

PA-059 **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.