

Gene technology to help healthy skin in Aboriginal Australians

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Researchers from the Walter and Eliza Hall Institute, Melbourne, have used cutting-edge genome technologies to reveal the genetic makeup of a widespread skin parasite causing serious health problems. Credit: Walter and Eliza Hall Institute

Australian researchers have used cutting-edge genome technologies to

reveal the genetic makeup of a widespread skin parasite causing serious health problems in Aboriginal communities.

The research team identified the genetic 'map' of the human parasitic scabies mite, accelerating research that could lead to new ways of preventing and treating scabies infestations and prevent lifelong complications for people in remote Aboriginal communities.

Scabies is a contagious and extremely itchy skin infestation caused by scabies mites. Scabies is rife in many remote Aboriginal communities in Australia, affecting one in two children and one in four adults each year.

Scabies infestations often become infected, causing serious - even lifelong or fatal - complications, such as bacterial blood infections (sepsis), and are associated with serious kidney and heart diseases.

The research was led by Associate Professor Tony Papenfuss from the Walter and Eliza Hall Institute and Dr Katja Fischer from the QIMR Berghofer Medical Research Institute, Queensland, and was published today in *PLoS Neglected Tropical Diseases*.

Genomic technologies are critical for finding ways to prevent and control scabies, Associate Professor Papenfuss said. "A shocking seven out of ten children in remote Aboriginal communities will contract scabies before they reach one year of age," he said.

Scabies wounds often become infected by Group A streptococcus bacteria, which can cause rheumatic fever, acute kidney disease and rheumatic heart disease. These infections have dramatic effects on life quality and expectancy.

"Genomic technologies have revolutionised how we treat many diseases, such as cancer," Associate Professor Papenfuss said. "We are excited

that we can now apply these technologies to tackle a major, yet neglected, health problem in Indigenous Australians."

To get the first insight into the genetic makeup of scabies mites, the team analysed DNA from the cellular 'energy factories' called mitochondria. Mitochondrial DNA evolves slowly compared with other types of DNA, making it useful for examining the relatedness of different parasite strains.

Dr Fischer said the team compared DNA sequences from human scabies mites with those from domestic pigs, which commonly have scabies. "One of the unexpected things we found was that one patient was infected with mites that were genetically more similar to pig mites than to human mites," she said. "This suggests it may be possible for certain animal strains of mites to infect humans, which we did not previously know was possible. If subsequent studies confirm this finding, it could have major implications for disease control programs."

Prior to this study, little was known about the genetic makeup of the scabies mite. Understanding the [genetic makeup](#) of the scabies mite would help identify how it becomes resistant to certain drugs and could suggest new strategies for development of novel therapeutics.

Associate Professor Papenfuss said that analysing the scabies mite was a challenge due to their tiny size. "We analysed thousands of [mites](#) to get sufficient DNA for sequencing and developed bespoke analysis methods to overcome DNA contamination from the host animal and bacteria in the wound."

Provided by Walter and Eliza Hall Institute

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