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NITheCS COLLOQUIUM:

The power of contemporary African DNA: Exploring human evolution and health in Africa

Prof Marlo Möller (Stellenbosch University)

DATE: Monday, 3 June 2024 | 16h00–17h00 SAST

VENUES:
- Neelsie Cinema, Stellenbosch University
- Online

ABSTRACT

Africa is home to some of the most genetically diverse populations in the world, with a population of over 1.2 billion people comprised of over 3,000 distinct ethnic groups and a wide range of unique genetic variations. Given the genetic diversity on the continent, it is generally accepted that humans evolved in Africa, but several opposing conceptual models representing our origins have been proposed. Our study sheds light on the divergence of human populations on the African continent and challenges traditional models, suggesting a new framework – represented by a tangled vine with offshoots – where stem populations separated, but continually exchanged genetic material. This work would not have been possible without sequencing the most genetically diverse human genomes in the world. Contemporary African DNA is not only key to understanding deep human history, but is central to implementing prevision medicine on the continent and answering other health-related questions.

BIOGRAPHY

Marlo Möller is a professor in the Division of Molecular Biology and Human Genetics, Stellenbosch University (SU) which houses the South African Medical Research Council (SAMRC) Centre for Tuberculosis (TB) Research. She is also an Associate Member of the Centre for Bioinformatics & Computational Biology at SU. Her primary research focus is on finding the human genetic underpinnings of TB and leverage the complex ancestry of South Africans to find novel genes and pathways involved. Her main strength is to provide a uniquely African emphasis on the current highly computational field of genetics as it impacts human disease. Combining these interests with her insights into the latest genetic analyses available have allowed the work on genetic susceptibility to TB to benefit from population genetics analyses and next generation sequencing.

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