205 Evaluation of SARS-CoV-2 spike protein response on PI3K agonist-mediated IL-8 release

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A novel coronavirus related to a condition known as a severe acute respiratory syndrome (SARS) in 2003 has now been confirmed as the source of the current COVID-19 pandemic. The spike protein of the virus plays a critical role in host cell entry, receptor recognition, and immune evasion. This protein is composed of two subunits, S1 and S2. SARS-CoV-2 spike protein, similar to SARS-CoV, also binds to the human receptor ACE2. We have used an in vitro cell model (HEK-293T) to evaluate the effects of PI3K agonist on the SARS-CoV-2 spike protein expression. Our results suggest that PI3K agonist-mediated IL-8 release may be a potential therapeutic target for COVID-19.

206 The distinct skin microbiota of congenital ichthyoses

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The skin microbiome is an important component of skin health and plays a crucial role in immune function. Congenital ichthyoses are a group of genetic skin disorders characterized by severe dry skin, hyperkeratosis, and ichthyosis. The skin microbiota of patients with congenital ichthyoses has not been well studied. We aimed to characterize the skin microbiota of patients with congenital ichthyoses and compare it to healthy skin. We collected skin samples from patients with congenital ichthyoses and healthy controls. We performed 16S rRNA gene sequencing to analyze the skin microbiome. Our results suggest that the skin microbiota of patients with congenital ichthyoses is distinct from healthy skin, with a lower diversity and abundance of beneficial bacteria. This study highlights the importance of considering the skin microbiome in the management of congenital ichthyoses.

207 Targeting of HDAC8 and HDAC9 in keratinocytes to enhance skin immune defense

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HDACs are a family of enzymes that regulate gene expression by modifying histone tails. They are involved in the regulation of skin homeostasis and have been implicated in skin diseases. We have previously shown that HDAC8 and HDAC9 play a role in the regulation of the immune response in keratinocytes. In this study, we aimed to further investigate the role of HDAC8 and HDAC9 in skin immune defense. We used a keratinocyte cell line and performed gene expression analysis via quantitative real-time PCR (qRT-PCR). We found that HDAC8 and HDAC9 expression increased in response to UV radiation or imiquimod application, thus validating the expression analysis via qRT-PCR. IFN-γ production was increased in HDAC8/9flox mice in response to UV radiation or imiquimod application, thus validating the expression analysis via qRT-PCR.

208 Eosinophil-derived IL-17 protects against epicutaneous Staphylococcus aureus infections

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Eosinophils are a type of immune cell that are involved in the regulation of immune responses. They are known to produce IL-17, a pro-inflammatory cytokine that is involved in the regulation of immune responses. In this study, we aimed to investigate the role of eosinophils in the regulation of immune responses against Staphylococcus aureus infections. We used a mouse model of epicutaneous Staphylococcus aureus infections and performed gene expression analysis via qRT-PCR. We found that eosinophils were recruited to the site of infection and produced IL-17. Our results suggest that eosinophils play a role in the regulation of immune responses against Staphylococcus aureus infections.

209 Epidermal interferon expression is positively regulated by Staphylococcus aureus in SLE and involves the STING pathway

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Staphylococcus aureus (S. aureus) is a common skin commensal that can cause infections in patients with atopic dermatitis (AD), psoriasis, and systemic lupus erythematosus (SLE). However, the mechanisms by which S. aureus regulates interferon expression are not well understood. In this study, we aimed to investigate the role of S. aureus in regulating interferon expression in patients with SLE. We used an SLE cell line and performed gene expression analysis via qRT-PCR. We found that S. aureus increased interferon expression in a dose-dependent manner. Our results suggest that S. aureus plays a role in regulating interferon expression in patients with SLE.

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