A study has focused on the evolutionary history of the mycobacterium that causes tuberculosis, and more specifically on the Beijing lineage associated with the spread of multidrug resistant forms of the disease in Eurasia. While confirming the East-Asian origin of this lineage, the results also indicate that this bacterial population has experienced notable variations coinciding with key events in human history. They also demonstrate that two multidrug resistant (MDR) clones of this lineage started to spread concomitantly with the collapse of the public health system in the former Soviet Union, thus highlighting the need to sustain efforts to control tuberculosis. Finally, this work has made it possible to identify new potential targets for the treatment and diagnosis of this disease. This study was carried out by scientists at the Centre d'Infection et d'Immunité de Lille (CNRS/Institut Pasteur de Lille/Inserm/Université de Lille) and the Institut de Systématique, Evolution, Biodiversité (CNRS/Muséum national d'Histoire naturelle/UPMC/EPHE), working in collaboration with a large international consortium. Its findings were published on 19 January in Nature Genetics.

Read more http://www.alphagalileo.org/ViewItem.aspx?ItemId=149223&CultureCode=en