



# Seminar(i)

**Deciphering the evolution of Mycobacterium tuberculosis throughout Africa and different hosts using genomics**

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Whole genome sequencing of Mycobacterium tuberculosis is being adopted for tuberculosis epidemiological investigation and drug resistance detection, leading to increasing genomic data and resources being available for analyses. However, the development of rapid typing tools based on genomic data requires a profound knowledge of the Mycobacterium tuberculosis complex (MTBC) genomic diversity and history. Our aim is to decipher the evolutionary history of the deeper nodes of the MTBC phylogeny, including MTBC animal ecotypes and M. africanum lineages, which are under sampled and insufficiently studied currently.

*WHERE?*

Seminar room – SS6  
(Institutes building floor -1)

*WHEN?*

Thursday 17/10/2019 – 12:00 h

*LANGUAGE?*

English