Background
Swaziland is a country with a high burden of tuberculosis (TB) and HIV. In 2009, the TB prevalence was 1275 per 100,000, the proportion of adults with HIV was 26%, and the TB/HIV co-infection rate was more than 80%. A drug-susceptibility study done in 2009 revealed the proportion of multidrug-resistant tuberculosis (MDR-TB) was 7.7% of new cases and 34% of previously treated cases. This study aimed to identify factors associated with MDR-TB in Swaziland.

Methods
A case-control study was designed, including 122 fully susceptible TB strains (controls) and 122 MDR-TB strains (cases). Genotyping analysis was applied to assess prevalent lineages and to identify dominant strain-families among the circulating MDR-TB strains. The level of clustering was studied to determine the impact of recent transmission on the dissemination of MDR-TB.

Results
Of 244 eligible strains, genotyping could be performed for 187 strains. 93 (49.7%) were fully susceptible to all five standard anti-TB drugs and 94 (50%) were multidrug-resistant. Through multivariate regression, clustering and being previously treated were identified as factors positively associated with MDR-TB. 120 strains (64%) were found to be prevalent in cluster. Clustering within the MDR-TB group was 89%, compared with 39% within the susceptible group. Clustering among MDR-TB strains were driven by two major clusters (N=18 and N=23), consisting of the two lineages X-type and S-type, together responsible for 49% of all clustered strains in the MDR-TB group or 44% of all MDR-TB strains.

Conclusion
MDR-TB in Swaziland was found to be largely driven by direct transmission, with two dominant lineages showing broad clonal expansion, thereby mediating transmission of drug-resistant TB. Because previous treatment was also independently associated with MDR-TB, acquired resistance is the other important factor in the occurrence and spread of the disease. However, primary MDR-TB seems to also play a part in the group of previously treated cases, most likely through incorrectly treating as susceptible TB, when patients already have undetected primary MDR-TB. More research is needed to better understand the role of genetic characteristics in the occurrence and spread of MDR-TB.

Frauke Jochims1, Elisabeth Sanchez2, Themba Dlamini3, Mathieu Bastard2, Stefan Niemann4

1MSF, Geneva, Switzerland; 2Epicentre, Paris, France; 3National Tuberculosis Control Programme, Mbabane, Swaziland; 4National Reference Centre for Mycobacteria, Borstel, Germany

Contact: frauke.jochims@geneva.msf.org

NOT FOR CITATION OR PUBLICATION