Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

LB736

Wearing N95 masks does not disrupt the facial skin microbiome

G Hillebrand[1], P Dimitriu[2,3], K Nguyen[3], K Malik[1], W Mohn[2,3] and R Kong[1] *1 Innovation and Science, Amway Corp, Ada, Michigan, United States, 2 The University of British Columbia, Vancouver, British Columbia, Canada and 3 Microbiome Insights, Inc., Vancouver, British Columbia, Canada*

The COVID-19 pandemic has elevated concern about mask-related skin problems like so-called 'maskne' which is likely rooted in the skin microbiome. We therefore determined if wearing an N95 mask affects the skin microbiome in a 3-day controlled study. On Day 1, subjects (n=10) followed their normal office routine without a mask. On Days 2 and 3, subjects wore an N95 mask (3M Model 8210) from morning to late afternoon (6 hours). The same mask was used both days. Microbiome diversity and composition (16S rRNA amplicon sequencing, V1-V3), stratum corneum (SC) barrier function (TEWL), SC hydration, skin redness and follicular porphyrins were measured on the cheek (masked site) and forehead (control site) each morning and afternoon. At the end of the study, a sample of each mask was collected for microbiome analysis. Mask wearing showed no significant effect on alpha (Shannon) or beta (Brays-Curtis) microbiome diversity. Mask wearing had no significant effect on *Cutibacterium acnes* relative abundance. Mask wearing corresponded to a small increase in the genus *Staphylococcus* relative abundance on Day 2 ($p=0.03$) but not Day 3. There was no significant effect of mask wearing on SC hydration or follicular porphyrins. TEWL and skin redness were elevated ($p<0.05$) on Day 2 and Day 3 on the masked cheek but not the unmasked forehead; values returned to baseline from Day 2 PM to Day 3 AM. Finally, the mask microbiome reflected that of the subject's skin; the relative abundance of *C. acnes* on the subject's mask correlated with that on the subject's cheek skin ($r^2=0.46$, $p<0.001$). In conclusion, wearing an N95 mask for 6 hours per day on two consecutive days under routine office work conditions did not significantly affect the diversity or composition of the skin microbiome and produced only transient changes in visible skin redness and barrier function. Longer term studies with different types of masks under non-office conditions are needed to further understand the influence of mask wearing on the skin microbiome.

LB737

Lack of stable housing as a risk factor for group A streptococcal skin and soft tissue infection among hospitalized adult patients

A Zakaria[1], K Abuabara[1], P Kim-Lim[2], L Fox[1], E Amerson[1,3] and A Chang[1,3] *1 Dermatology, University of California San Francisco School of Medicine, San Francisco, California, United States, 2 University of California Davis School of Medicine, Sacramento, California, United States and 3 Dermatology, Zuckerberg San Francisco General Hospital and Trauma Center, San Francisco, California, United States*

Background: Patients lacking stable housing face significant medical morbidity, including increased rates of skin and soft tissue infections (SSTIs). While outbreaks of invasive group A streptococcal (GAS) disease, such as sepsis and pneumonia, have been reported among persons experiencing homelessness, only a single small study has examined housing status as a risk factor for non-invasive GAS infections, such as SSTIs. Objective: To determine if housing status is an independent risk factor for GAS SSTIs. Methods: We performed a retrospective cross-sectional study of hospitalized adult patients receiving dermatology consult services at UCSF Moffitt-Long Hospital or Zuckerberg San Francisco General Hospital between March 2018 and March 2020 who were diagnosed with an SSTI and had skin microbiology data available. We developed logistic regression models to examine whether housing status was independently associated with GAS SSTI in unadjusted analysis and after adjusting for age, gender, alcohol use and injection drug use. Results: Our analysis captured 209 patients, with 150 having stable housing and 59 lacking stable housing. GAS was cultured from skin in 42% of patients lacking stable housing and 17% of patients with stable housing. In simple logistic regression, patients lacking stable housing had 3.51 times the odds (95% CI 1.80 to 6.84; $p<0.001$) of GAS positivity relative to patients with stable housing. In multiple logistic regression adjusting for potential confounders, patients had 3.95 times the odds (95% CI 1.87 to 8.38; $p<0.001$) of GAS positivity if they lacked stable housing. Conclusions: Our results suggest that medical providers caring for patients lacking stable housing should have a high index of suspicion for GAS in the setting of SSTIs and consider empiric GAS coverage with a first-line antibiotic.

LB738

Anti-inflammatory activity of traditionally used, bioactive mushrooms in skin

R Graziose[1,2], D Collins[2], T Low Dog[3], A Weil[4], S Schnittger[2], W Lee[6], S Green[6] and N Pernodet[2,5] *1 Origins Laboratories, Melville, New York, United States, 2 Estee Lauder Companies, New York, New York, United States, 3 Chief Medical Officer, Healthy Lifestyle Brands, Phoenix, Arizona, United States, 4 Director, Andrew Weil University of Arizona Center for Integrative Medicine, Tucson, Arizona, United States, 5 Material Science and Engineering, Stony Brook University, Stony Brook, New York, United States and 6 SUNY Downstate Medical School, New York, New York, United States*

Mushrooms have long been considered a valuable resource for both nutritional purposes and in traditional medicinal practices. In particular, increasing amounts of research demonstrate that many of the medicinally used mushrooms possess strong anti-inflammatory and immune-modulating properties. In the skin, as elsewhere in the body, inflammation is a natural response to external and internal insults (i.e. physical stimuli, stress, infection, sunlight) and if uncontrolled, can also impact skin cell function, matrix protein degradation, and accelerate skin aging. In this work, we describe how the inhibition of the recruitment and accumulation of neutrophils to the site of "irritation" (a hallmark of the inflammatory response) can reduce inflammation and help skin cells return to their optimal function. We show the ability of traditionally used, bioactive mushrooms to act on inflammation via this target and suggest a topical application of these mushroom extracts can reduce the visible signs of irritation.

LB739

A retrospective analysis of bacterial culture results and disease severity in a cohort of Hidradenitis Suppurativa patients

L Mittal[1], TM Andriano[1], G Benesh[1], H Hosgood[2] and SR Cohen[1] *1 Division of Dermatology, Montefiore Medical Center, Bronx, New York, United States and 2 Department of Epidemiology and Population Health, Albert Einstein College of Medicine, Bronx, New York, United States*

The role of bacteria in the initiation and progression of hidradenitis suppurativa (HS) is poorly understood. Likewise, the utility of swab bacterial cultures in guiding antibiotic therapy, a mainstay of treatment, remains controversial. We are seeking to determine if bacterial swabs reveal clinically useful trends in the relationship between bacterial profiles and HS severity. A retrospective chart review of 127 patients seen between March 2019 and November 2020 at the Einstein/Montefiore HS Center was performed. Disease severity was classified according to the HS-Physician Global Assessment (HS-PGA) scale. Chi-square and Fisher's exact tests were computed to analyze the differences in bacterial profile based on disease severity. Those with HS-PGA scores of ≥ 2 and swab bacterial cultures obtained at presentation were included in this study (mean age: 35.8±13.6, female: 70.1%). Participants were grouped by culture results: aerobic, anaerobic, aerobic plus anaerobic, or normal. Patients with aerobic cultures or mixed anaerobic plus aerobic cultures were more likely to have severe disease (HS-PGA 3-5) than mild disease (HS-PGA 2) ($p=0.03$), relative to patients growing anaerobic cultures at first visit. Furthermore, patients with Streptococcal species were more likely to have severe disease than mild disease ($p=0.03$). These findings suggest that superficial microbial cultures in HS may reveal trends in the relationship between bacterial profile and disease severity. Specifically, participants with severe disease were found to have predominantly aerobic or mixed aerobic plus anaerobic flora. Further longitudinal studies are necessary to analyze the shifting relationship between bacterial growth and disease severity in response to treatment.

LB740

SARS-CoV-2-associated 'covid toes:' multiplex immunofluorescent characterization of pathophysiology

JJ Moon[1], A Costa da Silva[2], JM Tran[1], C Kim[2], R Sharma[2], M Hinshaw[1], BE Shields[1], E Brooks[3], EW Cowen[3], A Singh[4], B Drolet[1], J Mays[2] and L Arkin[1] *1 Dermatology, University of Wisconsin-Madison School of Medicine and Public Health, Madison, Wisconsin, United States, 2 National Institute of Dental and Craniofacial Research, Bethesda, Maryland, United States, 3 Pathology and Laboratory Medicine, University of Wisconsin-Madison School of Medicine and Public Health, Madison, Wisconsin, United States, 4 Pediatrics, University of Wisconsin-Madison School of Medicine and Public Health, Madison, Wisconsin, United States and 5 Dermatology Branch, National Institute of Arthritis and Musculoskeletal and Skin Diseases, Bethesda, Maryland, United States*

Coincident with the start of the COVID-19 pandemic, dermatologists worldwide have reported an uncharacteristic increase in pernio or chilblains (aka 'COVID toes'). However, the lack of systemic illness, low PCR positivity and lack of consistent seroconversion have led some authors to postulate an epiphenomenon. SARS-CoV-2 spike protein has been identified in a limited number of skin biopsies in few publications, yet there remain conflicting reports regarding other SARS-CoV-2 associated proteins, the presence or absence of viral RNA, and a unifying pathophysiology. In cooperation with the COVID Human Genome Effort, our "COVID toes" biobank was established to identify both the genetic and immunologic basis and provide clinically relevant insights into targeted therapeutics. As of March 2021, we have enrolled 96 patients, creating a prospective biorepository with clinical data, saliva, serial blood collection, and skin biopsies. Here we aim to comprehensively investigate the conflicting findings, detail the inflammatory response, and identify the source of interferon signaling with multiplex immunofluorescence (IFA) and the RNAscope fluorescent assay to detect viral mRNA. Median patient age was 17 (range 2 − 72) and 44/96 (46%) were male. Preliminary IFA results demonstrate detection of SARS-CoV-2 components, robust MxA detection and plasmacytoid dendritic cell (pDC) colocalization, identifying PDCs as the likely primary source of IFN-I production and implicates an excessive localized IFN-I response in affected patients.