INFECTIOUS DISEASES (BACTERIAL, FUNGAL, VIRAL, PARASITIC, INFESTATIONS)

THE IMPACT OF SCABIES ON THE HEALTHY SKIN MICROBIOTA

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Introduction: We hypothesize that in the tropics scabies plays a significant role in the establishment, proliferation and transmission of opportunistic, pathogenic bacteria and forms a critical precursor of skin-borne infection that can lead to severe illness.

Methods: Whole metagenome analysis and 16S/ITS1 rRNA amplicon Illumina MiSeq sequencing.

Results: The first in vivo evidence endorsing this hypothesis came from a longitudinal pilot study in a scabies porcine model, demonstrating a drastic shift from commensal to pathogenic staphylococci in the skin with the onset of scabies infection. To investigate scabies infestations in humans we analysed metagenome data generated from DNA preparations of mite and skin material collected from severe crusted scabies patients in northern Australia. A remarkable preliminary finding is the high abundance of opportunistic pathogens. To define the microbiome in skin lesions of patients with common scabies in North Australia, India and France we analyse skin scrapings from a large cohort of patients sampling multiple body sites and including control samples from corresponding co- and contra-lateral healthy sites. The multi-centre project involves a large team of dermatologists, parasitologists, health workers, nurses and students. Given the association between scabies and secondary infections, there is a need to understand how anti-scabies treatment impacts on pathogens associated with the mite. Our work in the porcine model showed that at 5 weeks post treatment with ivermectin the healthy skin microbiota is not restored. In collaboration with Medicines Development for Global Health, we will study scabies lesions for their microbial content over time, compared to contralateral uninfected sites, during the course of treatment of patients enrolled in a moxidectin Phase II study.

Conclusions: This work will present the diversity and dynamics of microbes associated with human scabies and define molecular mechanisms that underpin this synergy, to provide the basis for improved treatment and management strategies.