a panel by skin zone-to-skin zone, we are all **different**. In fact, our skin microbiome is first determined by early microbial colonization right after birth (and delivery type has its impact\(^16\)), but is then matured with increasing microbial diversity by our life environment, especially during the first year of life.\(^17\) On this point, a study performed in 2015 on Korean twins tried to explore genetic and environmental effects on skin microbiome modulations.\(^18\)

Today, the diversity of skin-associated bacterial communities among people is more and more considered for forensics identification, with different skin microbiome profiling methods being developed.\(^19,20,21\)

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\(^8\) The Gut Microbiota and Autism Spectrum Disorders. Q Li et al., Front Cell Neurosci. 2017, 11, 120


\(^10\) Disruptive physiology: olfaction and the microbiome-gut-brain axis. J Bienenstock et al., *Brain Res Camb Philos Soc* 2018, 93, 390-403

\(^11\) The nasal microbiome mirrors and potentially shapes olfactory function. K Koskinen et al., *Scientific Reports* 2018, 8, 1296

\(^12\) Probiotics, prebiotics and symbiotics: a review. KR Pandey et al., *J Food Sci Technol*. 2015, 52, 7577–7587

\(^13\) Structure and function of the human skin microbiome. NN Schommer and RL Gallo, *Trends Microbiol.* 2013, 21, 666-668


\(^15\) The skin microbiome. EA Grice and JA Segre, *Nature Reviews Microbiology* 2011, 9, 244-253

\(^16\) Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. MG Dominguez-Bello et al., *PNAS* 2010, 107, 11971-11975

\(^17\) Diversity of the Human Skin Microbiome Early in Life. KA Capone et al., *J. of Inv. Dermatol.* 2011, 131, 2026-2032

\(^18\) Genetic associations and shared environmental effects on the skin microbiome of Korean twins. J Si et al., *BMC Genomics* 2015, 16, 992

\(^19\) Integrating the microbiome as a resource in the forensics toolkit. TH Clarke et al., *Forensic Science International: Genetics* 2017, 30, 141-147

\(^20\) The human microbiome: an emerging tool in forensics. JT Hampton-Marcell et al., *Microb Biotechnol.* 2017, 10, 228-230

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Studies also looked at demonstrating the impact of skin contact with other people - or animals! - on the microbiota composition. For instance, James Meadow and co-workers showed in 2013 the influence of a contact sport (roller derby in this case) on the modulation of skin microbial composition upon crossed bouts. Skin microbiome profiles of all players tended to overlap after tournament.

At the same time, Se Jin Song et al. showed the influence, on human skin microbial communities, of having a dog at home. They measured in particular that dog-ownership significantly increased the shared skin microbiota in cohabiting adults, and dog-owning adults shared more skin microbiota with their own dogs than with other dogs. Their results suggest that direct and frequent contact with our cohabitants (humans and pets) may significantly shape the composition of our skin microbial communities.

But microbes on our skin also communicate with our body, and in particular play an important role in our immune system, as was described by Julia Segre (see figure below). As a prolific expert in the field, Richard Gallo also demonstrated the link between cutaneous microbiota and skin health.

In fact, if most of the microbiome research is focused on the gut (skin microbiome scientific papers represent less than 4% of the total microbiome studies published every year, according to PubMed), knowledge on the association of skin disorders and the presence of typical microbial species is steadily increasing. It has to be noticed that microbial communities from the skin differs strongly from the microbiomes of other organs, as was measured by The Human Microbiome Project Consortium, and that it is furthermore constantly subject to external influences.

But despite this complexity and the lack of strong population surveys and skin epidemiologic studies, it has become clear that several skin disorders were correlated with alterations in microbial communities, where differences in the microbes present in diseased skin versus those present in healthy skin have been described. However, it is still not clear whether microbiome imbalance leads to skin pathologies, or whether underlying skin conditions result in a modification of microbial equilibrium.

Among the different correlations that have been identified and demonstrated, one can mention:
- atopic dermatitis with Staphylococcus aureus species (and a low-diversity skin microbiota),
- acne with Cutibacterium acnes and Staphylococcus,
- dandruff with Malassezia species and a disrupted balance between bacteria and fungi,
- psoriasis with an increase in Firmicutes (mainly Streptococcus and Staphylococcus) and Actinobacteria (mainly Corynebacterium and Pro-

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23 Significant changes in the skin microbiome mediated by the sport of roller derby. JF Meadow et al., PeerJ 2013, 1:e51
24 Cohabiting family members share microbiota with one another and with their dogs. SJ Song et al., eLife 2013, 2:e00458
25 Skin microbiota-host interactions. YE Chen et al., Nature 2018, 553, 427-436
26 Dialogue between skin microbiota and immunity. Y Belkaid and JA Segre, Science 2014, 346, 954-959
27 Functional microRNA expression in human skin xenografts. B Dreno et al., Experimental Dermatology 2017, 26, 798-803
28 The role of the skin microbiome in atopic dermatitis: a systematic review. RD Bjerre et al., British Journal of Dermatology 2017, 177, 1272-1278
29 Skin microbiome and acne vulgaris: Staphylococcus, a new actor in acne. B Dreno et al., Experimental Dermatology 2017, 26, 798-803
31 The balance of metagenomic elements shapes the skin microbiome in acne and health. E Barnard et al., Scientific Reports 2016, 6:39491
32 Characterization of the major bacterial-fungal populations colonizing dandruff scalps in Shanghai, China, shows microbial disequilibrium. L Wang et al., Experimental Dermatology 2015, 24, 381-400
33 Dandruff is associated with the conjoined interactions between host and microorganisms. Z Xu et al., Scientific Reports 2016, 6:24877
34 Collapse of human scalp microbiome network in dandruff and seborrheic dermatitis. T Park et al., Experimental Dermatology 2017, 26, 835-838
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pionibacterium), but above all linked with a lower microbial diversity.

Once again, it is the high diversity of the microbiota and the protection of its balance that prevails for a healthy skin microbiota.

### 3. Cosmetics and skin microflora

One of an additional role of microbes living on our skin is the production, or modulation, of body odors, in particular to produce axillary malodors by decomposition of apocrine sweat (usually by Corynebacteria), or foot odors from eccrine sweat.

In fact skin microbiota participates in the global olfactory “signature” of human skin. In 1953 first studies demonstrated the role of bacteria in the axillary odor formation, later followed by the work of famous dermatologist Albert Kligman.

**Deodorants** were thus the first cosmetic products developed to have an effect on our skin microbiota, with early studies on the effect of topical antibacterial agents on the axillary microbiome in 1963.

These discoveries were soon further exploited by Albert Kligman to develop new approaches to treat acne, while he coined the term “cosmeceuticals.” In addition, he developed new therapies to treat atopic dermatitis or rosacea, or even dandruff.

Today research on the axillary bacterial community and deodorants is still pursued, taking benefit of new technologies and regularly leading to better knowledge of the biochemical processes to malodors formation.

On this point, microbiota transplant that is operated from a healthy individual into a recipient to treat gastrointestinal diseases has inspired a much more disruptive approach to fight against armpit malodors.

Indeed its inventor, Chris Callewaert, experienced a successful, though of non-lasting effect, transplant of the skin microbiome from a ‘non-smelly’ donor to a ‘smelly’ acceptor, hence eradicating malodors. Still working on improving his approach, Chris Callewaert has since created "DrArmpit", a science communication platform where scientific research about armpit microbiology in relation to body odor is made available to the public.

Deep knowledge on gut microbiota functioning and in particular its beneficial modulation upon probiotics or prebiotics ingredients supply has served the cosmetic industry. Several products are available on the market, and the logic is simple: microorganisms that are good for our gut cannot be bad for our skin.

**Probiotics** are living microorganisms that are supplied to the gut (via ingestion) to rebalance an altered microbiome and modify its equilibrium towards a more healthy one. These are the classical *Bifidobacterium* or *Lactobacillus* we can find in yoghurt, for instance. Prebiotics, meanwhile, are food ingredients that promote the growth of beneficial microorganisms in the intestines.

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35 Community differentiation of the cutaneous microbiota in psoriasis. Av Alekseyenko et al., Microbiome 2013, 1:31
36 Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. A Tett et al., npj Biofilms and Microbiomes 2017, 3:14
38 Microbial flora and odor of the healthy human skin. HC Korting, Hautarzt. 1988, 39, 564-568
39 Mapping axillary microbiota responsible for body odours using a culture-independent approach. M Troccaz et al., Microbiome 2015, 3:3
40 Axillary odor; experimental study of the role of bacteria, apocrine sweat, and deodorants. WB Shelley et al., AMA Arch Derm Syphilol. 1953, 68, 430-446
41 The bacteria responsible for apocrine odor. AM Kligman and JS Strauss, J Invest Dermatol. 1956, 27, 67-71
44 Control of free fatty acids in human surface lipids by Corynebacterium acnes. RR Marples et al., J Invest Dermatol. 1971, 56, 127-131
46 Role of microorganisms in dandruff. JJ Leyden et al., Arch Dermatol. 1976, 112, 333-338
47 Deodorants and antiperspirants affect the axillary bacterial community. C Callewaert et al., Arch Dermatol Res. 2014, 306, 701-710
48 Towards a bacterial treatment for armpit malodour. C Callewaert et al., Experimental Dermatology. 2017, 26, 388-391
Probiotics and prebiotics can provide beneficial effects to the skin as these are targeted to favor those cutaneous microbial species which are believed to be ‘good’ for our skin. In both cases, the intention is to balance skin microbiota to enhance it.

However, since probiotics are living bacteria, there are quite a few hurdles before integrating them into our skin microbiome. Maintaining their integrity and survival in the cosmetic formulation is the first one, while the second is their lifetime and impact into the cutaneous microbiota itself, as gut and skin ecosystems are highly different. Thus, ‘probiotics’-containing beauty products are generally actually prebiotics, composed either of probiotics lysates or of ferment extracts.

In that field, communication to the consumers is key, and comes with their education. In fact, skin microbiome communication is booming in beauty magazines and professional press over the last two years, and blogs are flourishing talking about those little microbes that are best allies for our beauty.

For instance Elle Magazine, in 2015, named the probiotics as the “bacteria which makes us beautiful”. One year after, Vogue claimed probiotics an “invisible anti-aging shield”, which “by strengthening the skin microflora, also inhibits the ageing signs in formation”, and was followed by StyleCaster. While Fashionista encouraged to “start working probiotics into skincare routine”. In 2017, Elle Magazine, Madame Figaro, Shape and Vanity Fair all talked about probiotics and/or skin microbiome as being the new, unavoidable, solution for beauty. The Atlantic, The New York Times, Vanity Fair, and very recently Forbes, also dedicated at least an article on the subject.

As a summary, new cosmetic claims appear that are based on these microbiome ingredients, related to Age-Defying, New-Age, Healthy Hands, Detox Gentle, Rebalancing Masks, Probiotic or Biome-friendly.

4. Leading the way in skin microbiomics

Skin microbiome is, without contest, a full player in our beauty and well-being. But how do we assess it, how do we evaluate the impact of a cosmetic ingredient or end-product on the Stratum microbium™, and how do we demonstrate that its population is well balanced?

As we have seen it previously, most of the microbes living on our skin cannot be isolated and characterized under lab conditions, and therefore one has to target the entire genes set of the Stratum microbium™ to get the most of it. However, as genes from one species cannot be separated from the ones of its neighbour, a global approach called metagenomics was developed in the late 90s.

Metagenomics is a very powerful tool, but with a lot of potential pitfalls in study design, microbial DNA extraction and preparation, or sequences analysis for instance. As a “multi(tricky)step” procedure, precision, care and rigor are obligatory.

Metagenomics can be conducted via 2 different pathways, depending on your needs to be descriptive only (taxonomic profiling down to the genus, done from 16S ribosomal RNA analysis), or your wish to assess the functional potential and a detailed composition of your microbiome (done using whole genome sequencing techniques).

The different steps of such a taxonomic profiling study (the simplest of both approaches) have been nicely described by Heidi Kong and co-

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51 30 millions d’amies (au cm²). Vanity Fair Oct 20, 2017
52 Why Probiotic Beauty Products Are Great For Your Skin. C Shatzman, Forbes Jan 8, 2018
As a conclusion, typical taxonomic profiles (on the basis of microbiome taxonomic profiles (on the basis of microorganisms relative abundances), is nevertheless limited to bacteria. Thus, no information on other members of the microbiome – such as yeasts or fungi for instance – will be gathered, and relative abundances will be calculated only on the basis of bacterial families. In addition, 16S sequencing suffers from two constraints: the first is its lack of phylogenetic precision (taxonomic profiles can only be significantly estimated at the genus level minimum), and the second is its dependence to the variable region of the 16S rRNA gene that is used. Consequently, microbiota data have to be compared, from one study to the other, only if the procedure has been the same. Finally, PCR amplification of microbial DNA (to obtain enough material for sequencing) is often subject to bias from the choice of the primers.

As a conclusion, typical taxonomic profiles (bacterial genera relative abundance) that can be obtained are shown in the following figure (unpublished results).

While 16S sequencing provides a good estimate of who is there, the resulting data does not inform about any functional potential. To obtain such an information, and in addition to get an exhaustive (bacteria, fungi, yeasts...) description of the microbiota population down to the species (and sometimes the strains), one has to move towards whole genome sequencing (WGS), also called "shotgun sequencing".

In WGS sequencing all the pieces of DNA within a sample are cut up into small pieces, and all gene fragments are sequenced without any further selection or treatment. Once sequences data have been collected, computer analysis allows recreating the entire genome of all the organisms present in a sample. Gene fragments sequences are usually compared and assigned by alignment with databases of genetic information, and phylogenetic affiliation is compiled, including for unknown species. Finally, as all DNA information is decoded (and not only a fragment of the 16S gene), enzymes present in these microorganisms are identified at the same time, revealing the functional potential of the microbiota.

XC Morgan and C Huttenhower, in particular, have compared the two metagenomic approaches, and designed the following comparative process scheme.55

At Givaudan Active Beauty we master both techniques equally, with a particular know-how on cutaneous microbiota sample col-

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54 Performing skin microbiome research: A method to the madness. HH Kong et al., J Invest Dermatol. 2017, 137, 561-568

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As experts of skin microbiomics, we are dedicated to the development of new cosmetic ingredients linked with the Stratum microbium™. This exclusive knowledge enables us to understand cosmetic ingredients’ effect on skin microbiota, to design new ingredients acting directly on skin microbiota, and ultimately, to link skin microbiota composition to beauty.

As seen before, the overwhelming majority of products available on the market in this category are made of prebiotics, with a few of them containing probiotics. At Givaudan Active Beauty we also offer 2 products in that frame, in an approach that we name Balance to Enhance.

And to this skin microbiota leveraging range, we add 2 unique consumers’ driven approaches, which we call Protect to Care and Trigger to Activate.

The first concept is based on four observations: (i) our skin microbiota is beneficial for our beauty and well-being when it is well balanced, with a high microbial diversity; (ii) with the absence of any skin disorder, our current Stratum microbium™ represents our own healthy microbiome; (iii) applying any personal care products on our skin, including a prebiotic formula, could lead to a disturbance of our microbiome; and (iv) we are all unique.

Thus, a new ingredient, called Revivyl™ and developed for skin renewal activation, was shown to counteract the microbiome disturbance induced by the cosmetic base itself. In a way to Care of ourselves, Revivyl™ Protects our skin microbiome from external disturbance. This protection effect was demonstrated via a comparative 16S sequencing study, performed on the forearms of a panel of 19 women volunteers. After 2 weeks of treatment, Revivyl™ was shown to maintain the initial balance of the cutaneous microbial population, while a significant imbalance was observed by using the cosmetic vehicle only (see figure).

Protection of the skin microbiota balance using Revivyl™ (in this case, protects skin microflora equilibrium from an imbalance in Firmicutes provoked by the cosmetic base without Revivyl™)

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56 Life on Human Surfaces: Skin Metagenomics. A Mathieu et al., PLoS ONE 2013, 8, e65288
57 The future of skin metagenomics. A Mathieu et al., Research in Microbiology 2014, 165, 69e76
As a second unique alternative approach for skin microbiota leveraging products, we developed a strategy to Trigger the skin microbiome intrinsic capabilities to Activate ingredients and release their benefits. This is a precursor approach, in which the precursor, stable but inactive, is transformed by specific enzymes present in the cutaneous microbial community into an active ingredient, as illustrated in the following scheme.

In the case of our Brightenyl™ ingredient, launched in 2015 for skin brightening, redness decrease and pore size reduction applications, the required enzymes are alpha-glucosidases. Their presence was demonstrated by 2 parallel studies: a first incubation of Brightenyl™ with skin microbiota samples collected from the cheeks, forehead, nose, and forearms of 9 volunteers, and monitoring of precursor and active compounds using HPLC analysis. This showed the biological transformation of the inactive precursor into the desired active compound. And a second study done using Whole Genome Sequencing of DNA extracted from forehead microbiota samples collected on 2 volunteers, and which demonstrated the presence of several alpha-glucosidase genes to common bacterial species found on human skin (see table below for the most representative species).

With a similar approach based on the needs for enzymatic (esterolytic) activation of an inactive precursor, Questice® completes our range of Trigger to Activate approach ingredients.

With currently almost 1 trillion of microbiome data and solid expertise and know-how, we master the whole research process for microbiomics, from the swabbing to the DNA extraction and sequencing until the bioinformatics data analysis. Givaudan Active Beauty continues to develop active cosmetic ingredients, designed to activate, protect or balance the skin microbiota. Indeed, as we are all unique, future ingredients and end-products shall adapt to the uniqueness of their consumers and their microbial ecosystem.

In particular, future ingredients shall be designed to counteract aging physiological changes, which also impact skin microbial diversity. Recent studies showed, for example, a shift in skin microbiome composition correlated with chronological and physiological skin aging factors. Differences in aging skin microbiome are also observed between men and women, with variability depending upon the body area.

### Table: Bacterial Identification

<table>
<thead>
<tr>
<th>Bacterial Identification</th>
<th>Occurrence</th>
<th>Identity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Propionibacterium acnes</td>
<td>28</td>
<td>75-100%</td>
</tr>
<tr>
<td>Staphylococcus epidermidis</td>
<td>17</td>
<td>99-100%</td>
</tr>
<tr>
<td>Staphylococcus hominis</td>
<td>15</td>
<td>95-100%</td>
</tr>
<tr>
<td>Staphylococcus capitis</td>
<td>9</td>
<td>98-100%</td>
</tr>
<tr>
<td>Staphylococcus sp. AL1</td>
<td>8</td>
<td>99%</td>
</tr>
<tr>
<td>Staphylococcus warneri</td>
<td>8</td>
<td>99%</td>
</tr>
<tr>
<td>Staphylococcus haemolyticus</td>
<td>7</td>
<td>99-97%</td>
</tr>
<tr>
<td>Propionibacterium sp. HGH0353</td>
<td>6</td>
<td>97-99%</td>
</tr>
<tr>
<td>Propionibacterium acnes (HL103PA1)</td>
<td>5</td>
<td>75-100%</td>
</tr>
<tr>
<td>Propionibacterium acnes (JCM 18910)</td>
<td>5</td>
<td>99-100%</td>
</tr>
<tr>
<td>Propionibacterium sp. KPL2008</td>
<td>5</td>
<td>69-100%</td>
</tr>
<tr>
<td>Macroccoccus caseolyticus</td>
<td>4</td>
<td>75-99%</td>
</tr>
<tr>
<td>Micrococcus luteus</td>
<td>4</td>
<td>70-99%</td>
</tr>
<tr>
<td>Propionibacterium granulosum</td>
<td>4</td>
<td>85-96%</td>
</tr>
<tr>
<td>Dermacoccus sp. Elim185</td>
<td>3</td>
<td>93-95%</td>
</tr>
</tbody>
</table>

58 Aging-related changes in the diversity of women’s skin microbiomes associated with oral bacteria. N Shibagaki et al., Scientific Reports 2017, 7:105567
59 The microbiota and microbiome in aging: potential implications in health and age-related diseases. HJ Zapata and VJ Quagliarello, J Am Geriatr Soc. 2015, 63, 776-781
Looking more closely at certain species such as Archaea, Christine Moissl-Eichinger et al. revealed that archaea are more abundant in human subjects either older than 60 years or younger than 12 years as compared to middle-aged human subjects. This could open up the way to developing new anti-aging products based on archaeal signatures.

Finally, a very recent press release (Nov 30, 2017) revealed the discovery, by Amway in collaboration with Microbiome Insights, of two Corynebacteria species - one associated with younger people and the other with older people. The ‘old skin’ Corynebacteria species tend to displace the other during middle age (40-49). Interestingly, the two bacteria were found to be co-exclusive meaning they did not exist simultaneously at the same skin site. And furthermore, in addition to being associated with chronological age, the ‘old skin’ Corynebacterium was found to be associated with skin redness, wrinkles and age spots, suggesting it could be a target for treatment intervention.

Active Beauty
Givaudan Active Beauty Sales offices

Europe
Givaudan France SAS
17-23 rue de la Voie des Bans
FR-95100 Argenteuil (France)

Givaudan UK Ltd
Magna House
76-80 Church Street
Staines, TW18 4XR (United Kingdom)

North America
Givaudan Fragrances Corp.
40 W - 57th Street - Floor 17
NY 10019 - New York (United States)

Asia Pacific
Givaudan Singapore Pte Ltd
1 Pioneer Turn
627576 Singapore (Singapore)

Givaudan Shanghai Ltd
298 Li Shi Zhen Road
Pudong Zhang Jiang High Tech Park
201203 Shanghai (China)

Latin America
Givaudan do Brasil Ltda
Av. Engº Billings - 2185, Edificio 31, 1ºAndar - Jaguaré
05321-010 São Paulo - SP (Brazil)

global.cosmetic@givaudan.com

Active Beauty
Givaudan France SAS

Denis Wahler, Ph.D.
Global Manager Technology Partnerships
denis.wahler@givaudan.com
+33 761 088 944

60 Human age and skin physiology shape diversity and abundance of Archaea on skin. C Moissl-Eichinger et al., Scientific Reports 2017, 7:4039