223 Murine cutaneous microbiota composition is largely mouse strain dependent with microbiota changes during acute wound healing showing mouse strain specific responses. 

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To date little research has investigated the genetic determinants of cutaneous microbiota composition and how microbiota composition can effect acute wound healing. Here we used 114 mice totalling 30 different mouse strains from an advanced cross-breeding program, The Collaborative Cross, and performed large, 1.5x1.5cm, full excisional wounds of mouse dorsal skin. 16S rRNA sequencing immediately before wounding and at days 3 and 10 post-wounding show microbiota compositional changes are largely strain dependent with different mouse strains showing different changes in microbiota composition as a result of wounding. Principal component regression of centred-log ratio abundances and wound healing speed, time-to-wound closure, show an adjusted R-squared of 0.4 mm; n = 43, p < 0.03, were strongly associated with levels of serum androgens which are known to influence hormonal effects on the skin microbiome in individuals followed longitudinally has not been studied as systematically. In this prospective and longitudinal study, twelve healthy children were evaluated up to 6 years to investigate puberty-related changes in skin microbial shifts. Using 16S rRNA (V4-V3) amplicon sequencing with DADA2 analysis, bacterial and fungal communities of five different skin sites were analyzed and compared with serum hormone levels. The composition and the diversity of skin microbial communities varied in a sex-specific manner during childhood development. Furthermore, we revealed a positive feedback circuit between mTORC1 signaling and rosacea, in which LL37 activates mTORC1 signaling by binding to TLR2, which in turn enhances the expression of cathelicidin. Subsequently, cathelicidin LL37 derived from keratinocytes induces NET-asso- ciated IFNγ, TNFα, IL-17A were significantly attenuated in the skin of UVB-irradiated BMT mice with ROCK1 deficiency as compared to those transplanted with WT HSCs. In an ex vivo experiment, inhibition of neutrophil NET-associated IFNγ, TNFα, IL-17A were significantly reduced in PAF-treated neutrophils from ROCK1 deficient mice as compared to those from WT mice. Conclusion: Hematopoietic specific ROCK1 deficiency attenuates neutrophil NET release and NET-associated proinflammatory cytokine display in UVB-induced skin inflammation.

226 Effect of triamcinolone & manuka honey on Staphylococcus aureus growth & hemolytic activity.

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Atopic dermatitis (AD) is an inflammatory skin disease commonly treated with topical steroids (TS). Manuka honey (MH) is an antiseptic and anti-inflammatory agent containing the sugar methylglycoside, methylumbelliferone or MN. 16S RNA sequence data from five healthy subjects, each of whom underwent a blind, randomized, cross-over trial comparing topical triamcinolone acetonide (TAC) or MH alone. The study indicated that MH significantly reduced bacterial growth and hemolytic activity compared to TAC alone (p < 0.05).

227 A positive feedback loop between mTORC1 and cathelicidin promotes skin inflammation in rosacea.

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ROSacea is a chronic inflammatory skin disorder whose pathogenesis is unclear. Here, we focus on addressing the role of mTOR signaling in the pathogenesis of rosacea. We report that mTORC1 signaling is hyperactivated in both rosacea patients and mouse models. Functionally, both mTORC1 ablation and pharmacological inhibition by its specific inhibitors restrained the development of rosacea in an LL37-induced rosacea-like mouse model. On the contrary, hyperactivation of mTORC1 signaling in TSC2<sup>−/−</sup> mice exacerbated rosacea development. Furthermore, we revealed a positive feedback circuit between mTORC1 signaling and cathelicidin, in which LL37 activates mTORC1 signaling by binding to TLR2, which in turn enhances the expression of cathelicidin. Subsequently, cathelicidin LL37-derived cathelicidin mediated NET-asso- ciated IFNγ, TNFα, IL-17A were significantly attenuated in the skin of UVB-irradiated BMT mice with ROCK1 deficiency as compared to those transplanted with WT HSCs. In an ex vivo experiment, inhibition of neutrophil NET-associated IFNγ, TNFα, IL-17A were significantly reduced in PAF-treated neutrophils from ROCK1 deficient mice as compared to those from WT mice. Conclusion: Hematopoietic specific ROCK1 deficiency attenuates neutrophil NET release and NET-associated proinflammatory cytokine display in UVB-induced skin inflammation.

228 Shifts in the skin bacteria and fungi in healthy children transitioning through puberty.

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Skin microbial shifts among different age groups are known from several culture- and sequencing-based studies, the influence of sexual maturation on the skin microbiome in individuals followed longitudinally has not been studied as systematically. In this prospective and longitudinal study, twelve healthy children were evaluated up to 6 years to investigate puberty-related changes in skin microbial shifts. Using 16S rRNA (V4-V3) amplicon sequencing with DADA2 analysis, bacterial and fungal communities of five different skin sites were analyzed and compared with serum hormone levels. The composition and the diversity of skin microbial communities varied in a sex-specific manner during childhood development. Furthermore, we revealed a positive feedback circuit between mTORC1 signaling and rosacea, in which LL37 activates mTORC1 signaling by binding to TLR2, which in turn enhances the expression of cathelicidin. Subsequently, cathelicidin LL37 derived from keratinocytes induces NET-asso- ciated IFNγ, TNFα, IL-17A were significantly reduced in the skin of UVB-irradiated BMT mice with ROCK1 deficiency as compared to those transplanted with WT HSCs. In an ex vivo experiment, inhibition of neutrophil NET-associated IFNγ, TNFα, IL-17A were significantly reduced in PAF-treated neutrophils from ROCK1 deficient mice as compared to those from WT mice. Conclusion: Hematopoietic specific ROCK1 deficiency attenuates neutrophil NET release and NET-associated proinflammatory cytokine display in UVB-induced skin inflammation.

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