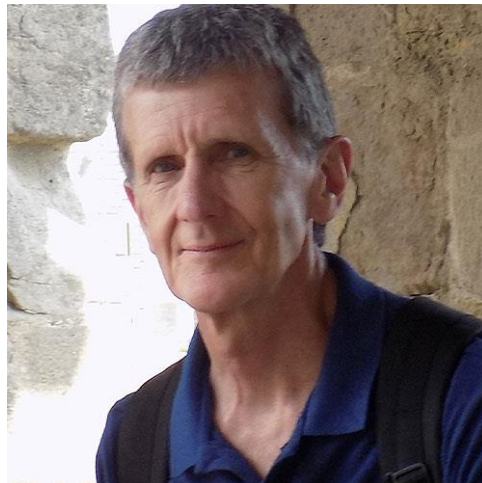


Key scientific breakthrough in HIV genetic research in people of African ancestry



Emeritus Professor Ayesha Motala



Dr Fraser Pirie



Dr Pravi Moodley

A global team of scientists and researchers including academics from UKZN and Omnigen Biodata Ltd, have discovered a genetic variant that may explain the naturally lower viral loads of HIV seen in some people of African ancestry. This global first discovery, that was reported in Nature, could lead to the development of new therapeutics and improve treatment options for those living with HIV.

This is the first new genetic variant associated with HIV infection identified in almost 30 years and highlights the importance of conducting genetic research in diverse populations, including those of African ancestry.

UKZN's Emeritus Professor Ayesha Motala; co-author of the Nature research paper; and Co-Chief Investigator of Discover Me South Africa explained, 'This piece of research is a real turning point for understanding HIV infections in African populations. The results of this study also demonstrate the importance of undertaking genetic research in African populations to enable discovery and address long-standing health inequities.' Other UKZN contributors include Dr Fraser Pirie, head of the Department of Diabetes and Endocrinology and Dr Pravi Moodley from the Department of Virology. Pirie said, 'I'd like to acknowledge the efforts of those that collected all clinical data and laboratory samples that made this study possible.'

HIV continues to be a major cause of illness and mortality, despite the existence of treatments which reduce viral loads. Viral load is the amount of virus that an individual has in their system and can vary widely between individuals infected with HIV. Higher viral loads are known to correlate with faster disease progression and increased risk of transmission. Viral load is influenced by several factors, including an individual's genetics. Considering the disproportionate impact of HIV on people living in Africa, more than 25 million people are HIV-positive on the continent, the researchers sought to better understand the role of genetics in HIV infection in African populations.

The study analysed the genetics of approximately 4000 individuals of African ancestry, living with HIV. A variant in the gene CHD1L, found to be specific to populations of African descent, was associated with reduced viral load. Experimental studies suggested this variant may play a role in limiting viral replication, although more research is required to fully understand how this occurs.

Professor Manjinder Sandhu, Faculty of Medicine at Imperial College London; co-author of the Nature research paper; founder & CEO of Omnigen Biodata; Principle Investigator of Discover Me UK and Co-Chief Investigator of Discover Me South Africa explained, 'With more than a million new HIV infections a year, it's clear that we still have a long way to go in the fight against HIV – we are yet to have a vaccine to prevent infection, have yet to find a cure and still see drug resistance emerging in some individuals. The next step is to fully understand exactly how this genetic variant controls HIV replication.'