

More about syphilis

Syphilis is an important and common disease in humans. It is caused by the bacterium *Treponema pallidum* ssp. *pallidum* and controversy surrounds its origin and subsequent spread across the world. Despite the close phylogenetic relationship of *T. pallidum* ssp. *pallidum* to the other ssp. *pertenue*, and *endemicum*, there is a paucity of information on the factors that lead to the protean clinical manifestations and transmission modes. This dearth of understanding is highlighted by a newly described simian *T. pallidum* strain that causes genital ulceration in baboons (*Papio anubis*). Despite its syphilis-like manifestation, this simian strain is genetically most closely related to human strains of the ssp. *pertenue* clade, which are known to cause yaws. Comparison of the genomes of various strains, in combination with our understanding of their clinical manifestations and immunopathobiology in human and non-human primates (NHPs), may provide further information about the origin, evolution, and pathogenesis of syphilis. Since the zoonotic potential of West African simian strains has already been reported, our research elucidates whether zoonotic transmission of these neglected tropical diseases occurs frequently in a natural environment. The identification of NHPs as a reservoir would make a strong impact to the success of future treponematoses eradication campaigns (e. g., WHO 2012).

It is hypothesized that non-venereal simian strains have evolved to produce syphilis-like manifestations more than once in the primate family OR that simian strains have recently begun to produce syphilis-like manifestations in response to changes in host immunological response or environmental changes. Furthermore it is open to question whether genetic polymorphisms lead to functional differences between the different *Treponema* strains and if these correlate with strain-specific clinical and immunological characteristics.

We follow a ‘one-health approach’, considering that human and wildlife health cannot be separated from each other. Scientifically, one of our core aspects of the project is the comparison of human and NHP *Treponema* isolates from Africa, especially in areas that are known as hotspots for *Treponema* infection in both humans and NHPs.

Selected references:

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