MOLECULAR TYPING AND DRUG RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS COMPLEX ISOLATES FROM JAMOT AND MBALMAYO DISTRICT HOSPITALS, CAMEROON

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Background Cameroon is a country where tuberculosis still remains a major public health problem. The aim of the present research was to evaluate the potential of molecular markers in predicting first-line drug resistance and to investigate the predominant genotypes representative of Mycobacterium tuberculosis strains in the Centre region of Cameroon.

Methods A total of 169 strains of M. tuberculosis isolate from the Centre Region of Cameroon were screened for mutations associated with first-line drug resistance by DNA sequence analysis. Spoligotyping and MIRU-VNTR (24 loci; mycobacterial interspersed repetitive units typing – variable number tandem repeat) were combined to identify clustered isolates.

Results Rifampicin-resistant strains had the rpoB mutations D516V, H526D or S531L; isoniazid-resistant strains had the mutations katG S315T or inhA promoter C15T; streptomycin-resistant strains had the mutations rpsL K43R, gidB V36G, H48N, P75S, L79W, or A138P; ethambutol-resistant strains had the mutation embB M306V. Among those M. tuberculosis isolates, 52.5% isolates were Cameroon genotypes followed by Haarlem genotype (22.1%). The frequencies of isoniazid, rifampin, streptomycin and multidrug-resistant isolates were equally distributed in Cameroon genotype strains and non-Cameroon strains. Furthermore, the analysis also shows the very low frequency of M. africanum since only 2.6% of isolates belong to this species.

Conclusions Mutations of common genes known to be involved in resistance had high specificities in detecting resistance. This study reveals the highly diverse M. tuberculosis population structure. It confirms a predominance of the Cameroon lineage in the Centre Region of Cameroon and the disappearance of M. africanum in Cameroon.