

## Genetic Diversity and Drug-resistance Patterns of Mycobacterium tuberculosis from Pulmonary Tuberculosis Patients in the South West and Littoral Regions of Cameroon

**Nkimbeng Desmond Akumtoh**

**University of Buea (Cameroon)**

In Cameroon, data, on Mycobacterium tuberculosis (Mtb) lineages, drug-resistance burdens and transmission patterns are lacking. Existing report is derived from conventional methods, with low resolution power. This study harnessed the potentials of whole-genome sequencing, to map the Mtb lineage diversity and Abstract drug-resistance patterns, in tuberculosis patients, in two regions of Cameroon, with relevance to tuberculosis prevention and control. Sputum samples were collected and cultured. A total of 125 Mtb DNA samples were extracted and whole genome sequenced. 88 high quality reads were obtained and used to determine Mtb lineage diversity and drug-resistance patterns, using TBProfiler tool. Three Mtb main lineages were identified, the Euro-American lineage (L4), being most abundant (98%). Nine sub-lineages were identified; L4-LAM\_10 Cameroon, being the most frequent (42%). L4-Congo (1%) and L2-Beijing (1%) genotypes, were new, not previously reported. Drug-resistance predictions, revealed overall drug resistance rate of 10.1%; rifampicin (3.4%), isoniazid (1.1%), streptomycin (1.1%) and second line drugs (4.5%). No multi-drug resistance, was identified. New drug mutations were found; Ser441Ala, His445Asp and Pro454Ser mutations, in the Rifampicin-rpoB gene, 386 delG, 115 delG and 315 delG in the Streptomycin-SIM/gid gene, the panDVal138Ala in the Pyrazinamide-panD gene and 1402 C>A mutations in the aminoglycosides-rrs gene. This study indicates that, the Mtb population in the Littoral and Southwest regions of Cameroon is diverse, suggesting on ongoing transmission. Although the prevalence of drug resistance is low, there are new drug resistant variants in circulation. Further investigation of the new genotypes and drug resistant variants is warranted.