Domanda estratta n. 2

Domande contenuto tecnico - prova colloquio

1) Descrivere le caratteristiche principali degli acidi grassi che compongono il sebo e illustrare i metodi analitici per la caratterizzazione degli isomeri posizionali di doppi legami.

2) Fornire la descrizione di un metodo di indagine lipidomica applicata all'analisi dei lipidi superficiali cutanei.

ROMA - Istituti Fisioterapici Ospitalieri -

Domanda estratta n. 2

Domande di informatica:

1) Dovendo realizzare un foglio di raccolta dati con Excel con 10 pazienti e 5 variabili (contenenti sia stringhe che numeri) come lo strutturesti?

2) Come si calcola la media aritmetica semplice con Excel?

Domanda estratta n. 2

Trends in
Microbiology

CellPress

Review

The epidermal lipid barrier in microbiome–skin interaction

Arnaud Kengmo Tchoupa,[1,2,3] Dorothee Kretschmer,[1,2,3] Birgit Schittek,[2,4] and Andreas Peschel[1,2,3,*]

The corneocyte layers forming the upper surface of mammalian skin are embedded in a lamellar-membrane matrix which repels harmful molecules while retaining solutes from subcutaneous tissues. Only certain bacterial and fungal taxa colonize skin surfaces. They have ways to use epidermal lipids as nutrients while resisting antimicrobial fatty acids. Skin microorganisms release lipophilic microbe-associated molecular pattern (MAMP) molecules which are largely retained by the epidermal lipid barrier. Skin barrier defects, as in atopic dermatitis, impair lamellar-membrane integrity, resulting in altered skin microbiomes, which then include the pathogen *Staphylococcus aureus*. The resulting increased penetration of MAMPs and toxins promotes skin inflammation. Elucidating how microorganisms manipulate the epidermal lipid barrier will be key for better ways of preventing inflammatory skin disorders.

Highlights

We are only beginning to understand how changes in skin microbiome composition are causes for, or consequences of, inflammatory skin diseases.

The lamellar membranes in the stratum corneum represent a barrier for loss of internal, or intrusion of external, molecules. At the same time, it is a source of lipid-derived nutrients and antimicrobials with crucial roles in microbiome–host interaction. The full range of lipid-hydrolytic enzymes and of fatty acid resistance mechanisms awaits further analysis.

Microbe-associated molecular patterns (MAMPs) are retained in skin lamellar membranes. How they are degraded there remains to be elucidated.

Defects in epidermal lipid barrier integrity are probably the reason for altered skin microbiome composition and increased penetration of MAMPs towards responsive keratinocytes and leukocytes in deeper skin layers, resulting in chronic inflammatory disorders.

Mammalian skin – an unusual habitat for bacteria

Moist and nutrient-rich body surfaces such as the mucous membranes of the gastrointestinal, respiratory, and genitourinary tracts are preferred colonization sites for most bacteria. However, some bacterial taxa have specialized in colonization of the dry and nutrient-poor mammalian skin surfaces. These microorganisms belong mostly to the Firmicutes and Actinobacteria phyla, together forming dynamic skin microbiomes [1–3]. The specific environmental conditions on mammalian skin are the result of the unique composition of the skin surface, which is governed by the corneocyte protein meshwork and by lamellar-lipid membranes, which form a tight diffusion barrier between the corneocytes of the stratum corneum (Figure 1A, Key figure) [4]. How bacteria affect, and are affected by, skin lamellar membranes has remained a neglected field of research. Several recent studies have shed new light on these processes, getting us closer to a comprehensive understanding of lipid-dependent skin microbiome–host interaction [5–9].

The skin microbiomes differ with respect to host species and body site, following in particular differences in humidity and sebaceousness [1]. Nevertheless, the microbial core taxa are similar on most body sites and differ only in relative abundance. Among the Actinobacteria phylum, members of the genera *Corynebacterium, Cutibacterium*, and *Micrococcus* belong to the most abundant skin colonizers [1]. Corynebacteria have very hydrophobic surfaces as a result of their mycolic acid outer membrane [10], which suits them well for interaction with skin lipids. Several species of the Firmicutes, including the genus *Staphylococcus* and some *Streptococcus* species, regularly colonize mammalian skin. In addition to bacteria, some fungal species, in particular from the genus *Malassezia*, are typically found on mammalian skin. The diversity and dynamics of human skin microbiomes have previously been reviewed in detail by other experts [1–3]. A recent skin metagenome-based study has extended our knowledge on microbial skin microbiome members, with the identification of several new taxa, many of which remain difficult to cultivate and to analyze [11].

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