——————— **Original Article** ———————

A MOLECULAR EPIDEMIOLOGIC ANALYSIS OF *MYCOBACTERIUM TUBERCULOSIS* AMONG FILIPINO PATIENTS IN A SUBURBAN COMMUNITY IN THE PHILIPPINES

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Abstract   [Background] The Philippines is designated as one of the high tuberculosis (TB) burden countries by WHO. We conducted a molecular epidemiologic analysis of *Mycobacterium tuberculosis* isolates collected from patients consulting at the health clinics in the city of Santa Rosa, Laguna, a suburban community in the Philippines. [Methods] A total of 116 *M.tuberculosis* isolates were characterized and genotyped using spoligotyping and 15 loci of variable number of tandem repeats of mycobacterial interspersed repetitive units (15 MIRU-VNTR). The strains were then compared with the international spoligotyping database (SpolDB4). Cluster analyses were done using 15 MIRU-VNTR and spoligotyping. [Results] Majority of the patients with pulmonary tuberculosis were young (18−29 year age group at 41.4%) and male (62.1%). 86/116 (74.1%) were sputum-smear positive and 43/116 (37.1%) had severe pulmonary tuberculosis. When the genotyping results were compared to the SpolDB4, there were 10 identified Spoligo-International-Types (SITs) with SIT 19 as the predominant SIT (89/116, 76.7%). 10 out of 116 (8.6%) did not match any SIT in the SpolDB4. The distribution of strains according to major *M.tuberculosis* clades was as follows : EAI2_Manilla (101/116, 87.1%; U 2/116, 1.7%; LAM2 1/116, 0.9%; EAI3_Ind 1/116, 0.9%; MANU2 1/116, 0.9%. Using univariate and multivariate analysis, there was no significant association shown between the EAI2_Manilla clade and SIT with patient characteristics such as sex and age groups as well as bacillary load based on sputum-smear positivity and severity of pulmonary tuberculosis. Using logistic regression, no patient characteristic, as well as bacillary load or severity of TB, were significant predictors for clade or SIT. Based on the molecular typing method used, spoligotyping identified 4 clusters and 20 genotypes (16 unique strains) with a Hunter-Gaston discrimination index (HGDI) of 0.409. 15 MIRU-VNTR identified 16 clusters and 69 genotypes (53 unique strains) with an HGDI of 0.960. The combination of spoligotyping and 15 MIRU-VNTR identified 11 clusters and 79 genotypes (68 unique strains) with the highest HGDI at 0.970. High case rate of TB among young people in this community suggests the high transmission rate of infection. However, in the absence of significant association between clustering and age, the interpretation of observed high cluster rate warrants caution, and requires further molecular and epidemiological observation. [Conclusion] This is the first molecular epidemiology study to show the distribution of genotypes of the *M.tuberculosis* strains, systematically and prospectively sampled, of the patient population in a suburban community in the Philippines. The combination of spoligotyping and 15 MIRU-VNTR identified 11 clusters and 79 genotypes (68 unique strains) with the highest HGDI at 0.970. High case rate of TB among young people in this community suggests the high transmission of infection. However, in the absence of significant association between clustering and age, the interpretation of observed high cluster rate warrants caution, and requires further molecular and epidemiological observation.

Key words : Tuberculosis, Molecular epidemiology, Spoligotyping, Variable numbers of tandem repeats, *Mycobacterium tuberculosis*, Philippines

Background

Tuberculosis (TB), long known to be a major cause of morbidity and mortality throughout the world, has for the past several decades been a neglected disease in both industrialized and developing countries. In 2011, there were estimated 8.7

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