

PA-084 **GENOTYPIC DIVERSITY AND DRUG SUSCEPTIBILITY PATTERNS AMONG *M. TUBERCULOSIS* COMPLEX ISOLATES RESPONSIBLE OF EXTRAPULMONARY TUBERCULOSIS IN CAMEROON FROM 2006–2015**

Justice Trésor Ngom,¹ Francioli Koro,¹ Celestin Godwe,¹ Clemence Adande,¹ Romaric Ateugieu,¹ Tatiana Onana,¹ Annie Ngono,¹ Yannick Kamdem,² Sara Ngo-Niobe,² François-Xavier Etoa³. ¹University of Douala, Cameroon; ²Centre Pasteur, Yaoundé, Cameroon; ³University of Yaoundé I, Cameroon

10.1136/bmjgh-2016-000260.116

Background Extrapulmonary tuberculosis can cause major irreversible health complications if it is diagnosed late and not well treated. In Cameroon, it remains neglected with very few data concerning its different forms, causing species and their drug susceptibility, while these data may help to understand the global epidemiology of tuberculosis in Cameroon.

Methods We have made a retrospective study on 215 clinical isolates stored in Centre Pasteur of Cameroon. Isolates were genotyped using spoligotyping to identify lineages and families, and the drug susceptibility patterns were determined through proportion method.

Results The primary resistance rate of isolates was 12.5%, among which 3.12% were mono-resistant to isoniazid, 1.56% to rifampicin and 3.9% to streptomycin. No mono-resistance was recorded for ethambutol. Multidrug-resistance rate to at least isoniazid and rifampicin was 3.12%. Spoligotyping revealed that 97.67% (210/215) and 2.32% (5/215) of extrapulmonary tuberculosis was caused by *Mycobacterium tuberculosis* and of *M. africanum*, respectively. *M. bovis* was absent. Spoligotyping lineages identified among the *M. tuberculosis* complex (MTC) showed a dominance of Cameroon family (40.46%). The other families were the ubiquitous T (36.27%), Haarlem (13.95%), U (6.04%) and LAM (1.39%). Ten spoligotypes had no SIT numbers. Only *M. tuberculosis* strains were associated to resistance. But there was no significant difference for drug resistance between MTC lineages.

Conclusions To the best of our knowledge, this study is the first to give the population structure of MTC strains causing extrapulmonary tuberculosis (ETB) and their drug susceptibilities. That shows the predominance of *M. tuberculosis* species and the very low contribution of *M. africanum* and *M. bovis* as the causative agent of ETB. It also shows that the population structure of this MTC is similar to that observed in pulmonary tuberculosis suggesting the dissemination of the pulmonary tuberculosis.