PUBLIC HEALTH MEDICINE

IDENTIFYING TUBERCULOSIS TRANSMISSION IN WESTERN AUSTRALIA USING MIRU GENOTYPING
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Introduction: Molecular genotyping of Mycobacterium tuberculosis has proven an increasingly useful tool in tuberculosis (TB) disease control programs internationally. Current molecular genotyping techniques focus on mycobacterial interspersed repetitive units (MIRU) typing, which determine the number of tandem repeat units at a given number of pre-specified loci [1]. This study aimed to examine the usefulness of routine MIRU genotyping to the Western Australian (WA) Tuberculosis Control Program, with a focus on assessing the level of local tuberculosis transmission and detecting unrecognised transmission.

Methods: All TB cases diagnosed in WA and notified to the WA Department of Health from 2012 to 2015 inclusive were eligible for inclusion. State laboratory genotyping records were matched with Department of Health records and WA TB Control Program notes to obtain demographic, clinical, contact tracing and available genotyping data. Data were used to create an overall epidemiological profile and identify genotype clusters of identical MIRU profiles. Genotype clusters were examined for epidemiological evidence of transmission enabling cases to be classified into four groups: ‘no transmission event’, ‘possible transmission event’, ‘likely transmission event’ or ‘laboratory cross-contamination event’. Unrecognised transmission was classified as those cases involved in a ‘likely transmission event’ not previously identified through traditional contact tracing techniques.

Results: The epidemiological profile of 544 eligible notifications was consistent with the recognised pattern of TB in WA occurring predominantly in the overseas born population (88.4%), particularly among young adult migrants recently arrived from TB-endemic countries. A diversity of genotypes demonstrated multiple strains of endemic transmission in the Aboriginal population. Of a total of 408 notifications with genotyping available, 357 (87.5%) were classified as ‘no transmission event’, 27 (6.6%) were involved in a ‘possible transmission event’, 23 (5.6%) in a ‘likely transmission event’ and 1 (0.3%) notification in a ‘laboratory cross-contamination event’. There were three previously unrecognised transmission events. Two events occurred amongst healthcare workers, one likely the result of a brief occupational exposure and one resulting from an undisclosed casual contact.

Conclusion: MIRU molecular genotyping of TB was a useful tool in revealing a low level of transmission of TB in WA. The majority of WA TB cases represent imported infection acquired in TB-endemic countries. MIRU genotyping, in combination with epidemiological assessment, detected several instances of otherwise unrecognised local transmission, including in healthcare workers. Results were consistent with other studies [2, 3]. Routine MIRU genotyping would act as a useful tool for incorporation into standard contact tracing processes within the WA Tuberculosis Control Program to assist in timely identification of local disease transmission.

References
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THE EFFECT OF PM10 ON ALLERGY SYMPTOMS IN ALLERGIC RHINITIS PATIENTS DURING SPRING SEASON
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Background/Introduction: Asian sand dust (ASD) that originates in the Mongolian Desert in the spring induces serious respiratory health problems throughout East Asia (China, Korea, Japan). PM10 (particulate matter with an aerodynamic diameter <10 μm) is a major air pollutant component in ASD. We studied the effects of PM10 on allergy symptoms in patients with allergic rhinitis during the spring season, when ASD frequently develops.

Methods: We investigated the changes in allergic symptoms in 108 allergic patients and 47 healthy subjects by comparing their 120-day symptom scores from February to May 2012. At the same time, the contributions of pollen count and PM10 concentration were also assessed. We also compared symptom scores before and 2 days after the daily PM10 concentration was >100 μg/m³.

Results/Outcomes: The PM10 concentration during the 120 days was <150 μg/m³. No significant correlations were observed between changes in the PM10 concentration and allergic symptom scores (p > 0.05). However, allergic symptoms were significantly correlated with outdoor activity time (p < 0.001).

Conclusion(s): These results demonstrate that a PM10 concentration <150 μg/m³ did not influence allergy symptoms in patients with allergic rhinitis during the 2012 ASD season.

References
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