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## Molecular characterization of *Mycobacterium tuberculosis* complex in Benishangul Gumuz Region, Western Ethiopia

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**Background:** The knowledge of genetic diversity of *Mycobacterium tuberculosis* in certain geographic region is needed for a better understanding of epidemiology of TB and could have implications for development of new diagnostics, drugs, and vaccines. The aim of this study was to provide preliminary information on the strains of *M. tuberculosis* circulating in Benishangul Gumuz Region.

**Methods:** Cross-sectional study was conducted in order to generate a preliminary data on the genetic diversity of *Mycobacterium tuberculosis* between November 2012 and April, 2013. *M. tuberculosis* isolates were characterized using region of difference 9 (RD9) and spoligotyping. The patterns of strains identified by spoligotyping were compared with the patterns registered in the SpolDB4 database of the Pasteur Institute.

**Results:** From a total of 53 smear positive samples, 34 (64.15%) were culture positive, of which, 33 samples were confirmed to be *M. tuberculosis* by RD9 deletion typing. Further characterization of these 33 isolates using spoligotyping lead to the identification of 24 individual spoligotype patterns, among which, 18 were unique while the remaining six were found in clusters containing two to four isolates. Of the 24 patterns identified by the present study, only six patterns were registered in SpolDB4 international database, while 18 patterns were not previously registered in the database. Grouping of the 33 isolates into the lineages showed that 19 (57.6%) isolates were members of Euro-American, 6 (18.2%) isolates were Indo-Oceanic while the remaining 8 (24.2%) could not be categorized to the presently known lineages.

**Conclusion:** In conclusion characterization of the *M. tuberculosis* strains showed the identification of new strains and lineages which could not match with the existing strains and lineages suggesting the localization of these strains and lineages in this Region. Hence, further research is required to identify and document the strains and lineages circulating in the Region.

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