

CAS Scientists Reveal the Genetic Basis of Drug Resistance in *Mycobacterium tuberculosis*

Tuberculosis (TB) is a chronic respiratory disease caused by *Mycobacterium tuberculosis* and is a serious threat to human health. Every year there are 1.3 million new cases of TB worldwide, 100,000 of which are multidrug resistant. The TB burden in China is the second highest in the world. The widespread occurrence of multidrug (MDR) and extensively drug-resistant (XDR) tuberculosis is making the treatment of TB more and more problematic.

Research on the mechanisms underlying drug resistance, one of the most important, difficult and competitive areas of TB research worldwide, has been carried out in the labs of Professors BI Lijun and ZHANG Xian'en at the Institute of Biophysics, CAS. On September 1st, 2013, *Nature Genetics* published their findings in an article entitled "Genome sequencing of 161 *Mycobacterium tuberculosis* isolates from China identifies genes and intergenic regions associated with drug resistance".

This article reports the collection and sequencing of 161 *Mycobacterium tuberculosis* isolates (44 drug-sensitive, 94 MDR and 23 XDR isolates) from 12 provinces across China, done in collaboration with Professor WAN Kanglin of the China Center for Disease Prevention and Control and BGI-Shenzhen. Comparative analysis of these genome sequences led to the discovery of 72 genes and 28 intergenic regions associated with drug resistance in addition to well-known drug resistance genes. The results of this study have broad application throughout China as the isolates were collected from throughout the country and provide many new avenues of research for investigating drug resistance mechanisms and the development of new TB drugs. The study also showed that TB patients in China are mainly infected by lineage 2 and lineage 4 strains of *Mycobacterium tuberculosis*, and that 95% of the lineage 2 strains were from the Beijing family, a family of strains

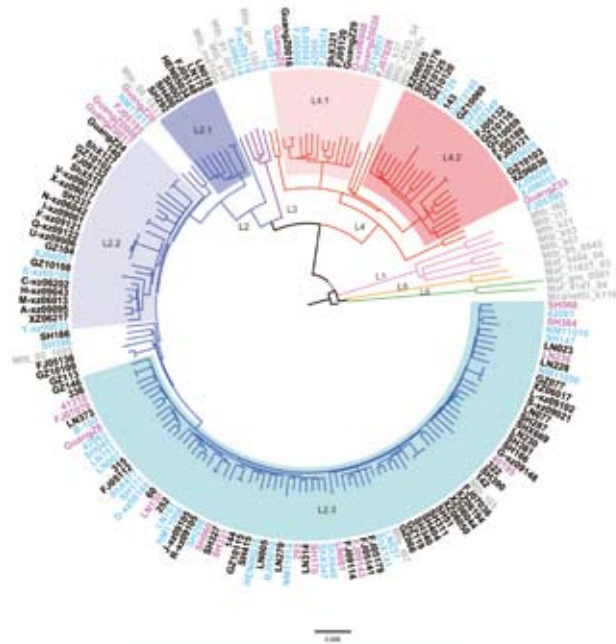


Figure 1 Phylogenetic analysis of *M. tuberculosis* isolates.

Phylogenetic analysis of the 161 *M. tuberculosis* isolates analyzed in this study. Isolates were sampled from 12 provinces and municipalities across China. Strains labeled in gray represent previously published genomes, those in blue drug-sensitive strains, those in black MDR strains, and those in pink XDR strains.

which has received significant attention as it is considered to be more virulent and prone to drug resistance than other strains.

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