a custom R script. Analyses of pathways, upstream regulators, and causal networks were conducted using ingenuity pathway analysis (IPA). **Results:** The molecular signatures of acne skin and the effect of PM2.5 on skin in vitro were compared at 3 levels: (1) gene expression, (2) pathway activity, and (3) upstream regulators. Significant concordant overlaps of both upregulated ($P < 3e\text{-}23$) and downregulated DEGs (P< .005) were observed in acne skin and PM2.5-exposed keratinocytes. However, for the PM2.5-exposed 3D skin model, significant overlap with acne skin was only observed for upregulated DEGs ($P < 8e\text{-}14$). Fold changes of DEGs in both acne and PM2.5-exposed data sets showed significant correlation (Pearson correlation coefficient > 0.6; $P < .001$). An IPA analysis identified 13 pathways commonly enriched in acne and PM2.5 data sets, including IL17, IL6, Toll receptor PPAR, LXR–RXR, and acute-phase response pathways. Common upstream regulators were further identified including TNFα, NFκB, CAMP, AhR, and IL17A. Finally, causal network analysis revealed several potential hub regulators shared in acne pathogenesis and PM2.5-exposed skin, including HIF1α, TNF, IL1α, and CCL5. **Conclusions:** Our analysis revealed significant concordant molecular signatures between acne and PM2.5-exposed skin. Biological insights from this study offer clues that build the causal links between air pollution and acne pathogenesis.

**Subject Category:** Environmental Hygiene
**Abstract Number:** SG-APSIC1094
**Impact of environmental pollution on skin antimicrobial peptide genes expression revealed by transcriptome profiling**
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**Objectives:** Pollution exposure is associated with several dermatological conditions including acne, atopic dermatitis, and psoriasis. Antimicrobial peptides (AMPs) are key effectors of innate defense, and some AMPs are involved in inflammatory skin conditions. In this study, we aimed to characterize expression changes of human AMPs under different in-vitro pollution exposures. **Methods:** RNA-seq profiling was conducted on normal human primary epidermal keratinocytes (NHEK) treated with either a vehicle control, or benzo[a]pyrene (BaP) and on pigmented living skin equivalent models (pLSE) treated with either a vehicle control, ozone, or vehicle exhaust. Differential expressed genes (DEGs) were identified with R scripts. DEGs of PM2.5 were obtained from the literature and the GEO database. Also, 180 human AMP genes were obtained from a UDAMP database. UpSetPlot was used to plot DEGs overlaps. MetaVolcano was used to identify frequently changed AMPs. **Results:** We used in-house and published transcriptome profiles to identify AMP genes that displayed altered expression under in-vitro pollution exposure. Of the 180 AMP genes under investigation, 37 showed significant changes in expression in at least 1 of the 5 experiments. Using MetaVolcano, 13 AMP genes were identified to be frequently and consistently changed. Several AMPs associated with inflammation and skin diseases were frequently upregulated, including S100A8, S100A9, LCN2, HBD3, RNASE7, and CXCL1. Only 3 frequently downregulated AMP genes were identified, including CXCL14, which is reported to be a noninflammatory AMP that is highly expressed in healthy skin and is downregulated in skin diseases. **Conclusions:** The data sets suggest that expression of both proinflammatory and homeostatic AMPs can be perturbed by pollution. These findings provide new clues to explain how pollution affects skin innate defense, host–microbe interactions and contributes to abnormal skin conditions. Normalizing aberrant AMP expression may be a potential approach to treat pollution associated skin disorders in the future.

**Subject Category:** Hand Hygiene
**Abstract Number:** SG-APSIC1107
**Effectiveness of interventions increasing surgical hand hygiene compliance at Hung Vuong Hospital**
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**Objectives:** Surgical handwashing is one of the most important measures to prevent surgical site infection (SSI). We evaluated the effectiveness of the intervention program on surgical handwashing compliance of healthcare workers (HCWs) at Hung Vuong Hospital. **Methods:** This research was conducted from July 2019 to November 2019 in 3 phases. In the first phase, we determined the surgical handwashing compliance rate before the intervention. In the second phase, we implemented an intervention bundle as follows. We provided reminders of compliance in the form of video screen and automatic timers at surgical handwashing sinks. We provided links and QR codes for online access and live streaming of instructional videos on implementation of the hospital's surgical hand sanitation procedures in the surgical handwashing area. We conducted direct monitoring to remind and guide HCWs to follow the procedures in combination with camera surveillance to accurately reflect compliance. Finally, we provided feedback in multiple steps: feedback to individual, feedback to head of department or department heads, cited names in briefings and sent names to the general planning department to suspend surgery privileges. In the third phase, we re-evaluated the surgical handwashing compliance rate after the intervention. **Results:** The total number of surgical handwashing checklists observed before and after the intervention was 787. The surgical handwashing compliance rate improved significantly from 48.8% to 71.8% (PR, 2.7; 95% CI, 1.98–3.57; $P < .01$). The compliance rate in camera monitoring also increased from 22.1% to 57.9% (PR, 4.8; KTC 95%, 3.14–7.47; $P < .01$). The compliances rates of both surgeons and scrub nurses improved significantly after the intervention ($P < .01$). Conducting the new surgical handwashing procedure increased from 90.2% to 99.5% after this intervention. **Conclusions:** This intervention program improved surgical handwashing compliance of HCWs.

**Subject Category:** Hand Hygiene
**Abstract Number:** SG-APSIC1122
**Observational study of handwashing sink activities in the inpatient setting**
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**Objectives:** The use of handwashing sinks for activities other than hand hygiene (HH) is associated with higher rates of β-lactamase–producing