INVITED REVIEW



Exploring the impact of solar radiation on skin microbiome to develop improved photoprotection strategies

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Abstract

The skin microbiome undergoes constant exposure to solar radiation (SR), with its effects on health well-documented. However, understanding SR's influence on host-associated skin commensals remains nascent. This review surveys existing knowledge on SR's impact on the skin microbiome and proposes innovative sun protection methods that safeguard both skin integrity and microbiome balance. A team of skin photodamage specialists conducted a comprehensive review of 122 articles sourced from PubMed and Research Gateway. Key terms included skin microbiome, photoprotection, photodamage, skin cancer, ultraviolet radiation, solar radiation, skin commensals, skin protection, and pre/probiotics. Experts offered insights into novel sun protection products designed not only to shield the skin but also to mitigate SR's effects on the skin microbiome. Existing literature on SR's influence on the skin microbiome is limited. SR exposure can alter microbiome composition, potentially leading to dysbiosis, compromised skin barrier function, and immune system activation. Current sun protection methods generally overlook microbiome considerations. Tailored sun protection products that prioritize both skin and microbiome health may offer enhanced defense against SR-induced skin conditions. By safeguarding both skin and microbiota, these specialized products could mitigate dysbiosis risks associated with SR exposure, bolstering skin defense mechanisms and reducing the likelihood of SR-mediated skin issues.

K E Y W O R D S

exposome, photoprotection, skin microbiome, solar radiation, ultraviolet radiation

Abbreviations: 6-HAP, 6-N-hydroxyaminopurine; AK, actinic keratosis; AMP, antimicrobial peptides; IL-6, interleukin 6; MAPK, mitogen-activated protein kinase; MED, minimal erythema dose; MMP, matrix metalloproteinase; NF-κB, nuclear factor kappa-light-chain-enhancer of activated B cells; PAMP/DAMP, pathogen/damage-associated molecular pattern; PLE, polymorphic light eruption; ROS, reactive oxygen species; SC, skin cancer; SCC, squamous cell carcinoma; SR, solar radiation; ssUV, solar-simulated UV; TEWL, transepidermal water loss; TGF-β, transforming growth factor beta; UV, ultraviolet; UVA, ultraviolet A; UVB, ultraviolet B; UVR, ultraviolet radiation; XO, Xanthine oxidase.

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INTRODUCTION

The skin provides a physical, chemical, and immunological protective barrier between the body and the environment.^{1,2} It hosts a community of a multitude of commensal microbes named the microbiota which is the collection of all genetic material of all its members.^{3,4} The microbiota forms together with the skin the microbiome is the first shield of the human body against external aggression and pathogens.^{5,6} The skin microbiome permanently coevolves and a healthy microbiota helps keep the host's health balanced by participating in the host's defense against exposome factors during his entire life.^{7–11}

The exposome comprises all external and internal factors to which the body is exposed, including solar radiation (SR), chemicals, pollutants, tobacco smoke as well as lifestyle factors, dietary habits, and infectious agents that a body encounters throughout its lifetime, from conception to death and that impact on its health.^{12–17}

A disturbed microbiome may be caused by exposome factors that include medication such as antibiotics, antiseptics, diet, skincare routines, exercise, pollution, and climate parameters as well as SR may result in dysbiosis or an unbalancing of the skin homeostasis.^{8,18–23} As a result of dysbiosis, inflammatory skin conditions and, potentially, skin cancer (SC) including melanoma may be observed.^{22,24–27} Moreover, exposome factors, are involved in skin photoaging, hyperpigmentary skin disorders, and other photodermatoses, especially in exposed areas of the skin.^{28–33}

The commensal microbes differ greatly by site, and the skin microbiome is regularly exposed to SR.³⁴ While both the positive and negative impact of SR on our health are well defined and understood, the understanding of the role of SR on the microbial dynamics of host-associated commensals of the skin microbiome is still in its infancy.³⁵

Currently recommended means to protect from excessive SR include adequate clothing, wearing a hat, and using sunscreens with high sun protection factors as well as avoiding prolonged exposure during midday.^{36–39}

Sunscreens have been marketed for decades to primarily protect the skin against SR-induced erythema that is mostly due to UVB exposure. Today, most broad-spectrum sunscreens provide protection against ultraviolet B (UVB) radiation and ultraviolet A (UVA) radiation. But visible and infrared light are also impacting the skin, especially in skin photoaging and hyperpigmentation.^{40,41} The present review provides an overview of what is known about the impact of SR on the skin microbiome and a perspective on innovative sun-protecting products that not only protect the skin but are also able to limit the negative impact of SR on the skin microbiome.

MATERIALS AND METHODS

A group of 10 dermatologists, scientists, and researchers specialized in skin photodamage and photoprotection reviewed 122 publications about the impact of SR, and the skin microbiome published between 1987 and 2023 and available from the PubMed and Research Gate databases.

Keywords alone or combined with each other included skin microbiome, photoprotection, photodamage, skin cancer, ultraviolet radiation (UVR), infrared light, visible light, solar radiation, skin commensals, skin protection, and pre- and probiotics During the second step, the experts discussed the potential of innovative sun protection and future strategies that may be able to leverage the skin microbiome to protect against the deleterious effects of SR.

RESULTS

While a rich literature is available about the impact of SR on the skin and the role of sunscreens to protect the body from SR, only little information is available about the potential impact of SR on the human skin microbiome, its consequences on the host's skin health and about novel approaches to protect the skin from SR exposome damage.³⁵

Solar radiation, skin microbiome, and immunity

UVR may directly or indirectly impact the skin microbiome.^{42,43} Shifts in the skin microbiome composition with bacteria responding differently, especially to ultraviolet A (UVA) and ultraviolet B (UVB) have been observed.^{35,44,45} Figure 1 shows how sun exposure affects the diversity and composition of the skin microbiota and how sunscreens help to maintain healthy skin and its microbiome.

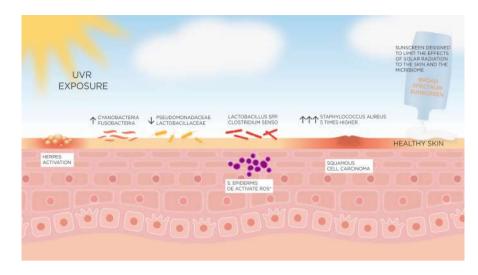


FIGURE 1 Sun exposure affects the diversity and composition of the skin microbiota. Following UVR exposure occurs an increase in *Cyanobacteria* spp., *Fusobacteria* spp, and decreased *Lactobacillaceae* spp. and *Pseudomonadaceae* spp. *Lactobacillus* spp., and *Clostridium* sensu were the most discriminately higher genera in the healthy skin microbiome. *Staphylococcus epidermidis* was shown to be able to generate electrons which deactivate ROS which otherwise cause cellular damage. Increase of Staphylococcus aureus in squamous cell carcinoma and in actinic keratosis.

A study compared two groups of healthy volunteers exposed to SR. One group, exposed to the sun in the summer, was compared with a group wearing clothes throughout the year including the summer period. The study compared the seasonal effects on the skin microbiome before and after summer. Three skin sites were sampled: the inner forearm, dorsal forearm, and cheek. No significant differences in the diversity of the microbiome were observed and no significant seasonal differences in high-abundance species at any of the sampling sites were observed, in any group. These findings suggest a certain stability of the skin microbiome, even after several months of exposure to SR. However, significant differences were observed in lowabundance species in the unprotected areas of the inner and outer arms in the group exposed to SR during the summer months. These changes in low-abundance species are of interest requiring further research.48

Willmott et al.⁴⁷ observed in a study published in 2023 a significant change in the microbial beta diversity after 4weeks of extensive exposure to sunlight at the forearm of the subjects compared to baseline suggesting that sun exposure affects the diversity and composition of the skin microbiota. Moreover, the overall composition of the skin microbiome may be long-term altered following UVA and UVB radiation at the back of the volunteers.⁴⁴ A general increase in *Cyanobacteria* spp., *Fusobacteria* spp., *Verrucomicrobia* spp., and *Oxalobacteraceae* spp., was observed. Conversely, *Lactobacillaceae* spp. and *Pseudomonadaceae* spp. decreased following UVR exposure. The latter decreased to a greater extent following UVA exposure.

In parallel, several species developed mechanisms to resist against this aggressor. These defense mechanisms are not only the result of selective pressure but also of the potential of UVR to damage DNA, increasing the mutational rate of microbes.⁴⁹ As a result, microbial species exhibit a vast array of natural adaptations to protect against UVR.^{50,51} For example, *Staphylococcus epidermidis* generated electrons deactivating ROS which otherwise cause cellular damage.⁵² *Micrococcus luteus* which uses carotenoid pigments and a high endonuclease activity limited the bactericidal effects of UVR.^{53,54}

The process of the alteration of the skin microbiota by UVR is not completely elucidated. The skin microbiota may be altered by microbial photoproducts including pyrimidine dimers and/or 6–4 photoproducts produced after UVR exposure. UVR may trigger a pathogen/damage-associated molecular pattern (PAMP/DAMP) response resulting in various microbial signals comprising oleic acid, LPS and/or porphyrins.^{55–58} The latter affect the overall immune signaling cascade, leading to inflammation, and an altered immune response.

Moreover, an increased production of natural antimicrobial peptides (AMP) by microbes or AMP produced by keratinocytes and controlled by microbes under exposure UVR may contribute to an altered immune response and a change of the microbial load by affecting the microenvironment. Under UVR stress conditions, the microbiome may trigger interleukin-1 and together with directly induced microbial signals, influence skin immunity by the release of various cytokines such as that of Th17 pathway. As a result, the keratinocyte effector function may be influenced through the production of interleukin-17, resulting in an altered AMP production affecting the microbiome.⁴² With UVR being able to suppress the body's immune response to infectious microorganisms, it may also be able to increase the risk of microbial infections or worsen existing infections due to UVR-caused dysbiosis and altered skin homeostasis. However, clinical evidence is still very low.⁵⁹

Table 1 provides an overview of data generated about the impact of solar radiation on the healthy skin microbiome.

Solar radiation and modulation of the skin microbiome response

Due to its capacity to adapt, to a certain extent, to exposome factors, the skin microbiota is able, to protect itself and its host against external aggression.

The release of protease enzymes by commensal microbes is involved in desquamation, renewal of the *stratum corneum*, biofilm, and bacteriocins production, as well as quorum sensing while sebum and free fatty acid production by the host participate in the regulation of the skin pH.^{6,60–62} Moreover, the release of lipase enzymes helps in the lipidic film surface breakdown process and urease enzymes participate in urea degradation. Commensal microbes also compete for nutrients and space and thus limit the invasion and reproduction of non-commensal potentially detrimental microbes through the release of antimicrobial peptides (AMPs).^{6,63}

A transcriptomic analysis in a mouse model revealed a different gene regulation in the presence or absence of the microbiota after UV exposure.⁴³ In the absence of the skin microbiota, UV exposure led to an increased release of pro-inflammatory cytokines such as IL-1b, IL-6, and IL-18rap. Conversely, in the presence of the microbiota, immunosuppressive cytokines such as IL-10, IL-10ra, IL-20rb, and IL-7r were more prevalent. These results confirm that microbes or microbial products have immunoregulatory effects and may participate in the protection against UV-induced skin neoplasia and modulate gene expression in the skin. Moreover, they may be able to influence the epidermal development and differentiation and wound healing.^{1,51,60,64–66} In addition, certain skin-resident microbes and microbial products are capable to regulate AMP expression induced by UVR, potentially through the production of pro-inflammatory cytokines.^{67,68}

UVR, microbiome dysbiosis, and skin cancer

Currently, evidence that UVR may cause skin cancer due to skin microbiome dysbiosis is low.^{44,69}

Nakatsuji et al.⁵¹ suggested that a specific strain of *S. epidermidis* that produces 6-N-hydroxyaminopurine (6-HAP) protects in a mouse model of photocarcinogenesis against the development of keratinocyte carcinomas. Additionally, the authors demonstrate that Intravenous injection of 6-HAP in mice suppressed the growth of B16F10 melanoma cells without evidence of systemic toxicity. This molecule inhibited DNA polymerase activity and the proliferation of tumor lines but not that of normal keratinocytes.

An animal study published in 2022 revealed a close link between melanoma progression and dysbiosis of the skin microbiome.²⁷ A significant difference in microbiome diversity and richness between melanoma tissue and healthy skin was observed. *Lactobacillus* spp., *Clostridium* sensu stricto 1, and *Corynebacterium* 1 were the most discriminately higher genera in the healthy skin microbiome, while *Fusobacterium* spp., *Trueperella* spp., *Staphylococcus* spp., *Streptococcus* spp., *and Bacteroides* spp. were discriminately abundant in the skin microbiome of melanoma lesions.

Kullander et al.⁷⁰ reported that *Staphylococcus aureus* (*S. aureus*) and squamous cell carcinoma (SCC) were associated with an almost five times higher colonization rate with *S. aureus* in SCC lesions than in healthy skin. However, the authors also stated that the study design did not allow to determine whether the association implies that *S. aureus* may influence carcinogenesis or if SCC has an increased susceptibility to *S. aureus*. But, with AK lesions being considered precursors of SCC, an increased colonization of *S. aureus* in AK may indicate a carcinogenic process from AK to SCC.^{70–72}

Skin microbiome and photoprotection

Today, there is large evidence of acute and chronic skin alteration caused by SR and especially by UVR and the benefits that sunscreens offer to reduce and prevent such damages.⁷³ However, information still mostly focuses on the protection of the skin as an organ, and data about the protective effect of sunscreens that contain prebiotics or probiotics that also protect the microbiota are sparse.^{74,75}

Probiotics and Postbiotics are recognized to help in maintaining human health in supporting disease prevention and management and, in the future, may potentially play a beneficial role in photoprotection.^{74,76–80} Table 2 provides a summary of all studies that assessed the benefit of pro and postbiotics as photoprotective ingredients.

UVR and the use of sun protective measures were reported to impact the relative bacterial abundances of the skin microbiome.¹⁰⁴ The proximity of *Micrococcus luteus* to *Corynebacterium* spp., *Streptococcus* spp., and *Staphylococcus* spp. in the observed interaction network associated with sunscreen was hypothesized to be an example of how *Micrococcus luteus* may be able to influence

	Reference	Burns et al. ⁴⁴	Burns et al. ⁴⁴	Schuetz et al. ⁴⁶	Willmott et al. ⁴⁷	Harel et al. ⁴⁸	Harel et al. ⁴⁸
	Impact of SR	Phylum level increase in <i>Cyanobacteria</i> , 1 <i>Fusobacteria</i> and <i>Verrucomicrobia</i> Family level decreases in <i>Lactobacillaceae</i> and <i>Pseudomonadaceae</i> Family level increase in <i>Oxalobacteraceae</i>	Phylum level increase in <i>Cyanobacteria</i> , 1 <i>Fusobacteria</i> and <i>Verrucomicrobia</i> Family level decreases in <i>Lactobacillaceae</i> and <i>Pseudomonadaceae</i> Family level increase in <i>Oxalobacteraceae</i> .	UV exposure led to higher abundance of <i>Cutibacterium</i> compared to <i>Lactobacillus</i> Application of SPF20 sunscreen prevented this relative change Placebo had no effect	Reduction of <i>Proteobacteria</i> at 28 days post-holiday in subjects that actively sought sun No differences by D28 and D84 post-holiday	Microbiomes of both groups generally lisimilar similar Significant differences in microbial composition between lifeguards and ultraorthodox detected in sun exposed sites (cheek, outer and inner arms) No significant seasonal difference in the microbiome within the ultraorthodox group	Increase in the abundance of Sphingomonas and Erythrobacteraceae after the summer
	Analysis method	16S rRNA sequencing	16S rRNA sequencing	16S rRNA sequencing	16S rRNA sequencing	16S rRNA sequencing	16S rRNA sequencing
	Collection method	Swabbing	Swabbing	Swabbing	Swabbing	Swabbing	Swabbing
	Subjects	Male (n=6) Fitzpatrick phototype I/II	Male (n=6) Fitzpatrick skin types I-II	Female (n = 10) Fitzpatričk skin type II–III Aged 20–45 years	Male $(n = 4)$ Female (n = 17) Healthy, white Northern European Mean age \pm SD: 33.6 \pm 6.4 years	Male	Lifeguards $(n = 10)$
•	Study design	Varying doses of UVB applied to the back Swab samples acquired prior to, immediately after, and 24h after UV exposure	Varying doses of UVB applied to the back Swab samples taken prior to, immediately after, and 24h after UV exposure.	Single-blind clinical trial SFF 20 sunscreen and placebo applied to two test areas on the back of prior to UV irradiation Treated and untreated zones exposed to 2 MED of UVA/UVB Skin surface swabs collected 2h after UV exposure	Skin swabs taken from extensor forearm prior to (d0) taking a holiday in a sunny destination (minimum of 7 days duration) Swabbing repeated upon return at d1, d28 and d84	Two groups: (1) Lifeguards, exposed yearly to direct sunlight and seawater throughout summer; (2) Ultraorthodox and always protected from direct sunlight Three skin sites were sampled: the inner forearm, dorsal forearm, and cheek.	Lifeguards exposed to SR throughout the summer Swabs collected at the beginning (May) and end (September) of summer
5	Dose	100, 150, 200, 250, 300, and 350 mJ/ cm ²	22, 27, 33, 39, and 47J/ cm ²	2 MED	Q	QN	QN
-	Wavelength	308 nm	340-400 nm	QN	Ϋ́Α	AN	AA
	Waveband	UVB	UVAI	Solar-simulated radiation (UVA/UVB)	Natural sunlight	Natural sunlight	Natural sunlight

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TABLE 2 Pro- and postbiotics for photoprotection—An overview of all studies performed with pro- or postbiotics.

Route of administration	Probiotic/Postbiotic	Species	Model	Stress	Photoprotective effects	References
Topical	6-N-hydroxyaminopurine-producing Staphylococcus epidermidis	Staphylococcus epidermidis	SKH-1 mouse	UVB	Suppresses UVB-induced tumor formation.	Nakatsuji et al. ⁵¹
Topical	Fermentable metabolite of Zymomonas mobilis	Zymomonas mobilis	SKH-1 hairless mouse	UVB	Restores TGF-β signaling Restores Procollagen I expression Reduces wrinkle formation	Tanaka et al. ⁸¹
Topical	Limosilactobacillus fermentum XJC60 Limosilactobacillus fermentum	Limosilactobacillus fermentum	Guinea pig	UVB	Prevents skin damage Reduces abnormal keratinization, hyperplasia, and edema Reduces MMP-1 expression Reduces inflammatory cell infiltration	Chen et al. ⁸²
Topical	Staphylococcus epidermidis (+ glycerol)	Staphylococcus epidermidis	ICR mouse	UVB	Reduces erythema and ulceration Reduces IL-6 levels Reduces hyperplasia	Keshari et al. ⁸³
Topical	Staphylococcus epidermidis ATCC 12228	Staphylococcus epidermidis	ICR mice	UVB	Reduces lipid peroxidation Reduces DNA damage	Balasubramaniam et al. ⁸⁴
Topical	Yeast	Saccharomyces cerevisiae	BALB/c mice	UVB	Reduces skin damage Reduces inflammatory cell infiltration	Lu et al. ⁸⁵
Topical	Lactobacillus reuteri DSM 17938	Lactobacillus reuteri	Reconstructed Human Epidermis (EpiDerm TM ; EPI-200, Mattek)	UVB	Reduces inflammatory cytokine production	Khmaladze et al. [%]
Topical	Lactobacillus reuteri DSM 17938 İysate	Lactobacillus reuteri	Ex vivo human skin explant Reconstructed Human Epidermis (EpiDerm ^{TN} ; EPI-200, Mattek)	UVB UVB	Reduced inflammatory cytokine production Reduces inflammatory cytokine production	Khmaladze et al. <mark>%</mark> Khmaladze et al. <mark>%</mark>
Topical	Vitreoscilla filiformis extract	Vitreoscilla filiformis	Clinical study on back skin (Placebo-controlled; <i>n</i> =5)	UVB	Reduces sunburn cell formation	Mahé et al. ⁸⁷
Oral	Bifidobacterium breve	Bifidobacterium breve	Hos:HR-1 hairless mice	UVB	Reduces erythema Reduces edema Reduces skin thickening Increases skin elasticity Reduces elastase expression Reduces inflammatory cytokine expression	Sugimoto et al. ⁸⁸
			Hos:HR-1 hairless mice	UVB	Reduces TEWL Increased hydration levels Reduces lipid and protein oxidation Reduces XO activity	Ishii et al. ⁸⁹
			Hos:HR-1 hairless mice	UVB	Reduces wrinkle formation Reduces erythema Reduces TEWL Increases lyudration levels	Satoh et al. ⁹⁰
					Reduces skin thickening Reduces histological damage Reduces inflammatory cytokine production	

Route of administration	Probiotic/Postbiotic	Species	Model	Stress	Photoprotective effects	References
Oral	Bifidobacterium animalis subs. lactis MG741	Bifidobacterium animalis	HR-1 hairless mice	UVB	Reduces wrinkle formation Reduces epidermal thickening Increases hydration Reduces TEWL Reduces MMP-3 expression Inhibits MAPK signaling Reduces inflammatory cytokine expression	Lee et al. ⁹¹
Oral	Bifidobacterium longum	Bifidobacterium longum	SKH-1 hairless mice SKH-1 hairless mice	UVB UVB	Reduces TEWL Reduces erythema Reduces wrinkle formation Increases hydration Reduces wrinkle formation Reduces epidermal thickening Increases antioxidant enzyme levels Increases Type I collagen expression Reduces inflammatory cytokine expression Reduces MMP expression	Hong et al. ⁹² Kim et al. ⁹³
Oral	Bifidobacterium longum + Galactooligosaccharide	Bifidobacterium longum	SKH-1 hairless mice SKH-1 hairless mice	UVB UVB	Infinitions MATA and NN-KB signating Reduces TEWL Reduces erythema Increases hydration Reduces wrinkle formation Reduces epidermal thickening Increases antioxidant enzyme levels Increases Type I collagen expression Reduces inflammatory cytokine expression Reduces MMP expression Inhibits MAPK and NF-kB signaling	Hong et al. ⁹² Kim et al. ⁹³
Oral	Lactobacillus acidophilus	Lactobacillus acidophilus	HR-1 hairless mice Hos:HR-1 hairless mice	UVB UVB	Reduces TEWL Reduces epidermal thickening Inhibits MAPF expression Inhibits MAPK signaling Reduces skin thickening Increases scalagen levels Increases skin hydration Reduces TEWL Inhibits MMP expression Increases antioxidant enzyme expression Inhibits inflammatory cytokine production Inhibits MAPK signaling	Im et al. ⁹⁴ Im et al. ⁵⁵
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Oral	Lactobacillus johnsonii La1	Lactobacillus johnsonii	Skh:hr1 mice	SSUV	Reduces edema Prevents UV-induced immunosuppression	Guéniche et al. ⁹⁶
Oral	Lipoteic acid from Lactobacillus mamnosus GG		Crl:SKH-1-hrBR hairless mice C57/BL6 mice C1:SKH-1-hrBR hairless mice	UVB+UVA UVB UVB	Reduces epidermal thickening Prevents apoptosis Reduces inflammatory cell infiltration Prevents immunosuppression Delays tumor formation Prevents UV-induced immunosuppression Reduces tumor growth	Weill et al. ⁹⁷ Friedrich et al. ⁹⁸ Friedrich et al. ⁹⁸
Oral	Lactobacillus plantarum HY7714	Lactobacillus plantarum	Hairless mice	UVB	Reduces epidermal thickening Reduces TEWL Increases hydration Increases ceramide levels	Ra et al. ⁹⁹
Oral	Lactobacillus johnsonii La1	Lactobacillus johnsonii	Clinical study on back skin (RCT; $n = 54$) Clinical study ($n = 60$ with Polymorphic Light Eruption) (skin area n/a)	ssUV UVA1	Prevents UV-induced immunosuppression Reduces PLE scores	Peguet-Navarro et al. ¹⁰⁰ Marini et al. ¹⁰¹
Oral	Lactobacillus johnsonii La1 + Carotenoids	Lactobacillus johnsonii	Clinical study $(n = 16)$ (skin area: buttocks)	NUss	Prevents UV-induced decrease in Langerhans cells Reduces melanin content	Bouilly-Gauthier et al. ¹⁰²
Oral	Lactobacillus johnsonii La1 + Carotenoids	Lactobacillus johnsonii	Clinical study (RCT; $n = 43$) (skin area: upper back)	ssUV	Increases MED Reduces ΔE^*	Bouilly-Gauthier et al. ¹⁰²
Oral	Lactobacillus johnsonii La1 + Carotenoids	Lactobacillus johnsonii	Clinical study (<i>n</i> = 80) (skin area: whole body dermatological evaluation)	Natural sunlight	Prevents sunburn Prevents sun intolerances (benign summer light eruption; labial herpes) Prevents sunspots More homogenous pigmentation	Bouilly-Gauthier et al. ¹⁰²
Oral	Lactiplantibacillus plantarum PBS067 (DSM24937), Lacticaseibacillus rhamnosus LRH020 (PBS070, DSM25568), and Limosilactobacillus reuteri PBS072 (DSM25175)	Lactiplantibacillus plantarum, Lacticaseibacillus mamnosus, Limosilactobacillus reuteri	SKH-1 hairless mice	UVB	Reduces TEWL Increases hydration levels Reduces erythema Reduces skin thickening Reduces wrinkle formation Inhibits MMP expression Inneases Type I collagen expression Increases expression of hydration-related proteins Reduces inflammatory cytokine expression Increases antioxidant enzyme levels Reduces lipid peroxidation Reduces ROS levels Inhibits MAPK signaling	Seo et al. ¹⁰³

nearby organisms or even the host skin and their abilities to increase their resistance against UVR by sharing metabolites.

In a recently published study, new insights into the response of the skin microbiome to UVR, as well as the potential protective effects of a sun-protecting sunscreen on the microbiome of UV-irradiated skin of the volunteers' back were given.⁴⁶ The authors reported that the alpha diversity of the skin microbes was more modified by inter-individual differences and by the application of sunscreens rather than by SR. After UVR, the abundance of Lactobacillus crispatus was negatively impacted without any sun protection, while the application of sunscreen provided a protection against UVR. Moreover, the use of sunscreen helped to maintain an interaction network with Micrococcus genus. UVA and UVB impacted differently on the survival rates of L. crispatus, Cutibacterium acnes, and Staphylococcus epidermidis. These findings may help for a better understanding of the complex interaction between the skin microbiome and UVR, highlighting the importance of sun protection in maintaining a healthy skin ecosystem to avoid dysbiosis that may damage the skin. Significant interindividual differences in the microbial composition were observed in each subject.

DISCUSSION

The skin microbiome is permanently exposed to external aggressors including SR. Genetic predisposition plays a significant role in determining individual susceptibility to solar radiation-induced dysbiosis and skin conditions. Impacting the host's microbiome results in modifications of the microbiota composition and of the host immunity including both innate and acquired immunity.^{7,8,42,105}

While evidence of the impact of SR on the skin as an organ is abundant, to date there are only few data available about the impact of SR on the skin microbiome. These data do yet not allow to confirm the hypothesis that SR components impact not only directly the immune responses of the body but also indirectly through modifications of the skin microbiome.³⁵ While the beneficial and deleterious impact of SR components on inflammatory skin diseases such as atopic dermatitis, psoriasis, and acne has been well described the microbiota may also play a role in the host's immune response during or following exposure to SR.^{13,42,44,106–118}

Investigating the global metabolic profile of the skin regarding the microbiome and UVR, as well as together with other environmental factors such as pollution or climate change, provided interesting and new insights into the dynamics and interactions between the skin metabolome, microbiome, and UVR creating new axes for the development of metabolite- or lipid-based claims to maintain skin health.¹¹⁹

While, again, there is no direct evidence that UVR has a deleterious impact on the skin microbiome and through this impact causes or worsens existing skin conditions, there is evidence that UVR destroys substances such as porphyrins which are absorbed in the long UVA range and especially in the visible range and which are produced by several microorganisms including the skin commensal *Cutibacterium acnes* and *Pseudomona aeru-ginosa*. Thus, UVR may impact on the skin microbiome composition leading to dysbiosis and an altered skin barrier.^{120,121}

Sun protective means exist to shield the body, and especially the skin, against UVR. These products were developed to protect the skin as an organ in itself but without considering their effect on its commensal inhabitants. Therefore, protecting the exposed areas of the skin and its commensal inhabitants may help to further protect the host and maintain a balanced skin microbiome. Novel sun-protecting products containing pre and probiotics and other beneficial ingredients may potentially help to protect the skin microbiota from SR damages and help to limit the exposome-induced immunosuppression of the host.^{74,76–80}

In addition to topical sunscreens, the use of oral photoprotective supplements rich in antioxidants such as *Polypodium leucotomos* extract and green tea may play a crucial role in mitigating the dysbiosis induced by solar radiation exposure, thus maintaining a healthier skin microbiome.¹²²

In 2021, Souak et al.⁷⁴ reported that the skin microbiota may be a source of compounds with indirect photoprotective properties and several commensal bacteria are able to block UV radiation or absorb its deleterious impact, while others have anti-inflammatory and antioxidative properties. Clinical investigations have supported the concept that probiotics may be beneficial in preventing or reversing the negative impact of UVR on the body.³⁵ Other work supported this idea of potential benefits of novel therapeutic strategies using pro- and pre-biotics to modulate the skin response to UVR including not only the protection of the host but also to enhance the therapeutic effects of UVR in inflammatory skin conditions.¹²³

While this concept seems appealing, currently only sparse information is available that shows that modulating the skin microbiota in supplying such care helps to reduce immunosuppression and strengthen the skin microbiome against SR.

In conclusion, safeguarding both the skin and its microbiota can help reduce the risk of dysbiosis caused by solar radiation (SR), thereby supporting skin defense mechanisms and lowering the likelihood of SR-related skin conditions. Furthermore, the incorporation of topical sunscreens with film-forming properties as a vehicle not only offers effective sun protection but also enhances the skin barrier, potentially aiding in the preservation of a healthy microbiome by reducing the penetration of harmful UV radiation and environmental stressors. Among our recommendations, it is imperative to conduct more studies to comprehend the influence of solar radiation and its individual component wavebands on the skin microbiome. Also, more studies about the potential long-term consequences of solar radiation exposure on the skin microbiome and the implications for chronic skin conditions and aging. Additionally, there is a need for further investigations assessing the impact of sunscreens on the skin microbiome. Moreover, more high-quality clinical studies are needed to explore the use of oral and topical pro- and postbiotics and other therapeutic interventions targeting the skin microbiome to mitigate the effects of SR. Additional research is necessary to validate this emerging concept of microbiota protection against solar radiation.

AUTHOR CONTRIBUTIONS

All authors participated in the discussion, literature review, and read and approved the manuscript.

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CONFLICT OF INTEREST STATEMENT

YG, SS, GL, HWL, JK, and TP have received honoraria from ISDIN. JPC is a consultant for ISDIN. AB, CT, and EJ are employed by ISDIN who financed the publication expenses.

DATA AVAILABILITY STATEMENT

The data that support this work are available from the corresponding author upon reasonable request.

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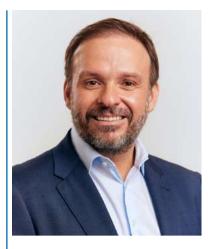
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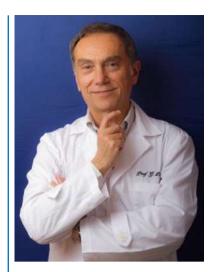
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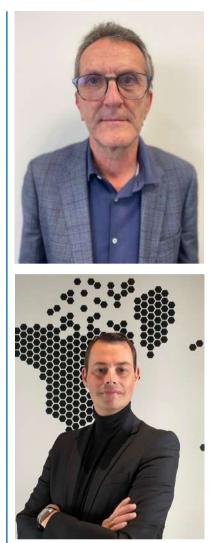


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CEO of Dermatologic Photototherapy Private Clinic in Rome and Columbus Light Clinic in Milan. Dr. Leone is esteemed as President of the European Society for Photodermatology (ESPD), having been elected in 2016. He contributes to various journals, including "Der Hautarzt" and "Photodermatology, Photoimmunology, and Photomedicine PPP". With extensive memberships and editorial roles, Dr. Leone is a respected figure in dermatology worldwide.



Anthony Brown completed his PhD at Imperial College, London, UK before undertaking postdoctoral research the University at of Oxford, UK. He is currently Preclinical Manager at ISDIN, a cosmetics company based in Barcelona, Spain.



Carles Trullas Degree in Chemistry and MSc from the University of Barcelona. Since 1983 he has been working in the field of skin care and photoprotection. He is co-author of 60 papers published in peer-reviewed international scientific journals.

Eric Jourdan is a French Pharmacist (PharmD) and a Dr in Cellular and molecular biology (PhD). He dedicates his last 25 years to study skin biology in diverse environments. From fundamental research to different private companies as the R&D and innovation director. He is involved for many

years to understand Exposome and skin interrelations.



Henry W. Lim is the former Clarence S. Livingood chair and chairman of the Department of Dermatology, Henry Ford Health, Detroit, Michigan, USA. Dr. Lim has served as president of the American Academy of Dermatology

(AAD), American Society for Photobiology, and International Union of Photobiology. He is the current president of the International League of Dermatological Societies. He was awarded an Honorary Membership of the AAD. Dr. Lim is honorary member of the following international dermatological societies: Austria, France, the Philippines, China, the Baltics, Spain, Taiwan, Peru and CILAD. He is an internationally recognized expert in photodermatology including photoprotection.



Krutmann Jean obtained his MD from the University of Münster in 1986. After several stays abroad he became associate professor at the University Hospital for Dermatology of Freiburg. From 1994 until 2001 he was a full professor/deputy director of the University Hospital

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Thierry Passeron Professor is chair and of Dermatology at the University Hospital of Nice. He also heads the laboratory INSERM U1065 team 12. C3M, dedicated to the study of molecular mechanisms

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