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SIDA, TUBERCULOSE E
DOENÇAS OPORTUNISTAS**

LIVRO DE RESUMOS

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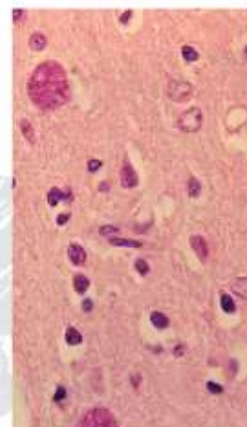
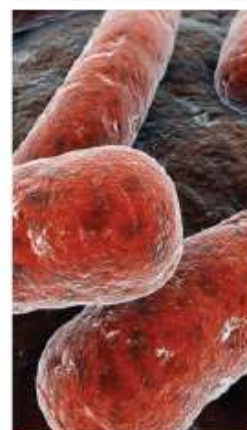
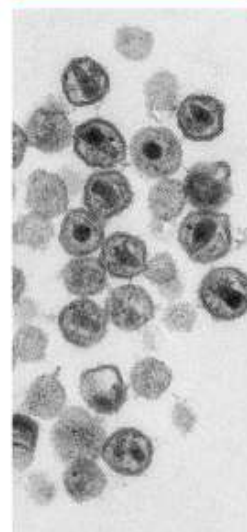
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TUBERCULOSIS ACROSS THE SEAS: CPLP-TB - A JOINT EFFORT IN CATALOGUING *MYCOBACTERIUM TUBERCULOSIS* GENETIC DIVERSITY IN THE LUSOPHONE SPACE

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Abstract

The Community of Portuguese Language Speaking Countries (CPLP) comprises nine countries across four continents, accounting for 7.2% of the world's land area, and where tuberculosis (TB) is still a cause of public health concern. A marked variation in TB incidence (23 to 551 cases per 100 000 inhabitants) can be observed across the different member-states and, despite of this, a considerable gap in the knowledge on the *Mycobacterium tuberculosis* population structure and country-level geospatial distribution still exists.

To address this we have gathered a comprehensive set of molecular and phenotypic drug susceptibility data on approximately 1150 different clinical isolates, from different partners, across 5 distinct Portuguese-speaking countries. This initial dataset comprises molecular genotypic data obtained by either 12, 15 or 24-*loci* Mycobacterial Interspersed Repetitive Unit – Variable Number of Tandem repeat (MIRU-VNTR) and/or Spoligotyping.

The complete dataset therefore includes *M. tuberculosis* clinical isolates from Portugal (n≈370), Angola (n≈80), Guinea-Bissau (n≈13), Mozambique (n≈14) and Brazil (n≈680). To make this data available to the scientific community and public health authorities we have developed CPLP-TB, an online database coupled with web-based tools that enable exploratory data analysis. This new tool specifically directed at CPLP countries include advanced data analysis capability together with graphical visualization tools (e.g. dendrogram and choropleth mapping).

As a public health tool, it is expected to contribute for a deeper knowledge on the combined population structure and strain circulation between countries, thus enabling the assessment of strain specific trends in a broader macroepidemiological context. Furthermore, this new tool provides a new framework for inter-laboratory cooperation on TB molecular epidemiology.