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Authors: Norbert Reiling, Susanne Homolka, Thomas A. Kohl, Christine Steinhäuser, Katharina Kolbe, Stefan Schütze, Julius Brandenburg



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**Shaping the niche in macrophages: Genetic diversity of the *M. tuberculosis* complex and its consequences for the infected host**

Norbert Reiling<sup>1,\*</sup>, Susanne Homolka<sup>2</sup>, Thomas A. Kohl<sup>2</sup>, Christine Steinhäuser<sup>1</sup>, Katharina Kolbe<sup>1</sup>, Stefan Schütze<sup>3</sup>, Julius Brandenburg<sup>1</sup>

<sup>1</sup>Microbial Interface Biology

<sup>2</sup>Molecular and Experimental Mycobacteriology, both at the Research Center Borstel, Leibniz Center for Medicine and Biosciences, 23845 Borstel, Germany

<sup>3</sup>Institute of Immunology, Christian-Albrechts-University of Kiel, 24109 Kiel, Germany

\*Corresponding Author:

PD Dr. Norbert Reiling  
RG Microbial Interface Biology  
Research Center Borstel  
Leibniz-Center for Medicine and Biosciences  
Parkallee 22  
23845 Borstel  
Germany

Phone: +49-4537-188 4860

Fax: +49-4537-188 6860

Email: nreiling@fz-borstel.de

**Abstract:**

Pathogenic mycobacteria of the *Mycobacterium tuberculosis* complex (MTBC) have co-evolved with their individual hosts and are able to transform the hostile environment of the macrophage into a permissive cellular habitat. The impact of MTBC genetic variability has long been considered largely unimportant in TB pathogenesis. Members of the MTBC can now be distinguished into three major phylogenetic groups consisting of 7 phylogenetic lineages and more than 30 so called sub-lineages/subgroups. MTBC genetic diversity indeed influences the transmissibility and virulence of clinical MTBC isolates as well as the immune response and the clinical outcome. Here we review the genetic diversity and epidemiology of MTBC strains and describe the current knowledge about the

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